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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Run

June 28, 2005, 09:42:27 е ::

// Search time 26.0601 Seconds
(without alignments)
1631.912 Million cell updates/sec

442

US-10-622-237-2 Title:

1 MASVVLPSGSQCAAAAAAA......AIINAEGGQNNSEEKKEYFI Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

length: 0 length: 2000000000 seq Minimum DB s Maximum DB s

Minimum Match 0% Maximum Match 100% Listing first 45 summaries Post-processing:

pirl:* pir2:* pir3:* PIR 79:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote hypothetical prote hypothetical prote poliovirus recepto poliovirus recepto poliovirus recepto neural cell adhesi pRZ delta - human poliovirus recepto poliovirus recepto poliovirus recepto poliovirus recepto neural cell adhesi connectin/titin - neurotrimin - rat cell adhesion mole cell adhesion mole cell adhesion mole elastic titin - hu neuromusculin - fr neural cell adhesi neural cell adhesi PRR2 alpha - human opioid-binding pro surface glycoprote adhesion molecule opioid-binding cel cell adhesion mole perlecan precursor opioid-binding pro Description SUMMARIES T08732 T720992 T720992 T720992 T720992 T683437 T444194 T444194 T68099 T68099 T68099 T742639 T742633 T742633 T742633 T7369 T736 Length DB 55176 51176 Query 268 263.5 263.5 263.5 247.5 247.5 244.5 240.5 24 223.5 223 228.5 218.5 218.5 217 216.5 216.5 216.5 Score Result Š.

s-gicerin precurso	carcinoembryonic a	limbic-system-asso	cell surface glyco	opioid-binding pro	heparan sulfate pr	connectin 3B - chi	differentiation an	CD22 homolog/B lym	B-cell adhesion pr	neogenin - chicken	nephrin - human	alcam - human	neural cell adhesi	duttl protein - mo
150419	A36319	JC4776	I38049	JC1238	S18252	PN0568	I49583	A46512	JH0371	150600	T37190	I39428	LJCHNL	T30805
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9.0	, o	0.6	0.6	9.0	8.9	8.9	8.9	6.8	8.8	8.8	8.7	9.8	9.8	9.8
9.5	206 9.0													195.5 8.6

ALIGNMENTS

4. ?.		9	~	-	~	-	m	0	m	N		
<pre>protein DKFZp566B0846.1 - human (fragment) iomo sapiens (man) fun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-200 i T08732 fler, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, the Protein Sequence Database, May 1999 number: Z16474 1-407 <ott> rences: UNIPROT:Q9Y412; EMBL:ALOS0071 ial source: fetal kidney; clone DKFZp566B0846</ott></pre>	Match 11.7%; Score 268; DB 2; Length 407; ocal Similarity 26.7%; Pred. No. 1.5e-11; s 84; Conservative 60; Mismatches 123; Indels 48; Gaps	120 GRYFCQLYTDPPQESYTIITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPAT	176 IIRWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGN	61 HIDW-EGDLGEMESTITSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKD	231 LQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQH	115 IRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDG	291 AVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTT	173 LLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTTLQPTIQWHPST	343 TTTTTTTTTTLLILTDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLI-	233 ADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGGALFIVLVSVLAGIFC	394ILGRYFARH 402	286 YRRRIFRGDYFAKN 300
RESULT 1 T08732 hypothetical C;Species: 1 C;Date: 11-C C;Accession: C;Accession: A;Accession: A;Reference A;Reference A;Roccession: A;Roccession: A;Roccession: A;Roccession: A;Roccession: C;Genetics: C;Genetics: A;Note: DKF?	Query Match Best Local Matches 8	oy Dp	ζ	qq	λΌ	ор	<i>λ</i> ο	qa	ò	QQ	È	qq

13;

CPAT 175

230

9

1PQH 290 EKD 114

1PDG 172

342 232 285

RESULT 2 T20992 hypothetical protein F15G9.4a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T20992; T24733

TI- 393

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preliminary; translated from GB/EMBL/DDBJ
                            A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYMLYVYDPPTTIPP
                                                                                                     A; Experimental source: clone
                                                                                                                                                                                                                                                                                                                                                          A; Gene: him-4; F15G9.4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: JC4024
                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: X
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Hemicentin precursor - Caenorhabditis elegans

Cispeciaes: Generorhabditis elegans

Cispeciaes: Generorhabditis elegans

Cispeciaes: Generorhabditis elegans

Cispeciaes: Generorhabditis elegans

Cibate: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004

Ciscession: T43290; T20993; T24734

Rivogel, B.E.; Hedgecock, E.M.

Submitted to the EMBL Data Library, June 1998

A; Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-A; Reference number: Z22396

A; Recession: T43290

A; Residues: 1-5198 +VOG>

A; Residues: 1-5198 +VOG>

A; Residues: 1-5198 +VOG>

A; Residues: 1-5198 +VOG>

A; Cross-references: UNIPROT:076518; EMBL:AF074901; PIDN:AAC26792.1

R; Sulston, J.

Submitted to the EMBL Data Library, December 1994

A; Reference number: Z19355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: X
A;Introns. 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
                                                                                                                                                                   EMBL: Z47068; PIDN: CAA87335.1; GSPDB: GN00028; CESP: F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2310 CPA-TGKPEPDÍTWFKDGEAIHIENIADIIPNGELNG--------NÓLKITRIK 2354
                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-5175 <W12>
A;Cross-references: EMBL:447070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CESP:F15G9.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 VTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPL----KDSRFQLLNFSSSEL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIQKD-TAVEGEEIEVN 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----NTELKGKSEVEEWSDMYTVTSQLMLKVHK 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVH---IQMTYPLQGLTREGDALELTCE 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIGKPQPVMVTWVRVDDEMPQHAVL----SGPNLFINNLNKTDNGTYRCEASNIVGKAHS 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.5%; Score 263.5; DB 2; Length 5175; 24.6%; Pred. No. 8.2e-10; tive 66; Mismatches 129; Indels 71;
R,Sulston, J.
submitted to the EMBL Data Library, December 1994
A,Accession: T20992
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DMR
A,Molecule type: DMR
A,Residues: 1-5175 < WIL>
A,Cross-references: UNIPROT:0810L3; EMBL:Z47068; PII
A,Experimental source: clone F15G9
                                                                                                                                                                                                                                                                                  A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                            R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTAMASKPATTIRWFKG-----
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87; Conservative
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A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1
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R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubre Gene 155, 261-265, 1995

A;Title: Complementary DNA characterization and chromosomal localization of a human gene A;Reference number: JC4024; MUID:95237621; PMID:7721102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rikershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24734

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5198 «WI2-

A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone T09B9
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PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
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A,Map position: 11q23-11q24
A,Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor: transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>F;1-50/Domain: signal sequence #status predicted protein #status predicted <Pre>F31-518/Product: poliovirus receptor-related protein #status predicted <Pre>CMM>
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poliovirus receptor related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52 VTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPL----KDSRFQLLNFSSSEL
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A,Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 11.5%; Score 263.5; DB 2; Best Local Similarity 24.6%; Pred. No. 8.3e-10; Matches 87; Conservative 66; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2310 CPA-TGKPEPDÍTWFKDGEAIHIENIADIIPNGÉLNG
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F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted Query Match 10.9%; Score 248; DB 2; Length 518; Best Local Similarity 25.4%; Pred. No. 5.3e-10; Matches 105; Conservative 60; Mismatches 154; Indels 94; Gaps 20;	Db 164 IGPQSVAVARCVSTGGRPPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVEVGRAD 223 Qy 215 GVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQ 274
Qy 74 IQLINPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP 131 : :	Qy 275 PVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP 334
Qy 132 QESYTTITULVPPRNLMIDIQKD-TAVEGEBIEVNCTAMASKPATTIRWFKGNTELK 187	Qy 335 TIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
QY 188 GKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLE 238	RESULT 6 A44194
Qy 239 VQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSG 295	poliovirus receptor (clone AGM-alpha-1) - green monkey C;Species: Cercopithecus aethiops (green monkey, grivet) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 C;Accession: A44194
Qy 296 PNLFINN-LNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTT 354	<pre>R;KOlKe, S.; 18e, 1.; Sato, Y.; YoneKawa, H.; Gotoh, O.; Nomoto, A. J. Virol. 66, 7059-7066, 1992 A;Title: A second gene for the African green monkey poliovirus receptor that has no puta A;Reference number: A44194; MUID:93059651; PMID:1331508</pre>
Qy 355 LTIITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFT 408 Db 346HGRRAGPVPTAIIGGVAGSILLVLIVVGGIVVALRRRHTFKGDYST 392	A;Accession: A44194 A;Stutus: preliminary A;Molecule type: DNA A;Reaidues: 1-417 <koi></koi>
	A,Cross-references: UNIPROT:P32506; GB:S48777 C;Superfamily: pollovirus receptor; immunoglobulin homology C;Keywords: transmembrane protein F;259-314/Domain: immunoglobulin homology <imm></imm>
	Query Match Best Local Similarity 23.5%; Pred. No. 7.8e-10; Matches 108; Conservative 70; Mismatches 192; Indels 90; Gaps 18;
policylrus receptor mPVR - mouse C'Species Mus musculus (house mouse) C'Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004 C'Accession: A53437	Qy 13 AAAAAAAPPGLRLELLLEFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNK 68
R.Acki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A. J. Biol. Chem. 269, 8431-8438, 1994 Aftitle: Amino acid residues on human poliovirus receptor involved in interaction with F. A;Reference number: A53437; MUID:94179228; PMID:8132569	QY 69 SDDSVIQLANPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS1 116 ::::
A;Accession: A53437 A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA	OY 117 SDEGRYPCQLYTDPPQESYTTITVLVPPRNLMIDIOKDTAVEGEEIBV-NCTAMASK 172
A; Residues: 1-330 (ADAN) A; Gross-references: UNIPOT: P32507; GB:D26107; NID:g475017; PIDN: BAA05103.1; PID:g825507 A; Experimental source: C57/BL6, brain A; Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)	110 BDEGNIIC-LEVIFPEGGSKSVDIMMKVLAREQN-TABVQK-VQLIGKEVFVARKVSIGGR 173 PATTIRWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVT
C.Superfamily: poliovirus receptor; immunoglobulin homology F;47-133/Domain: immunoglobulin homology <imm></imm>	Db 173 PPAHITWHSDLGGMPNTSQAPGFLSGTVTVTSLMILVPSSQVDGKSVTCKVEHESFE 229 Qy 229 GNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP 288
Query Match 10.8%; Score 247.5; DB 2; Length 530; Best Local Similarity 22.1%; Pred. No. 6e-10; Matches 91; Conservative 63; Mismatches 166; Indels 91; Gaps 14;	230 KPQLLTVNLTVYYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTMGPLP
Qy 15 AAAAAAPPGLRLRLLLLPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQV 66	289 QHAVLSGPNLFINNINKTDNGTRCEASNIVGKAHSDYMLYYYDPPTTITPTTTTT
Qy 67NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS 105 : : :	
OY 106 ELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIE 163 : : : : :	Cy 404 GTYFTHEAKGADDAADATAIINAEGGQNNSEEKKE 439
Qy 164 VNCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLKVHKEDD 214	RESULT 7 HLMSP3

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A; Molecule type: mRNA
A; Residues: 1-725 < KUD>
A; Residues: 1-725 < KUD>
A; Cross-references: UNIPROT:073633; DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g31
A; Experimental source: heart
C; Comment: This protein mediates and regulates various cell-cell interactions through bot
C; Superfamally: neural cell adhesion molecule; fibronectin type III repeat homology; immun
E;413-475/Domain: immunoglobulin homology < 1RMs
F;512-589/Domain: fibronectin type III repeat homology <3FR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      199 KDIQVIVNVPPTIQARQLRVNATAKMAEŠVVLSCDADGFPDPEISWLKKGEPIEDGE-EK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160 EEIEVNCTAMASKPATTIRW-----FKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            213 DDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGK 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POPVMVTWVRVDDEMPQH-----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS 324
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C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 ARAAALLPSRSPPTPLLWPLLLLL----LLETG-AQDVRVQVLPEVRG------QLGGT
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C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 26.5'
Matches 90; Conservative
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Best Local Similarity 22.6
Matches 111; Conservative
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                             A;Accession: JE0099
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poliovirus receptor homolog precursor - mouse
C.Species: Mus musculus domesticus (western European house mouse)
C.Species: Mus musculus domesticus (western European house mouse)
C.Species: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: AJ8211
R;Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A;Reference number: AJ8211, MUID:92219365; PMID:1560525
A;Accession: AJ8211
A;Molecule type: DNA
A;Residues: 1-467 <MOR>
A;Residues: 1-467 <MOR>
A;Cross-references: UNIPROT:P32507; GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-354/Domain: extracellular #status predicted <EXT>
F;47-133/Domain: immunoglobulin homology <IPM3>
F;267-322/Domain: immunoglobulin homology <IPM3>
F;267-322/Domain: immunoglobulin homology <IPM3>
F;267-322/Domain: intracellular #status predicted <ITMN>
F;375-467/Domain: intracellular #status predicted <ITMN>
F;375-370/Distance <ITMN </ITMN>
F;375-467/Domain: intracellular #status predicted <ITMN>
F;375-467/Domain: intracellular #s
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JEBO09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 LPPTTERVSQVTWQRLDGTVVAAFHPS----FGVDFPNSQFSKDRLSFVRARPETNADLR 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPEN-------HAEAQEVT 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 GVKVTCRVEHESFEEPILLPVTLSVRYPPEVSIS-GYDDNWYLGRSEAI-LTCDVRSNPE 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDYDWSTISGVPPASAVAQGSQLLVHSVDRMVNTTFICTAINAVGTRAEQVILVRDIP 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QA-----SR----SR----SR-----SR-----DVGPLVWGAVGGTLLVTLLAGGFLALI 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 IGPQSVAVARCVSTGGRPPARITWISSLGGEAKDTQEPGIQAGTVTIISRYSLVPVGRAD 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 AAAAAAPPG----LRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEV---ATISCQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V------NCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLKVHKEDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 IILGRYFARHKGTYFTHEAKGADDA------ADADTAIINAEGGONNSEEKKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    201; Indels 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.7%; Score 244; DB 1
21.0%; Pred. No. 9e-10;
ive 74; Mismatches 2
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g &	108 AKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKN-QA 166 150 DIQKDTAVEGEEIEVNCTAMASKPATTIRWFKG-NTELKGKSEVEEWSDMYTVTSQLMLK 208	Qy 349 TTTTLTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVPAMLCLLIILGRYFARHK 403
qa Vo	167 EAQKVTFSQDPTTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAGTVTVTSRFTLV 226 209 VHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXFPQVHIQMTYPLQGLTREGDALELICE 268	RESULT 11 RWHUDT Policying receptor splice form delta precursor - human
ପ୍ର ଓ	227 PSGRADGVTVTCKVEHESFEEPALIPVTLSVRYPPEVSIS-GYDDNWYLGRTDA-TLSCD 284	NAIternate names: politorirus receptor H20B C;Species: Homo sapiens (man)
දු දු	269 AIGKPOPWMTWVRVDDEMPOHAVLSGPNLFINNLÄKTBONGTKEGEASNIL 328 285 VRSNPEPIGYDMSTISGIFFPISAVAQGSQLVIHAVDSLFNTIFVCTVINAVGMGRAEQVI 344	C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Ju1-2004 C;Accession: A43024; B31496 E. R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Takeg
ò	329 YVYDPPTTIPPPTTTTTTTTTTTTTTTTTT 388	EMBO J. 9, 3217-3224, 1990 Ajrile: The poliovirus receptor protein is produced both as membrane-bound and secreted Ajreference number: \$12048; MUID:31006015; PMID:2170108
Op (ATGGIIGGIIAAIIATA	A, Accession: A43024 A, Molecule type: DNA
දි සි	389 LCLLILGKKFAKHKGTYFTHEAKGADDAADAD	A;kesidudes: 1-392 <koi> A;Crose-references: UNIPROT:P15151; EMBL:X64116 A;Note: 67-Ala was also found</koi>
λ	430 GONNSEEKKEYF 441	R;Mendelsohn, C.L.; Wimmer, B.; Racaniello, V.R. Cell 56, 855-865, 1989 A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and ex
qq	429 ASEHSPLKTPYF 440	A;Reference number: A90910; MUID:89168426; PMID:2538245 A;Accession: B31496
RESULT 1 R44194	10	A;Molecule type: mkNA A;Residues: 1-66, '4, (8-392 <men> A/ross-references: GR-M374406</men>
polioviz C;Specie	<pre>cus receptor (clone AGW-delta-1) - green monkey is: Cercopithecus aethiops (green monkey, grivet)</pre>	C.Common: The normal function of this receptor is unknown. Membrane-bound and soluble for C.Genetics:
C;Date: C;Access	30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004	A;Gene: GDB:PVR; PVS A;Cross-references: GDB:120324; OMIM:173850
K; KOIKE, J. Virol	, 5.; 18e, 1.; Sato, 1.; Yonekawa, H.; Goton, O.; Nomoto, A. 1. 66, 7059-7066, 1992 3. second gene for the African green monkey noliovirus recentor that has no nuta	A;Map position: 1941s.2-1941s.2 A;Introns: 27/1; 143/1; 25/1; 281/2; 331/1 C.Sunarfamily: noliovirus recentor: immunocilobulin homology
A;Refere A;Access		C'REYNOTGE: 11 FETTATIVE SPLICING; duplication; glycoprotein; receptor; transmembrane prot P;1-20/Domain: signal sequence #status predicted <81G>
A;Statue A;Molecu	s: preliminary	F;21-392/Product: poliovirus receptor delta #status predicted <mat> F;21-343/Domain: extracellular #status predicted <ext></ext></mat>
A; Kesidi A; Cross- C; Superf	A;KeBIQUBes 1-542 KKOL7 A;Cromerferences: UNIRROT:P32506; GB:S48817 C;Superfamily: poliovirus receptor; immunoglobulin homology	F;152-L25/Domain: immunoglobulin homology <imm1> F;159-223/Domain: immunoglobulin homology <imm3> F;259-314/Domain: immunoglobulin homology <imm3></imm3></imm3></imm1>
F;259-31	14/Domain: immunoglobulin homology <imm></imm>	F;344-367/Domain: transmembrane #status predicted <tmn> F;368-392/Domain: intracellular #status predicted <int></int></tmn>
Query Match Best Local (Matches 10)	/ Match Local Similarity 24.0%; Pred. No. 1.1e-09; nes 101; Conservative 60; Mismatches 178; Indels 81; Gaps 16;	r;49-123,166-221,266-312/DIBULINGE BONGS: #Status predicted F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status prf
ò	AAAAAAPPGIRLILLILFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNK	Query Match 10.5%; Score 240; DB 1; Length 392; Best Local Similarity 25.9%; Pred. No. 1.4e-09; Matches 107; Conservative 54; Mismatches 176; Indels 76; Gaps 17;
g 8	ARTWAAAWPPLLLTLLELSWPPPGTGDIIVQAPTQVPGFLGBSVTLPCYLQVPG	[:
<u></u>	59 SUDSVIQUENTRYILITERDERFLENDSREQUENTSSSELNVSLINVS	Db 2 ARAWAAAWPILIVALIVLSWPPPGTGDVVVQAPTQVPGFLGDSVTLPCY 50
ò	117 SDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIEV-NCTAMASK 172	Qy 65 -QVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS 115 Db 51 LOVPNMEVTHVSOLTWTRHGESGSMAVFHOTOGPSYSESKRLEFVAARLGAELRNASLRM 110
qq		116ISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEV-NCT
કે ક	173 PATTIRWFKGNTELKGKSEVEEWSDMYIVTSQLMLKVHKEDDGVPVICQVEHPAVT 228	111
3 <i>&</i>		168 AMASKPATTIRWFKGNTELKGKSBVEBW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPA
q	230 KPQLLTVNLTVXYPPEVSIS-GYDNNWYLSQNEA-TLTCDARSNPEPTGYNWSTTMGPLP 287	168
ò		DD 228 FEXPOLLTYVITYYYPPEVSIS-GYDNWYLGONEA-TLTCDARSNPEPTGYNWSTTWGP 285
qq	288 PFÁVAQGAQLLIRPVDKPINTTFICNVTNALGARQAELTVQVKEGPPSEFSGMSSN 343	QY 287 MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTT 346

us-10-622-237-2.rpr

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A,Accession: S09600
A,Molecule type: mRNA
A,Residues: 1-1088 «KRI»
A,Fesidues: 1-1088 «KRI»
A,Cross-ferences: UNIPROT.P16170; EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g21461)
A,Note: the authors translated the codon AAA for residue 970 as Leu
C,Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mole
C,Comment: Several forms of NCAM are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of a large cytoplasmic domain for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #status predicted
(covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             neural cell adhesion molecule long domain form precursor - African clawed frog N;Alternate names: NCAM-180
N;Alternate names: NCAM-180
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Mar-1993 #sequenc_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: S09600
R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.
Nucleic Anids Res. 17, 10321-1035; 1989
A;Title: Primary structure and developmental expression of a large cytoplasmic
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                                                       227 VTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDE 286
                                                                                                                                                                                                           287 MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTT 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  258 ISFNEDQSEMTIHHVEKDDEAEYSC-IANNQAGEAEATILLKVYAKPKITYVENKTÄVEL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160 EEIEVNCTAMASKPATTIRW-----FKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKE 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 DEITLICEA-SGDPIPSITWRIAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 213 DDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGK 272
                                                                                                   228 FEKPOLLTVVNLTVYYPPEVSIS-GYDNNWYLGQNEA-TLTCDARSNPEPTGYNWSTTMGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 KDVTVIEGEVATISC---OVNKS----DDSVIOLLN----PNRQTIYFRDFRPLKDSRFQL
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                                                                                                                                                                                                                                                                                                                                                              347 TITITITITITIDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYF 399
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                                                                                                                                                                                                                                                                  Length 1088;
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F;618-679/Domain: fibronectin type III repeat homology <FN3B>
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Best Local Similarity 26.2<sup>3</sup>
Matches 89, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                  poliovirus receptor splice form alpha precursor -.human
N.Alternate names: poliovirus receptor H20A
N.Alternate names: poliovirus receptor H20A
N.Contains: poliovirus receptor beta
C.Species: Homo sapiens (man)
C.Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C.Accession: 312048; A31466
R.Kooike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take ERBO J. 9, 3217-3224, 1990
A.;itie: The poliovirus receptor protein is produced both as membrane-bound and secreted A;feference number: S12048; MUID:91006015; PMID:2170108
A.Accession: S12048
A.Accession: S12048
A.Residues: 1-417 < KOI>
A.Kooss-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA454
A.Residues: C7-Ala was also found
A.Note: the gamma form has 331-Gly and lacks residues 332-384
R.Hendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A.Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A.Reference number: A90910; MUID:89168426; PMID:2538245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Genee: GDB:VR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19413.2-19413.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane proc;Keywords: algoral sequence efstatus predicted <SIG>F:21-417/Product: poliovirus receptor alpha #status predicted <PVRA>F;21-343/Domain: extracellular #status predicted <EXTP>F:21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>F;21-325/Domain: immunoglobulin homology <IMMI>F;42-125/Domain: immunoglobulin homology <IMMI
F;42-125/Domain: immunoglobulin homology <IMMI
F;42-125/Domain: immunoglob
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A;Residues: 1-66, A', 68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 FGLRVEDEGNÝTC-LFVTFPQGSRSVDIWLRVLAKPON-TAEVOK-VQLTGEPVPMARČV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMASKPATTIRWFKGNTELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPA 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTV-----IEGEVATISC- 64
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                                                                                                                       347 ITTTTTTLTILTITDSRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLIILGRYF
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7:368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn)
Query Match 10.5%; Score 240; DB 1; Length 417; Best Local Similarity 25.9%; Pred. No. 1.5e-09; Matches 107; Conservative 54; Mismatches 176; Indels '
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Cypecies: Galus gallus (chicken)
Cypecies: Galus gallus (chicken)
Cypecies: Galus gallus (chicken)
Cypate: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
CyAccession: T42633
R;Yajima, H.; Ohtsuka, H.; Kawamura, Y.; Kume, H.; Murayama, T.; Abe, H.; Kimura, S.; Mabochem. Biophys. Res. Commun. 233, 160-164, 1996
A;Title: A 11.5-kb 5'-terminal cDNA sequence of chicken breast muscle connectin/titin re A;Reference number: 222221; MUID:96254045; PMID:8660363
A;Accession: T42633
A;Accession: T4263
A;Accession: T4263
A;Accession: T4263
A;Accession: T4263
A;Accession: T4263
A;Accession: T4263
A;Crosser-references: UNIPROT:098918; EMBL:D83390; NID:g1513029; PIDN:BAA11908.1; PID:g151
C;Keywords: skeletal muscle
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4. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed neuroper: IS65S1; MUID:95198094; PMID:7891157
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                                                                       -OESYTTITVLVPPRNLMIDIQKDTAVE---GEEIEVNCTAMASKPATTIRWFKGNTELK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 GKSEVEEWSDMYTVTSQLMLKVHKEDDG---VPVICQVEHPAVTGNLQ-TQRYLEVQYKP 243
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372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCEVFAH 425
                                           PQPVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 SVIQLLNPURQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 CAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDD 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156551
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                                                                                                                                DYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTDSRAG 364
                                                                                                                                                            ::: | |:: | :: | :: | EFILVQADTPSS---PAIRKVEPYSSTVMIVFDEPDSTGG 521
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A;Molecule type: mRNA
A;Residues: 1-344 <RES>
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Best Local Similarity 23.99
Matches 86; Conservative
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C; Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
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                                                                                                                                                                                                                                                                                                                                                                                                                  85 YFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTD-PPQESYTTITVLVP 143
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                                                                                                                                                                       Gaps
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                                                                                 DB 2; Length 344;
                                                                             Query Match 10.1%; Score 230; DB 2; Length 34 Best Local Similarity 26.2%; Pred. No. 6e-09; Matches 84; Conservative 53; Mismatches 137; Indels
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ð		18	81	<u>8</u> -	NTE -	LKGKS	EVEEN	NGS1	YTY	SOLMLKVH	KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPV1 CQVEHPAVTGNLQTQRYLEVQ	AVTGNLQ	TORYLEVO	240
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          LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTLTI 357
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                                         358 ITDSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-22192378; PubMed-12202822; DOI=10.1126/science.1072356;
Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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97.8%; Score 2232.5; DB 2; Length 445;
Best Local Similarity 97.5%; Pred. No. 5.2e-151;
Matches 434; Conservative 2; Mismatches 6; Indels 3;
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GO; GO:0004520; C:3ynaptic vesicle; IDA.
GO; GO:000515; F:protein binding; IPI.
GO; GO:0007155; F:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007155; F:call adhesion; IDA.
GO; GO:000716; P:synaptogenesis; IDA.
InterPro; IPR003158; IQ C2.
InterPro; IPR003585; Neurexin-like.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AFS594-XANOI614.1; --
EMBL; AB183399; BAD30018.1; --
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SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Synaptic cell adhesion molecule 1 (RA175 isoform c)
Name=1gsf4a; Synonyme=RA175;
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MEDLINE-2226620; PubMed=12242005; DOI=10.1016/S0378-1119 (02) 00835-1; Pukami T., Satch H., Fujita E., Maruyama T., Fukuhara H., Rukami T., Satch H., Fujita E., Maruyama T., Fukuhara H., Rukami T., Satch H., Fujita E., Maruyama T., Fukuhara H., Takamoto S., Momoi T., Murakami Y.; Murakami Y.; Identification of the Talci gene, a mouse orthologue of the human turn suppressor TSLCI gene."; Tender 25:7-12 (2002).

EMBL; AF434663; AAL86736.1; -. BRL; AF434663; AAL86736.1; -. BRL; AF434663; AAL86736.1; -. BRC; Go:0016021; C:integral to membrane; TAS.

GO: GO:001621; C:integral to membrane; TAS.

GO: GO:001515; F:protein binding; IPI.

GO: GO:000515; F:protein binding; IPI.

GO: GO:000715; P:protein binding; IPI.

GO: GO:000715; P:protein binding; IPI.

RO: GO:000715; P:protein binding; IDA.

InterPro; IRR003589; Neurexin-like.

Roi GO:0007416; P:synaptogenesis; IDA.

InterPro; IRR003585; Neurexin-like.

Roi GO:0007416; 19; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTI 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                        445
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                                                                                                                                                                           DTAIINAEGGONNSEEKKEYFI 442
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SM00408; IGC2; 1.
E; PS50835; IG LIKE; 3.
CE 445 AA; 48664 MW;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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nes 436; Conservative
                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Igsf4a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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PROSITE; I
SEQUENCE
                                                                 361
                                                                                                                                                                                                421
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   361
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301 LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTT
                                                                                                                EVOYKPOVHIOMIYPLOGLTREGDALELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPN
                                                                                                                                              241 EVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN
                                                                                                                                                                                                                                              IT------DSRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTY
                                                                                                                                                                              LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTLTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078966, AAH78966.1;
InterPro; IPR003599; Ig.
InterPro; IPR00710; Ig-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                             407 FTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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SMART; SM00409; 1G; 3.
SMART; SM00408; 1Gc2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10116;
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                               300
                                                                                                                                                                                                         | ITDSRAGEEGSIRAVDHAVIGGVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDA 417
                                                                           EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 297
                                                                                                                                                                             360
                                                                                                                                                                                                                            RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL 237
                                                                                                                                           LPINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTLTI 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQXDTAVEGEEIEVNCTAMASKPATTI 177
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                                                                                              MASVVLPSGSQCAAA---AAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEG
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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SMART; SM0408; IGc2; 1.
PROSITE; PS5085; IG LIKE; 3.
SEQUENCE 456 AA; 49787 WW; 3226E866A4BCIC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
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Pred. No. 3.6e-150;
2; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                            456 AA.
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Best Local Similarity 95.4'
                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                           Q8R5M8;
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                                                                                                                                                                                                                                                                                                                                                      301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTT - LTIIT 359
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                                    1 MASVVLPSGSQCAAAAAAAAPGLRLRLIJLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                                                                                                                                                                                                                                                                                                                                                           301 NNIAKTDNGTYRCEASNIVGKAHSDYMLYVYDTTATTEPAVHGLTQLPNSAEELDSEDLS
                 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fulita E., Aikawa K., Momoi T.;
Submitted (UUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB183400; BAD30019.1; -.
EMBL; AB183400; BAD30019.1; -.
GO; GO:0016021; C:synapse; IDA.
GO; GO:0008021; C:synapse; IDA.
GO; GO:0008021; C:synaptic vesicle; IDA.
GO; GO:000815; F:protein binding; IPI.
GO; GO:00155; P:cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
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InterPro; IPR003599; Ig.
InterPro; IPR003599; Ig.-2.
Pfam; PR00047; Ig; 3.
SWART; SW00409; IG; 3.
SWART; SW00409; IGC2; 3.
SWART; SW0051 IGC2; 3.
SWART; SW0051 IGC2; 3.
SWART; SW0061 IGC2; 3.
SWART; SW0061 IGC2; 3.
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Last annotation update)
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25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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Name=RA175;
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                                                                                                                                                                                                                                                                                                                                                  RWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL 240
                                                                                                                                                                                                                                                                                                                                                                                                        EVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIS 117
                                                                                                                                                                                                                                                    DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTI 177
                                                                                                                                                                                                                                                                                                                    RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL 237
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                                                                                                                 1 MASVVLPSGSQCAAA---AAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEG
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

TISSUE=Whole embryo;
Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AK075502;
BAC11657.1;
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                                                                                  8; Indels
                                                Length
Hypothetical protein.
SEQUENCE 476 AA; 51853 MW; 486A43D37082C8FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50835; IG_LIKE; 3.
443 AA; 48648 MW; 046B43AA156F6F64 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0AR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human).
                                               Score 2186; DB 2;
Pred. No. 1.2e-147;
1; Mismatches 8;
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003585; Neurexin-like.
                                               95.8%;
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SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
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                                                                Best Local Similarity 91.0
Matches 433; Conservative
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SEQUENCE
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                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 297
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                           31;
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0
                                                                                    DB 2; Length 417;
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                                                                                                                           5; Indels
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  SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
                                                                                90.7%; Score 2071.5; DB 2
91.7%; Pred. No. 1.5e-139;
ive 1; Mismatches 5;
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                                                                                Query Match 90.7%;
Best Local Similarity 91.7%;
Matches 408; Conservative
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                                                         EVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSIS
                                                                                                                                         DEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGBEIEVNCTAMASKPATTI
SEQUENCE FROM N.A.
STRAIN-C57BL/6; TISSUE-Brain;
MEDLINE-22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
MEDLINE-22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingal T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
Implications of nectin-like molecule-
2/IGSF4/RA175/SgIGSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
R EMBL, A7813188; AA002381.1;
EMBL, A3813189; AA002020.1;
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:0045202; C:synapse; IDA.
R GO; GO:0005021; F:protein binding; IPI.
R GO; GO:0007155; F:protein binding; IPI.
R GO; GO:0007155; P:protein binding; IDA.
R InterPro; IPR007110; IG-like.
R InterPro; IPR003598; IG-2.
R InterPro; IPR003598; IG-2.
R Pfam; PR00047; ig; 2.
SWART; SM00294; 4.1m; 1.
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-077-2003 (TrEMBLrel. 25, Last sequence update)
25-077-2004 (TrEMBLrel. 28, Last annotation update)
Nectin-like molecule 2 (RAI75 isoform d).
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EVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 297
                                                                                                                                                                            241 EVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPN 300
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                                     RWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYL
                  DEGRYFCQLYTDPPQESYTT1TVLVPPRNLM1D1QKDTAVEGEE1EVNCTAMASKPATT1
                                                                                 RWFKGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Hippocampus; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninol P., Hayashizaki Y.; High-efficiency Full-length CDNA cloning."; Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
library, clone:290073606 product:immunoglobulin superfamily, member
4, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CSTEL/6J; TISSUE=Hippocampus; MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; MEDLINE=20530913; PubMed=11076861; DOI=5.0.1101/gr.152600; Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishina T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; TISSUE-Hippocampus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y., "Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of new Genome Res. 10:1617-1630(2000).
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STRAIN=C57BL/61; TISSUE-Hippocampus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                               LFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
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STRAIN-C57BL/6J; TISSUE-Hippocampus;
The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Igsf4a;
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MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
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                                                                                             RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0065202; C:synappei; DA.

GO; GO:0008021; C:synappei; DA.

GO; GO:0016338; P:calcium-independent cell-cell adhesion;

GO; GO:000715; P:cell adhesion; IDA.

GO; GO:000715; P:cell adhesion; IDA.

InterPro; IPRO07110; Ig-like.

InterPro; IPRO0710; Ig-like.

PFam; PF00047; ig; 2.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB092414; BAC66173.1; -.
EMBL; AB183402; BAD30021.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE-Spleen cell-derived;
Ito A., Koma Y., Nagano T.;
Submitted (GEP-2002) to the EMBL/GenBank/DDBJ databases.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
02-OCT-2004 (TrEMBLrel. 28, Last annotation update)
A secretion form of SGIGSF/TSLCI (RALTS isoform e).
Name=Igsf4a; Synonyms=RA175, sSGIGSF/STSLC1;
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Pred. No. 5.6e-112;
0; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                336 AA.
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; PSS0835; IG LIKE; 3.
E 336 AA; 37155 MW;
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97.9%;
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Best Local Similarity 97.9
Marches 327; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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PROSITE; E
SEQUENCE
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Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer."; Genome Res. 10:1757-1771(2000).
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Pred. No. 4e-111;
0; Mismatches 6; Indels
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SEQUENCE 336 AA; 37157 MW; FF887FAF4EFDF120 CRC64;
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
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(TrEMBLrel. 25, I
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Matches 325, Conservative
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Q922H8
ID Q922H
AC Q922H
DT 01-MA
DT 01-OC
DE Necti
      RAARARA BARAA BARA
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Last sequence update) Last annotation update)

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KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTC
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                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:00045202; C:synappic; Vesicle; IDA.
GO; GO:000515; C:synappic vesicle; IDA.
GO; GO:000515; F:protein binding; IPI.
GO; GO:00155; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR003158; Ig c2.
InterPro; IPR003588; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 295;
                                                                                                                                       Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AF061260; AAC67243.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00047; 1g; 2.
SMART; SM00294; 4.1m; 1.
SMART; SM04081; 1Gc2; 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6F488 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.8%; Score 1526; DB 2;
98.6%; Pred. No. 8.2e-101;
iive 1; Mismatches 3;
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Name=IGSf4a; Synonyms=ra175c;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.6°
Matches 291, Conservative
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Mus musculus (Mouse)
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SEQUENCE FROM N.A.
                                                             NCBI_TaxID=10090;
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Gaps

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MEDLINE-2263149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; MEDLINE-2263149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Pujida E., Soyama A., Momoi T.; Puman lung cancer, is a cell adhesion molecule."; Puman lung cancer, is a cell adhesion, IDA. Coj. GO:0005215; Piprotein binding; Pla.

GO; GO:0005215; Piprotein binding; Pla.

GO; GO:0007155; P: Protein binding; Pla.

GO; GO:0007155; P: Protein binding; Pla.

GO; GO:0007155; P: Protein binding; Pla.

GO; GO:0007165; P: Protein binding; Pla.

R GO; GO:0007165; P: 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 295;
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           GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Neurexin-like.
Pfam; PF00047; ig; 1.
SMART; SM00404; ig; 1.
SMART; SM00404; ig; 1.
PROSITE; PS00818; IGc2; 1.
PROSITE; PS00835; IG LIKE; 2.
SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175B.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 65.0%; Score 1483; DB 2;
Best Local Similarity 95.9%; Pred. No. 9.7e-98;
Matches 283; Conservative 3; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Igsf4a; Synonyms=ra175b;
Mus musculus (Mouse).
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R MGD; MGI:1889272; Igsf4a.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:00045202; C:synapse; IDA.

R GO; GO:0008512; C:synaptic vesicle; IDA.

R GO; GO:0005515; F:protein binding; IPI.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007156; P:synaptogenesis; IDA.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003598; Ig-2.

R InterPro; IPR003598; Neurexin-like.

R Pfam; PR00047; ig: 1.

R SMART; SM00409; IGC2; 1.

R SMART; SM00408; IGC2; 1.

R PROSITE; PS56035; IGC2; 1.

R PROSITE; PS56035; IG LIKE; 2.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Pred. No. 3.5e-99;
2; Mismatches 3; Indels 11;
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Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Las
01-OCT-2003 (TrEMBLrel. 25, Las
Adhesion protein RA175A.
Name=Igsf4a; Synonyms=ra175a;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65.9%;
94.8%;
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KKEYFI 306
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Gaps
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Query Match 61.1%; Score 1394; DB 2; Length 289; Best Local Similarity 91.9%; Pred. No. 2.1e-91; Matches 271; Conservative 3; Mismatches 15; Indels 6
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Search completed: June 28, 2005, 09:53:49 Job time : 113.883 secs

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GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-622-237-2 Perfect score: Title:

2283 1 MASVVLPSGSQCAAAAAAA.....AIINAEGGQNNSEEKKEYFI 442 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_16Dec04:* •• Database

geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003as:* geneseqp2003as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

SUMMARIES

	. e	cel	1ym	tum	pol	nov	Pro	hum	p53	p53	Pro	Pro	PRO	PRO	PRO	PRO	hum	sec	sec	sec	sec	sec	PRO	hum	sec
ü	Protein	Нишап	Human	Human	Human	Human	Human	Novel	Human	Novel	Human	Human	Human	Human	Human	Human	Novel	Human							
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56	27	28	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic; antirheumatic, dermatological; antiproliferative; antiartexiosclerotic; anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; cronn's disorder; inflammatory disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human. Protein encoded by human secreted protein gene #11. AAB25619 standard; protein; 442 AA. (first entry) 21-NOV-2000 AAB25619; RESULT 1 AAB25619

Homo sapiens.

WO200029435-A1

25-MAY-2000.

99WO-US025031. 27-OCT-1999; 98US-0105971P. 28-OCT-1998;

(HUMA-) HUMAN GENOME SCI INC

Υ; Wei Kenny JJ, Moore PA, Ni J, Ruben SM, Olsen HS, Young PE, Greene JM;

WPI; 2000-387742/33.

Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.

Disclosure; Page 182-183; 803pp; English.

The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAAB06066-8480623 encode the 12 secreted protein sequences given in AAB0506-825533. The human secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the

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Location/Qualifiers
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  antiarthritic; antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; and antiatiosclerotic; anticancer; vulnerary; antiviral; antibacterial; and antifungal activity. The proteins, polypeptides, agonists and antidonists and to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addisor's disease, rheumatoid arthritis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, Crohn's disease and nephritis; hyperproliferative disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; ardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; ardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; ardiovascular disorders e.g. coronary and the treatment of infectious diseases. The human secreted protein gene and the treatment of infectious diseases. The human secreted protein gene #11 and protein sequences are represented in sequences AAAB06516 and AAB25586. Sequences AAAB0677-A80682 represent genes related to the
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activities of the proteins include: immunosuppressant; anti-inflammatory;
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New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders.
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                                                                                                                                                                                                                                                                                                                                                  HCSRP
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                                 The present sequence is a novel human cell surface receptor protein (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 312256 from the cDNA library LUNGNOTO2, which was made from RNA isolated from lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 g3779242. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and melanoma, immune disorders such as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as between a disease, multiple sclerosis and espilepsy. Polymucleotides encoding HSCRP may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP matibodies may be used as
                                                                                                                                                                                                                                                                                                                           antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRE and for disapposis of HCSRP-related disorders. HCSRP and its catalytic or immunogenic fragments are useful for drug screening using libraries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MASVVLPSGSQCAAAAAAAAAPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
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B7-L1; T cell proliferation; natural killer cell; NK; tumour cell;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 2283; DB 3; Length 442; 100.0%; Pred. No. 8.3e-158; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human lymphoid derived dendritic cell adhesion molecule.
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Claim 1; Page 81-82; 97pp; English
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Best Local Similarity 100.
Matches 442; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 442 AA;
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The present amino acid sequence is the human lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B-1 and cytoplasmic region of BP-Li. Human LDCAM is expressed in breast, retina, feetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of corgan and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel molecules designated LDCAM are capable of altering or modulating T
biological activity, quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response.
                                                                                                                                                        39. .442
/label= Mature_human_LDCAM_polypeptide
57. .69
                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-Glycosylation site"
375. .395
/label= Transmembrane_domain
                                                                                                                                                                                                                                                                                                                  /note= "N-Glycosylation site"
304. .306
/note= "N-Glycosylation site"
                                                                                                                                                                                                                                                        /note= "N-Glycosylation site"
                                                                                                                                                                                                                                                                     113. .115
/note= "N-Glycosylation site"
165. .167
                                                                                                                                                                                                                        "N-Glycosylation site"
                                                                                                              l. .374
/label= Extracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                 396. .442
/label= Cytoplasmic_domain
                                                                                                                                            . .38
/label= Leader_peptide
                                                                                                Location/Qualifiers
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N-PSDB; AAZ50882
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                                                                                                                                            Peptide
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Gaps

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100.0%; Score 2283; DB 3; Length 442; 100.0%; Pred. No. 8.3e-158; tive 0; Mismatches 0; Indels 0;

Conservative

Matches 442;

Query Match Local

Similarity

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subject. The method comprising contacting a cell component of a proliferating cell with a reagent that detects level of the cell component in the proliferating cell and determining modification in the level of the cell component in proliferating cell as compared with a healthy cell, where modification indicates disorder associated with TSLC1. The method is useful for detecting a cell proliferative disorder (e.g. liver, lung or pancreatic cancer) associated with tumour suppressor lung cancer i (TSLC1) in a subject. The invention is useful in gene therapy and for treating a cell proliferative disorder such as lung cancer (human non-small cell lung cancer), liver cancer (hopatocaellular carcinoma) or pancreatic cancer associated with modification of TSLC1 production, where a reagent which modulates (preferably, increases) TSLC1 level in the cells, is employed. The present sequence is human TSLC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, vulnerary, dermatological, neuroprotective, nootropic, cancer, antiparkinsonian, immunostimulant, cytostatic; immunosuppressive, antidiabetic; antiallergic, gene therapy, wound healing; tissue repair; burn; central nervous system disorder, Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
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100.0%; Score 2283; DB 5;
Best Local Similarity 100.0%; Pred. No. 8.3e-158;
Matches 442; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
lung; pancreatic cancer; cell proliferative disorder; cytostatic;
                                        RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
                                                                                                                                                                       RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVGGEEIEVNCTAMASKPATTIRWF
                   MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                                                                   TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; hepatocellular
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(LIUD/)
(CROC/)
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                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93532). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABB63053) or an antibody (III) to (II).

(II) and (III) are useful for diagnostic evaluation of disorders.

(I) is useful for gene therapy of diseases and (III) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, parkinson's, Huntington's and amylotrophic lateral sclerosis, diabetes and allergies. Note: The sequence data for this patent din not form part of the printed specification, but was obtained in electronic format directly from Wilco at the printed specification, but was obtained ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISCQVNKSDDSVIQLINPNRQTIYFRDFRPLKDSRFQLINFSSSELKVSLTNVSISDEG 120
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                                                                                                                                                                                                                           New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies.
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                                                                                                                                                                                                                                                                                                      Claim 20; SEQ ID NO 262; 284pp + Sequence Listing; English.
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                                                                                                                                  Zhou P, Xue AJ, Ren F, Zhang J, u C, Drmanac RT, Wehrman T;
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100.0%; Pred. No. 8.3e-158;
tive 0; Mismatches 0;
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                                         31-AUG-2001; 2001WO-US027093
                                                                       01-SEP-2000; 2000US-00654935
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                                                                                                                                  Asundi V, Zh
Wang D, Liu
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                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                               N-PSDB; ABQ93304.
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                                                                                                                                Tang YT,
Zhao QA,
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54 identical to 18 human controllection fargures contained in American Type Culture Collection (Arcc) deposit No. defined in the specification, its species homologue, a variant of the polymuclectide having a polymuclectide capable of wariant of the polymuclectide having a polymuclectide capable of having a mucleotide sequence of only A or T residues. Also included are recombinant vectors, host cells (for producing the polympetide), the secreted polympetide (comprishing a sequence that is at least 95% category of protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polympetide, diagnoshing, treating, preventing or medical condition by administering the polymetide that seal of the polympetide (comprishing a sequence that is at least 95% categories, variant, allelic variant or species homologue), antibodies that specifically bind to the polympetides, diagnoshing, treating, preventing or ameliorating a medical condition by administering the polymetide or the species homologue) and activity in a biological assay (by expressing the convergence and sequence in a cell, isolating the supernatant, and detecting an activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greene JM;
                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; antiinflammatory; immunomodulator; neuroprotective; hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive;
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                                                                                                                                                                                                                                                                                                                                                                               Human novel secreted protein from gene 11 #3.
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DTAIINAEGGONNSEEKKEYFI 442
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                                                                                                                                                                     ADA27144 standard; protein; 442
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Crocker PR;
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19-APR-2000; 2000US-0198407P
30-OCT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836353.
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LIU D.
CROCKER P R.
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GREENE J M.
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27-FEB-2003

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in a biological assay and identifying the protein in the supernatant having the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune a disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the tissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other intertitional components. The present is a secreted protein of the
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Sequence 442 AA;

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240
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                                                                        1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                             Gaps
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100.0%; Score 2283; DB 6; Length 442; 100.0%; Pred. No. 8.3e-158;
                             0; Indels
                            0; Mismatches
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              Best Local Similarity
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Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
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                                                                                                     ADE54238 standard; protein; 442 AA
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ADE54238
IID ADE5
IID
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polyneptides or their antibodies. The polynucleotide or the compound to minum (c.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene for therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the specification) but was obtained in electronic form directly from will on the printed for the printed for the specification and pared nerve endervential to the printed for the printed for this patent did not form part of the printed for the printed for the form of the f 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240 New composition comprising two or more isolated polypeptides, useful for .; 0 Length 442; Indels preparing a medicament for treating pain in an animal 100.0%; Score 2283; DB 7; 100.0%; Pred. No. 8.3e-158; tive 0; Mismatches 0; Costigan M; ftp.wipo.int/pub/published_pct_sequences Claim 1; Page; 1017pp; English. Befort K, 14-AUG-2001; 2001US-0312147P. 01-NOV-2001; 2001US-0346382P. 26-NOV-2001; 2001US-0333347P. 14-AUG-2002; 2002WO-US025765. GEHO) GEN HOSPITAL CORP Local Similarity 100. Les 442; Conservative WPI; 2003-268312/26. GENBANK; NP_055148. Woolf C, D'urso D, (FARB) BAYER AG. Sequence 442 AA; Query Match 8 ò g ò q ò g

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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300

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                                                                                                                  61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDGG
                                                    MASVVLPSGSQCAAAAAAAPPGLRIRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                                   MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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   Mismatches
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human p53 modifying protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid sequence, or its allelic variant, a fragment of the CDNA sequence, or its fragment, domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein associated
                                                                                                           YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                         SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
                                               nucleic acid molecule, useful for preparing a medicament for venting, treating or ameliorating a medical condition e.g. cancer,
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                                                                                                                                                                                                                                                                                                                                                                                            human; secreted protein; cancer; liver disorder; hepatitis; neural disorder; Alzheimer's disease.
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                                                                                                                                                                                                                                                                                                                                                               Novel human secreted protein #11 associated protein #1
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Pred. No. 8.3e-158;
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liver disorders or neural disorders.
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27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
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MOORE P A.
WEI Y.
GREENE J M.
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Best Local Similarity
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Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
Human, p53 modifier, cytostatic, cancer, cytostatic, antiangiogenic,
antiapoptotic, p53 pathway, breast cancer, colon cancer, kidney cancer,
lung cancer, ovarian cancer, angiogenesis, cell cycle,
apoptotic disorder, cell proliferation disorder.
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modulating agent, by contacting an assay system comprising a purified HM polypeptide (human orthologue of genes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but for the presence of the test agent, the system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M3) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator that specifically binds to a HM polypeptide comprising an HM amino acid contacting a cell defective in p53 function size contacting the analysism of that specifically binds an HM polypeptide comprising an HM amino acid sequence, where p53 function is restored, modulating (M3) a p53 pathway. In a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a disease in a patient (comprising; (a) obtaining a biological sample of rome the patient; (b) contacting the sample with a probe for HM comparison indicates a likelihood disease). (M1) is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. (c) ridentifying modulators of the p53 pathway, such as, angiogenesis, apoptotic or cell the p53 pathway, such as, angiogenesis, apoptotic or cell confideration of the cell, so that the cell undergoes normal confideration of the cell, so that the cell undergoes normal confideration disorders (HP p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, also useful for reating defects in the p53 pathway such as angiogenic, represents a human p53 p
                                                                                                                                   invention relates to identifying (M1) a candidate p53 pathway
Example 2; Page 469-470; 678pp; English
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Sequence 442 AA;

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                                                                                                                                             TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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                                                                                          MASVVLPSGSQCAAAAAAAAAPPGLRIRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                                   Gaps
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99.9%; Score 2280; DB 6; Length 442; 99.8%; Pred. No. 1.4e-157;
                                 Indels
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                                   Matches 441; Conservative
                Best Local Similarity
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 Query Match
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Human p53 modifying protein, SEQ ID 191
ABO07231 standard; protein; 442 AA.
     (first entry)
     13-AUG-2003
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Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.

Homo sapiens,

WO200299122-A1.

12-DEC-2002.

03-JUN-2002; 2002WO-US017382.

05-JUN-2001; 2001US-0296076P

10-OCT-2001; 2001US-0328605P. 15-FEB-2002; 2002US-0357253P.

(EXEL-) EXELIXIS INC.

Funke RP; Li D, Belvin M, Francis-Lang H, Friedman L, Plowman GD,

2003-156859/15. N-PSDB; ACD13404. Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agente that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.

Example 2; Page 557-559; 678pp; English.

The invention relates to identifying (M1) a candidate p53 pathway

modulating agent, by contacting an assay system comprising a purified HM

colypeptide (human orthologue of genes that modify the p53 pathway in

Drosophila) or nucleic acid with a test agent under conditions, where but

for the presence of the test agent under conditions where but

correcting a cell detective in p53 pathway of a cell (comprising

contacting a cell defective in p53 function with a candidate modulator

Also included are modulating (M2) a p53 pathway of a cell (comprising

contacting a cell defective in p53 function with a candidate modulator

that specifically binds to a HM polypeptide comprising an HM amino acid

sequence, where p53 function is restored), modulating (M3) a p53 pathway

in a mammalian cell (comprising contacting the cell with an agent that

specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4)

contacting an aptient (comprising) (a) obtaining a biological sample

from the patient; (b) contacting the sample with a probe for HM

expression; (c) comparing the results with a control; and (d) determining

whether the comparison indicates a likelihood disease) (M1) is useful

for identifying modulators of the p53 pathway. A probe for HM expression

contacting applications, where disease or disorder prognosis is related

therapeutic applications, where disease or disorder prognosis is related

the p51 function of the cell, so that the cell undergoes normal

condition of the cell, so that the cell undergoes normal

condition or progression through the cell undergoes normal

conditions and the cell, so that the cell undergoes normal

conditions and the cell, so that the cell undergoes normal

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conditions and the cell, so that the cell undergoes normal

conditions and the cell proliferation disorders. The present sequence

conditions and the cell proliferation disorders. The present sequence

conditions are presented and possible to the p53 pathw

Sequence 442 AA;

Query Match

99.9%; Score 2280; DB 6; Length 442;

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Claim 1; Page; 1017pp; English
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                                                                  61 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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                                                                                                         RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
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                                               MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
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                            1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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           Gaps
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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           0; Indels
99.8%; Pred. No. 1.4e-157; ive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human Protein AAF69029, SEQ ID NO 7525.
                                                                                                                                                                                                                                                                                                                       DTAIINAEGGONNSEEKKEYFI 442
                                                                                                                                                                                                                                                                                                                                                                             ADE61605 standard; protein; 442
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-AUG-2002; 2002WO-US025765
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         Matches 441; Conservative
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GENBANK; AAF69029.
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 Best Local Similarity
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, cor human polynucleotides or a polynucleotide acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound to pain and a pharmaceutical composition a method for identifying a compound useful in treating condulates its activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more condulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene charapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the specification but was obtained in electronic form directly from WIPO at the form is the form the content of the printed for this patent did not form part of the printed form is the form the content of the form the content of the form the content of the form of the form of the form of the fo
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Pred. No. 1.4e-157;
1; Mismatches 0;
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Best Local Similarity 99.8%;
Matches 441; Conservative 1
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standard; protein; 442

240

300 300 420

361 SRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420

442

421

SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA

NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTLTITTD 360

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361

301

RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF

121

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61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG

KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ

181 181 241

YKPQVH1QMTYPLQGLTREGDALELTCEA1GKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFI

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                             Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                                                                                             Costigan M;
                              Human Protein AAF69029, SEQ ID NO 7528,
                                                                                                                                                                                             Befort K,
                                                                                                                                                                                                                                                        Claim 1; Page; 1017pp; English.
                                                                                                                                       14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                        14-AUG-2002; 2002WO-US025765
                (first entry)
                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP. (FARB ) BAYER AG.
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GENBANK; AAF69029.
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                                                                                          WO2003016475-A2
                                                                            Homo sapiens
               29-JAN-2004
                                                                                                         27-FEB-2003
ADE61608;
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating comprises its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a human procein (shown in Table 2 of the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed or expected the specification but was obtained in electronic form directly from WIPO at the sequence data for this patent did not form directly from WIPO at the sequence data for this patent did not form and directly from WIPO at the sequence data for this patent did not form 
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Matches 441;
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Conservative

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Human, PRO protein, tumour necrosis factor family, TNP, cytokine, secreted protein, transmembrane protein, inflammation disorder.
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        442
                                                  AAY17830 standard; protein; 440 AA.
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97US-0069711P.
97US-0069334P.
97US-0069334P.
97US-0069425P.
97US-0069694P.
97US-0069604P.
97US-0069604P.
97US-0069604P.
97US-0069604P.
97US-0069604P.
97US-0069604P.
                                                                                                      Human PRO355 protein sequence.
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                                                                                      (first entry)
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N-PSDB; AAX80055.
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                                                                                                                                                   Homo sapiens
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11-DEC-1997;
11-DEC-1997;
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17-DEC-1997;
18-DEC-1997;
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09-FEB-1998
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                                 RESULT 13
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Modified-site
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   The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-prolliferative and immunosuppressive activity. The proteins and polynucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
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                                                                                                                                                                                                                                                                                                                                                         1 MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
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Nucleic acids encoding PRO secreted and transmembrane proteins
                                                                                                                                                                                                                                                                                 Score 2263; DB 2; Length 440;
Pred. No. 2.4e-156;
0; Mismatches 0; Indels 2
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/label= Signal peptide
9. .15
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                                   Claim 12; Fig 27; 123pp; English
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Best Local Similarity 99.5
Matches 440; Conservative
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
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d diagnostic
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A, Godowski PJ, Grimaldi CJ, Gurney AL;
, Napier MA, Roy MA, Tumas D, Wood WI;
                                                                                                                                                                                                                        'note= "Tyrosine kinase phosphorylation site"
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designated as PRO polypeptides, useful as pharmaceutical and
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233. .240
                                                                                                                                                                                                                                                                                                                                         307. .313 /note= "N-myristoylation site"
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'note= "N-myristoylation site"
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/note= "N-myristoylation site"
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                                          /note= "N-glycosylation site"
111. .115
/note= "N-glycosylation site"
"N-glycosylation site"
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/label= Transmembrane domain
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/note= "N-myristoylation
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                                                                                                            163. .167
/note= "N-glycosylation
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98US-0112850P.
98US-0113296P.
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Gerritsen ME, Goααια
Tr, Kljavin IJ,
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ME, Goddard
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16-DEC-1998;
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30-MAY-2000; 2
02-JUN-2000; 2
05-JUN-2000; 2
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                                                                                                                                                                                118
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                                                                                                           1 MASVVLPSGSQCAAAAAAAAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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                                                                            1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                            Gaps
                                              .;
7
               Length 440;
                                              Indels
                                              ·,
          Score 2263; DB 3;
Pred. No. 2.4e-156;
0; Mismatches 0;
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2000WO-US005841.
2000US-0187202P.
2000US-0186968P.
2000US-0189328P.
          99.1%;
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2000US-0190828P.
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                                            Conservative
                              Similarity
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21-MAR-2000; 2
28-MAR-2000; 2
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                                            440;
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           Query Match
Best Local
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adernal, lung, colon, cursast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
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29-MAR-2000; 2000US-0193053P.
30-MAR-2000; 2000US-0193053P.
44-APR-2000; 2000US-0194449P.
44-APR-2000; 2000US-0194647P.
11-APR-2000; 2000US-0195975P.
11-APR-2000; 2000US-0195975P.
11-APR-2000; 2000US-019610P.
11-APR-2000; 2000US-019610P.
18-APR-2000; 2000US-019610P.
18-APR-2000; 2000US-01991397P.
25-APR-2000; 2000US-0199550P.
25-APR-2000; 2000US-0199550P.
25-APR-2000; 2000US-0199554P.
25-APR-2000; 2000US-0199554P.
25-APR-2000; 2000US-0199554P.
25-APR-2000; 2000US-0199554P.
25-APR-2000; 2000US-0199654P.
17-MAY-2000; 2000US-0199654P.
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2000US-0209832P.
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Smith V, W
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qa	119	
ò	181	KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLGVQRYLEVQ 240
QQ	179	KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 238
Š	241	YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
qa	239	YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 298
ò	301	NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT 360
οp	299	NILNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTT 358
ò	361	SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
qa	359	SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
ò	421	DTAIINAEGGONNSEEKKEYFI 442
qa	419	

Search completed: June 28, 2005, 09:50:06 Job time : 121.548 secs LANS OF STREET, STREET

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Perfect score:

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1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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US-09-945-87-61

US-09-945-87-61

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US-09-944-396-61

US-09-944-396-61

US-09-944-432-61

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Sequence 111, App
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Sequence 10, Appli
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Sequence 136, App
Sequence 20, Appl
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Sequence 2, Appli
                                                                                                    June 28, 2005, 09:53:58; Search time 112.927 Seconds (without alignments) 1505.131 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/NCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/ptodata/2/pubpaa/NS08_NEW_PUB.pep:*
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22: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-778-1878-2
US-09-984-130-136
US-09-984-130-136
US-10-302-041-20
US-10-302-041-20
US-10-303-107-1
US-10-303-616-262
US-10-698-408-2
US-10-015-1115-110
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                                                                                                                                                                                                                                                                         1717557 seqs, 384547976 residues
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                 RESULT 3
US-09-984-130-136
US-09-984-130-136
; Sequence 136, Application US/09984130
; Publication No. US20030055231A1
; GENERAL INFORMATION:
; APPLAL INFORMATION:
; TITLE OF INVENTION: 12 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: 12 nouses.
FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2001-04-19
PRIOR FILING DATE: 1001-04-19
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1998-10-27
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SEQ ID NOS: 149
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US-09-984-130-136
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    RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
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                                                                                                                     241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
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100.0%; Pred. No. 2.4e-160;
iive 0; Mismatches 0;
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Fatent No. US20020168712A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
TILLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILLE REPERENCE: 2873-US
CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 2001-02-06
FRIOR PILING DATE: 1999-08-05
FRIOR APPLICATION NUMBER: US 60/095,672
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-07
FRIOR FILING DATE: 1999-08-07
FRIOR FILING DATE: 1990-08-07
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ORGANISM: homo sapiens
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Sequence 1, Application US/10403107
Publication No. US20030165974A1
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: YOSHINORI, Muramaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/10/403,107
CURRENT FILING DATE: 2003-03-28
PRIOR PRILING DATE: 2001-08-15
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CURRENT APPLICATION NUMBER: US/10/302,041
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/778,510
FRIOR FILING DATE: 2001-02-07
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 20
LENGTH: 442
TYPE: PRT
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ORGANISM: Homo sapiens
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US-10-302-041-20
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SOFTWARE: Patentin ver
SEQ ID NO 1
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                                                                                                                                       Sequence 136, Application US/09836353A

Publication No. US20030129685A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REPRENCE: PF489P1

CURRENT FILING DATE: 2001-04-18

PRIOR APPLICATION NUMBER: 60/198,407

PRIOR FILING DATE: 2000-04-19

PRIOR FILING DATE: 1999-10-27

PRIOR PELING DATE: 1999-10-27

PRIOR PELING DATE: 1999-10-27

PRIOR PILING DATE: 1999-10-27

PRIOR PILING DATE: 1999-10-27

PRIOR PILING DATE: 1999-10-27

PRIOR PELING DATE: 1998-10-28

NUMBER OF SEQ 1D NOS: 147

SOSTWARE: PALENTIN VET. 2.0
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TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
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  421 DTAIINAEGGONNSEEKKEYFI 442
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Best Local Similarity 100.
Matches 442; Conservative
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                                                                                                    RESULT 4
US-09-836-353A-136
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181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
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                                                                                                                                                                                                                                                                                                               DB 15; Length 442;
                                                                                                                                                                                                                                                                                                                                                            Indels
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TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR PILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 2283; DB 15; Best Local Similarity 100.0%; Pred. No. 2.4e-160; Matches 442; Conservative 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 111
LENGTH: 442
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Publication No. US20040044181A1
GENERAL INFORMATION:
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CORGANISM: Homo sapiens
US-10-015-115-111
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, ORGANISM: Homo sapiens
US-10-363-616-262
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US-10-363-616-262
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APPLICANT: Li, Li
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APPLICANT: Li, Li
APPLICANT: Padigaru, Muralidhara
ITILE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
ITILE OF INVENTION: Using the Same
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: 60/248,153
FRIOR APPLICATION NUMBER: 60/248,153
FRIOR PELICATION NUMBER: 60/249,598
FRIOR PELICATION NUMBER: 60/264,240
FRIOR APPLICATION NUMBER: 60/264,240
FRIOR APPLICATION NUMBER: 60/266,127
FRIOR APPLICATION NUMBER: 60/266,127
FRIOR APPLICATION NUMBER: 60/266,127
FRIOR PELICATION NUMBER: 60/266,127
FRIOR FILING DATE: 2001-01-26
FRIOR FILING DATE: 2001-02-02
FRIOR FILING DATE: 2001-02-16
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                                                      Length 442;
                                                                                                      0; Indels
                                                    100.0%; Score 2283; DB 14; 100.0%; Pred. No. 2.4e-160;
                                                                                                        0; Mismatches
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Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
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APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
                                                 Query Match 100.
Best Local Similarity 100.
Matches 442; Conservative
  US-10-403-107-1
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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300
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                       181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
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| Publication No. US20050058642A1 |
| GENERAL INFORMATION: |
| APPLICANT: GALIBERT, Laurent J. |
| APPLICANT: YAN, Wei |
| TITLE OF INVENTION: ANTAGONISTS OF LDCAM AND METHODS OF USE |
| TITLE OF INVENTION NUMBER: US/10/898,408 |
| CURRENT APPLICATION NUMBER: 60/490,027 |
| PRIOR PFLING DATE: 2004-07-25 |
| NUMBER OF SEQ ID NOS: 13 |
| SOFTWARE: Patentin version 3.2 |
| LENGTH: 442
                                                                                                                                                             181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ
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Pred. No. 2.4e-160;
Mismatches 0; Indels 0;
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100.0%; Score 2283;
Best Local Similarity 100.0%; Pred. No. 2.4
Matches 442; Conservative 0; Mismatches
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ORGANISM: homo sapiens
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US-10-898-408-2
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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVKVDDEMPQHAVLSGFNLFI
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100.0%; Pred. No. 2.4e-160;
iive 0; Mismatches 0;
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Publication No. US20040204568A1
GENERAL INFORMATION
GENERAL INFORMATION
FILE APPLICANT: Baum, Peter R.
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REPERENCE: 2873-US
CURRENT FELING DATE: 2003-07-17
CURRENT FILING DATE: 2003-07-17
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US/09/778,187B
PRIOR APPLICATION NUMBER: PCT/US99/17905
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIN VERSION 3.1
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Best Local Similarity 100.
Matches 442; Conservative
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                       241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
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                                                                                                                                                        361 SRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLILGRYFARHKGTYFTHEAKGADDAADA
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
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99.5%; Pred. No. 7e-159;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                      421 DTAIINAEGGONNSEEKKEYFI 442
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; Sequence 61, Application US/09866028
; Patent No. US20020058309A1
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Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
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Filvaroff, Ellen
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Matches 440; Conservative
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APPLICANT: Botstein, David
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Tumas, Daniel
Wood, William
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ORGANISM: Homo Sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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APPLICANT: Guo, Xiaojia
APPLICANT: Gragolli, Esha
APPLICANT: Gragolli, Esha
APPLICANT: Shimkets, Richard A
APPLICANT: Taupier, Raymond J
APPLICANT: Ti, Li,
APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
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Pred. No. 3.9e-160;
1; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR APPLICATION NUMBER: 60/248,153
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-17
PRIOR FILING DATE: 2001-01-26
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR FILING DATE: 2001-02-02
PRIOR FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/309,261
PRIOR FILING DATE: 2001-07-10
PRIOR PRILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR PRILING DATE: 2001-07-31
PRIOR PRILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR SPLING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-07-31
PRIOR FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 205
                                                421 DTAIINAEGGONNSEEKKEYFI 442
                         DTAIINAEGGONNSEEKKEYFI 442
                                                                                                                                                                            ; Sequence 110, Application US/10015115; Publication No. US20030207800A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                  Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
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Best Local Similarity 99.8
Matches 441; Conservative
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US-10-015-115-110
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59 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 118
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                                             PRIOR APPLICATION NUMBER: 60/146,229
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: December 1, 1998
PRIOR PILING DATE: December 1, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 22, 1999
PRIOR PILING DATE: December 22, 1999
PRIOR APPLICATION NUMBER: 90/254,311
PRIOR APPLICATION NUMBER: PCT/US99/21252
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: No. US20020102647Alember 30, 1999
PRIOR PILING DATE: No. US20020102647Alember 30, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PECT/US99/28301
PRIOR PILING DATE: PECT/US99/28301
PRIOR PILING DATE: PECMER: PCT/US99/28301
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Pred. No. 7e-159;
0; Mismatches 0;
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PRIOR FILING DATE: February 11, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 3, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR FILING DATE: DECEMBER: J. 2000
PRIOR PILING DATE: DECEMBER: J. 2000
PRIOR PILING DATE: PEBRIOR SEQUIO 6520
PRIOR PILING DATE: PEBRIOR SEQUIO 6520
PRIOR PILING DATE: PEBRIOR SEQUIO 6520
PRIOR PILING DATE: PEBRIARY 28, 2001
NUMBER OF SEQ ID NOS: 120
FILING DATE: December 16, 1998
APPLICATION UNDBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
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Best Local Similarity 99.5
Matches 440; Conservative
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ORGANISM: Homo Sapien
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                                                          SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
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CURRENT FILING DATE: 2001-09-26
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PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR PELICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069,335
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR PILING DATE: December 16, 1997
PRIOR PILING DATE: December 17, 1997
PRIOR PILING DATE: December 19, 1997
PRIOR PILING DATE: Pebruary 5, 1998
PRIOR PILING DATE: Pebruary 5, 1998
PRIOR PILING DATE: Pebruary 9, 1998
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Patent No. US20020102647A1
GENERAL INFORMATION:
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Filvaroff, Ellen
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Goddard, Audrey
Godowski, Paul
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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Hillan, Kenneth
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99.5%; Pred. No. 7e-159;
.ive 0; Mismatches 0; Indels
                PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 22, 1998
PRIOR PILING DATE: December 12, 1998
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: December 1, 1998
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: December 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 16, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PEDLUARY 11, 2000
PRIOR PILING DATE: PEDLUARY 22, 2000
PRIOR PILING DATE: PEDLUARY 22, 2000
PRIOR PILING DATE: MARCH 30, 2000
PRIOR PILING DATE: PEDLUARY 28, 2001
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Matches 440; Conservative
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FILING DATE:
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APPLICANT: Naples, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Milliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLCI
CURREMY PAPLICATION NUMBER: 05/06/944,457
CURREMY APPLICATION NUMBER: 09/866,028
PRIOR PLILNG DATE: 2001-09-26
PRIOR PLILNG DATE: December 10, 1997
PRIOR PLILNG DATE: December 11, 1997
PRIOR PLILNG DATE: December 12, 1997
PRIOR PLILNG DATE: December 12, 1997
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PRIOR PLILNG DATE: December 17, 1997
PRIOR PLILNG DATE: PEDVLATION NUMBER: 60/069,017
PRIOR PLICATION NUMBER: 60/070,440
                                NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPFTTTTTTTTTTTTTTTTTTT
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                                                                299 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTT
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                                                                                                                                                                                                                                                                                                                     ; Sequence 61, Application US/09944457; Patent No. US20020110859A1; GENERAL INFORMATION:
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
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Pred. No. 7e-159;
0; Mismatches 0; Indels
                                         PRIOR PILIGIO DATE: December 22, 1998

RIOR PILIGIO DATE: December 22, 1998

RRIOR PILIGIO DATE: JULY 28, 1999

PRIOR FILING DATE: September 16, 1998

RRIOR FILING DATE: December 1, 1998

RRIOR FILING DATE: December 1, 1998

RRIOR FILING DATE: December 16, 1999

RRIOR FILING DATE: December 16, 1999

RRIOR FILING DATE: JUNE 22, 1999

RRIOR FILING DATE: September 16, 1999

RRIOR FILING DATE: December 16, 1999

RRIOR FILING DATE: December 1, 2000

RRIOR APPLICATION NUMBER: PCT/US90/2831

RRIOR FILING DATE: December 1, 2000

RRIOR APPLICATION NUMBER: PCT/US00/0441

RRIOR FILING DATE: PEDRUARTY 11, 2000

RRIOR RILING DATE: REDATARTY 11, 2000

RRIOR APPLICATION NUMBER: PCT/US00/0441

RRIOR FILING DATE: REDATARTY 21, 2000

RRIOR APPLICATION NUMBER: PCT/US00/0441

RRIOR FILING DATE: MATCH 3, 2000

RRIOR APPLICATION NUMBER: PCT/US00/0441

RRIOR FILING DATE: MATCH 3, 2000

RRIOR FILING DATE: December 1, 2000

RRIOR FILING DATE: December 1, 2000

RRIOR FILING DATE: DECEMBER: PCT/US00/0520

RRIOR RPLICATION NUMBER: PCT/US00/0520

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RRIOR FI
                              LICATION NUMBER: 60/113,296
December 16, 1998
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Best Local Similarity 99.5
Matches 440; Conservative
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TITLE OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC FILLE OF INVENTION: ACIDS ENCODING THE SAME FILLE APPLICATION NUMBER: US/09/44,862

CURRENT APPLICATION NUMBER: US/09/26

PRIOR PELICATION NUMBER: 00/1-09-26

PRIOR PELING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/06/3134

PRIOR APPLICATION NUMBER: 60/06/3134

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 12, 1997

PRIOR PLING DATE: December 12, 1997

PRIOR PLING DATE: December 16, 1997

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PRIOR PLING DATE: Pecember 19, 1998

PRIOR PLING DATE: Pecember 19, 1998

PRIOR PLING DATE: Pecember 19, 1998

PRIOR PLING DATE: Pebruary 9, 1998
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Grimaldi, Christopher
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Gerritsen, Mary
Goddard, Audrey
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APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI YKPOVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI

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181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240

9-949-016-7563 Sequence 7563, Ap 8-429-742-2 Sequence 2, Appli Sequence 10044, A 8-949-016-11044 Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6.78, Ap 8-435-956A-1 Sequence 6.15, Appli Sequence 6.15, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6.15, Appli Sequence 1, Appli Sequenc	ALIGNMENTS 10 Designated B7L1 /778,510 /US99/17906 095,663	ore 2283; DB 4; Length 442; ed. No. 9e-192; Mismatches 0; Indels 0; Gaps 0;	PPGIRIRILILILESAAALIPTGDGONLFTKDVTVIEGEVA 60 	TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120 	OESYTTITULVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180 	KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQ 240
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APPLICANT: Godowski, Paul J
APPLICANT: Godowski, Paul J
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kljavin, Ivar
APPLICANT: Rajer, Mary
APPLICANT: Najer, Mary
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/09/866,028
CURRENT APPLICANT: NUMBER: US/09/866,028
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Best Local Similarity 99.5%; Pred. No. 5.1e-190;
Matches 440; Conservative 0; Mismatches 0;
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Patent No. 6794288
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eston, Dan
APPLICANT: Ferrara, Napoleone
                    Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61
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Fatent No. 6556493
GENERAL INFORMATION:
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: THE VOSHINORI, Muramaki
APPLICANT: REEVES, Roger
APPLICANT: VOSHINORI, Muramaki
FILLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILLE REFERENCE: JUH1770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT PILLING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
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                                                                            DTAIINAEGGONNSEEKKEYFI 442
                                                                                                     DTAIINAEGGONNSEEKKEYFI 442
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Patent No. 6642360
GENERAL INFORMATION
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 442; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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US-09-866-028-61
                                                                                                                                                                           RESULT 2
US-09-930-803-1
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Query Match
Best Local Similarity 99.5
Matches 440; Conservative
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; ORGANISM: Homo Sapien
US-09-944-457-61
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US-09-778-510-22
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                                                                                                   APPLICANT: NOTAMERIA (1947
TITLE OF INVENTION: ACIDE ENCODING THE SAME
PILES BEREBENE: 2001-09/2944,457
CURRENT APPLICATION NUMBER: 05/06/05 134
PRIOR PELING DATE: 2001-09/2944,457
PRIOR APPLICATION NUMBER: 05/06/05 134
PRIOR PELING DATE: DOCEMBER (1949)
PRIOR APPLICATION NUMBER: 05/06/9335
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1949)
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR APPLICATION NUMBER: 05/06/9316
PRIOR PELING DATE: DOCEMBER (1) 1997
PRIOR PELING DATE: DOCEMBER (1) 1999
PRIOR PELING DATE: POLING NUMBER: (2) 1999
PRIOR PELING DAT
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APPLICATION NUMBER: PCT/US99/28313
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Godowski, Paul
Grimaldi, Christopher
                                             Gurney, Austin
Hillan, Kenneth
                                                                                              Kljavin, Ivar
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KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  359 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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TITLE OF INTERINCENTON: Molecules Designated B7L1
FILE REFRENCE: 2844 US
CURRENT APPLICATION NUMBER: US/09/778,510
                                            PRIOR APPLICATION UNDERS: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: Pebruary 11, 2000
PRIOR FILING DATE: Pebruary 11, 2000
PRIOR PILING DATE: Pebruary 22, 2000
PRIOR FILING DATE: February 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: Pebruary 28, 2001
LING DATE: December1, 1999
PLICATION NUMBER: PCT/US99/30095
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Patent No. 6512095
GENERAL INFORMATION:
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88 DFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNL 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 SIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 LLLQAAASKNKVKGSQGQFPLTQNVTVVEGGTAILTCRVDQNDNTSLQWSNPAQQTLYFD 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31 LLFSAAA---LIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 39.5%; Score 902; DB 2; Length 444; Local Similarity 44.6%; Pred. No. 1.1e-70; nes 194; Conservative 74; Mismatches 137; Indels
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                                                                                                                                                                                    15270-002810US
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Fatent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Reim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend an
                  APPLICATION NUMBER: US/08/659,984A FILING DATE: 07-UN-1996 CLASSIFICATION: 436 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/485,152 FILING DATE: 07-JUN-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                             NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 1527(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGGONNSEEKKEYFI 442
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                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGDALELICEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AAPPGLRLRILILILSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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Patent No. 5940400

GENERAL INFORMATION:

APPLICANT: Anderson, John P.

APPLICANT: Sinha, Sukanto

APPLICANT: Jacobson-Croak, Kirsten L.

TITLE OF INVENTION: Assays for Detecting Beta-Secretase

TITLE OF INVENTION: Inhibition

NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor

CITY: San Francisco

STATE: California
                                                                                                                                                                                                                                         Length 423
                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                   Score 2169; DB 4;
Pred. No. 8.4e-182;
1; Mismatches 4;
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
SPRIOR FILING DATE: 22
SOFTWARE: PAtentin Ver. 2.0
                                                                                                                                                                                                                                       95.0%;
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 98.8°
Matches 418; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC OPERATING SYSTEM: SOFTWARE: Patentin
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EYF 423
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US-08-659-984A-5
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                                                                                                                                                 LENGTH: 423
                                                                                                                            SEQ ID NO 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LMLKVHKEDDGVPVICQVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 ILTCESKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILFLNKTDNGTYRCEATWTIGQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     374 P----DHALIGGIVAVVVFVTLCSIFLIGRYLARHKGTYLTNEAKGAEDAPDADTAIINA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 DFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     197 LDFRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPL 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         264 ELTCEAIGKPOPVMVTWVRVDDEM--POHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---DSRAGEEG 367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 LLFSAAA---LIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39.5%; Score 902; DB 3; Length 444; 44.6%; Pred. No. 1.1e-70; Live 74; Mismatches 137; Indels
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              322 AHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT
: Two Embarcadero Ctr., 8th Floor
San Francisco
California
                                                                                                                                                                                                                                                                                                                                                     15270-002210US
                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,53
                                                                                                                                        PC-DOS/MS-DOS
                                                                                                         E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                 NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15;
TELECOMMUNICATION:
TELEPHONE: 415-326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 EGGONNSEEKKEYFI 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                             444 amino acids
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Best Local Similarity 44.6
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                      94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                               FILING DATE
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; Sequence 1, Application US/08659984A

RESULT 8 US-08-659-984A-1

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70 WHELSISVSDVSLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPQISGFSSPVMEGDLMQ 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 164 VNCTAMASKPATTIRWFKGNTELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 SSELKVSLTNVSISDEGRYFCOLYTDPPOESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         221 QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 RVDHESLANATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPLILTCESKGKPLPEPVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             280 WVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 LPTIIPSLTTATVTTVALTTSPTTSSIRDPNALAGONGP----DHALIGGIVAV 362
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                   APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                        ADDRESSEE: Townsend and Townsend and Crew STREET: Two Embarcadero Ctr., 8th Floor CITY: San Prancisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
APPLICANT: Anderson, John P. APPLICANT: Sinha, Sukanto APPLICANT: Jacobson-Croak, Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FELECOMMUNICATION INFORMATION
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INFORMATION FOR SEQ ID NO: 1:
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Best Local Similarity 45.1%
Matches 189; Conservative
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REGISTRATION NUMBER: 2
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COMPUTER READABLE FORM:
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307 LPTIIPSLTTATVITTVAITTSPTTSSIRDPNALAGQNGP----DHALIGGIVAV 362
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-- DSRAGEEGSIRAVDHAVIGGVVAV 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 PQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKG-K 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 IQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMP----QHAVLSGPNLFINN 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             303 LNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTS 362
                                                                                         384 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
                                                                                                                71 DSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57 DSSLQWSNPAQQTLYFGEKRALRDNRIQLVSSTPHELSISISNVALADEGEYTCSIFTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 IR---PEPAHPREGOKLLLHCEGRGNPVPQQYVWVKEGSEPPLKMTQESALIFP----F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 AAAAAPPGLRLRLLLLFSAAALIPTG----DGQNLFTKDVTVIEGEVATISCQVNKSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 APAASP----VPLLLLL--ACSWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 AGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 398;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.7%; Score 745.5; DB 4; 39.1%; Pred. No. 5.2e-57; iive 74; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                        Molecules Designated B7L1
                                                                                                                                                                                                                                                                                                          APLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7;
FILE REPERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 4
LENGTH: 398
    338 PPPTTTTTTTTTTTTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         423 AIINAEGGONNSEEKKEYFI 442
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US-09-778-510-6
Sequence 6, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
                                                                                                                                                                                                                                            Sequence 4, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 39.1%
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus
                                                                                                                                                                                                     RESULT 10
US-09-778-510-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVT 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RVDHESLNATPQVAMQVLEIHYTPSVKI---IPSTPFPQEGQPLILTCESKGKPLPEPVL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WVRVDDEM--POHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 VVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEGSQVNAEEKKEYFI 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44 GQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION 1435
PRIOR APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTONNEY/AGBAT INFORMATION:
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
                                                                                                                                                                APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Pamela S.
APPLICANT: Anderson, John P.
TILLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15270-002210US
                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                           Sequence 1, Application US/08660531
Patent No. 6221645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-236-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 421 amino acids
IYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 45.14
Matches 189; Conservative
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                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Chrysl
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                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                         US-08-660-531-1
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907, 794A
CURRENT APPLICATION NUMBER: US 60/1414
PRIOR APPLICATION NUMBER: US 60/143, 048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 TITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGK-SEVEEW 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 PGLRIRILLILLESAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQL
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32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.9e-56;
Matches 166; Conservative 73; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRIOR FULLING DATE: 1999-12-05
PRIOR FPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-05
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR FILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PLING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 309-12-30
PRIOR FILING DATE: 309-12-30
PRIOR FILING DATE: 300-01-05
PRIOR FILING DATE: 300-01-05
PRIOR FILING DATE: 300-01-05
PRIOR FILING DATE: 300-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US99/28214
FILING DATE: 1999-11-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1999-11-29
APPLICATION NUMBER: PCT/US99/28313
                           Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
                                                                                                                                            Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-11-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Gaps
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Baum, Peter
rTON: Molecules Designated B7L1
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                                  FILE REFERENCE: 2844-USE DEBIGNATED CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER: 60/095,663
NUMBER: PRIOR PILING DATE: 1998-08-07
NUMBER: PRIOR FILING DATE: 1998-08-07
SEQ ID NO 6
LENGTH: 398
                                                                                                   ьк: PCT/US99/17906
1999-08-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 84, Application US/09907794A
Patent No. 6635468
GENERAL INFORMATION:
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
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Gerber, Hanspeter
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Best Local Similarity 38.6'
Matches 166; Conservative
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     389 GGDDKKEYFI 398
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                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapien
  APPLICANT: Baum,
TITLE OF INVENTION:
FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-907-794A-84
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PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-29
PRIOR PLING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-30
PRIOR PILING DATE: 1999-11-20
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-06
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 1999-13-30
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Patent No. 668451
GENERAL INFORMATION:
APPLICANT: Genencech, Inc.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 38.6
Matches 166; Conservative
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US-09-905-125A-84
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                                                                               253 LQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYR 312
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                                       PNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPP
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CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT PILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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PILING DATE: 1999-07-26
FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
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APPLICATION NUMBER: PCT/US99/21090
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APPLICATION NUMBER: PCT/US99/20944
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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Williams, P. Mickey
Wood, William, 1
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Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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Ashkenazi, Avi
Botstein, David
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Eaton, Dan L.
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                                                                                   44; Gaps
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32.4%; Score 739; DB 4; Length 39 38.6%; Pred. No. 1.9e-56; ive 73; Mismatches 147; Indels
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APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERSINCE: 1046-61-7-10
FRICK APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2000-00-10
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR FILING DATE: 1999-00-13
FRIOR APPLICATION NUMBER: US 60/130,000
FRIOR PELING DATE: 1999-00-15
FRIOR PELING DATE: 1999-00-15
FRIOR PELING DATE: 1999-00-15
FRIOR PELING DATE: 1999-10-20
FRIOR PELING DATE: 1999-10-20
FRIOR PELING DATE: 1999-11-30
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR PELING DATE: 1999-12-30
FRIOR APPLICATION NUMBER: PCT/US99/30095
FRIOR PELING DATE: 1999-12-30
FRIOR APPLICATION NUMBER: PCT/US99/30095
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FRIOR PELING DATE: 1999-12-30
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38.6%; Pred. No. 1.9e-56;
Live 73; Mismatches 147; Indels 44; Gaps
                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher
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Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
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Hillan, Kenneth, J.
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Stewart, Timothy A.
Tumas, Daniel
                                                         Gerber, Hanspeter
Gerritsen, Mary E
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Best Local Similarity 38.6 Matches 166; Conservative
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CORGANISM: Homo sapiens
US-09-902-775A-84
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123 LVTVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQED 182
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137 TITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGK-SEVEEW 195
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
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PRIOR FILING DATE: 2000-02-22
PRIOR PEDITCATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
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FILING DATE: 1999-07-28
APPLICATION NUMBER: PCT/US99/20594
FILING DATE: 1999-09-08
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Grimaldi, Christopher
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Stewart, Timothy A.
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Gerritsen, Mary E.
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Mather, Jennie P.
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183 PNGKTFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTFTAMIRPDPP 242
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32.4%; Score 739; DB 4; Length 398;
Best Local Similarity 38.6%; Pred. No. 1.9e-56;
Matches 166; Conservative 73; Mismatches 147; Indels 44; Gaps
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-09-15
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR PLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/2813
PRIOR PILING DATE: 1999-11-29
PRIOR PILING DATE: 1999-11-20
PRIOR PLING DATE: 1999-12-02
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Job time : 32.659 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-906-700-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             373
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

June 28, 2005, 09:42:27; Search time 24.9399 Seconds (without alignments) 1631.912 Million cell updates/sec

US-10-622-237-4 2197 1 AAPPGLRLRILLILLSAAAL.....TAIINAEGGQNNSEEKKEYF 423 Title: Perfect score:

Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283416 seqs, 96216763 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote		ď					neural cell adhesi	poliovirus recepto		Н	н			elastic titin - hu	connectin/titin -	neuromusculin - fr	neural cell adhesi	neural cell adhesi	50K glycoprotein p	PRR2 alpha - human	opioid-binding pro		surface glycoprote	adhesion_molecule	perlecan precursor		cell adhesion mole	opioid-binding pro
SUMMARIES		T08732	T20992	T43290	HLMSP3	JC4024	A53437	168093	JE0099	A44194	B44194	IJXENE	RWHUPD	RWHUPA	156551	I38346	T42633	T13669	JE0100	JN0635	JC5519	153960	803199	JC4025	A45254	JH0506	A38096	B42632	A42632	JC1239
	DB	7	N	~	Н	7	~	7	~	~	~	Н	-		~	~	~	~	7	-1	~	7	7			~		~	7	7
	Length	407	5175	5198	467	518	530	538	725	417	392	1088	392	417	344	7962	4162	1011	725	1092	338	478	345	345	588	588	4391	815	932	345
d	양소	12.3	11.9			11.1	11.1	10.9	10.8	10.8	10.7	10.7	10.6	10.6	10.5	10.4	10.3	10.2	10.1	10.1	10.0	10.0	9.9		9.6	7.6	9.6	9.6	9.6	9.5
	Score	270	261.5		246.5	244	243	238.5	238	237	234.5	234	232.5	232.5	231	228.5	226	225	222	222	220.5	220	217.5	215.5	215.5	214	212	210.5		
	Result No.	-	7	m	4	2	9	7	89	6	10	11	12	13	14	15	16	17	18	19	20	. 21	22	23	24	25	26	27	28	29

s-gicerin precurso cell surface glyco	limbic-system-asso	differentiation an	CD22 homolog/B lym	B-cell adhesion pr	carcinoembryonic a	alcam - human	neogenin - chicken	opioid-binding pro	cell adhesion mole	DM-GRASP precursor	heparan sulfate pr	nephrin - human	connectin 3B - chi	neural cell adhesi
I50419 I38049	JC4776	149583	A46512	JH0371	A36319	139428	150600	JC1238	C42632	JH0464	\$18252	T37190	PN0568	IJHUNG
~ ~	N	~	~	~	~	7	~	~	7	~	~	7	~	П
584 646	338	862	868	847	702	583	1443	338	765	587	3707	1241	1323	761
9.5	9.4	9.4	9.4	9.4	9.3	9.3	9.5	9.1	9.1	9.1	0.6	6.8	8.9	8.8
209.5	206.5	206.5	206.5	206	204	203.5	202	200.5	200.5	200	197	196.5	195	193
		_				_	_	_	_	_	^1	_	_	

ALIGNMENTS

RESULT 1 T08732 T08732 T08732 T08732 T08732 C; Date: 11-Jun-1999 #text_change 09-Jul-2004 C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C; Accession: T08732 Symmitted to the Protein Sequence Database, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999 A; Reference number: 216474 A; Accession: T08732 A; Residues: 1-407 <0TT> A; Cross-references: UNIPROT: 09Y412; EMBL: AL050071 A; Cross-references: UNIPROT: 09Y412; EMBL: AL050071 A; Experimental source: fetal kidney; clone DKFZp566B0846 C; Genetics: A; Note: DKFZp566B0846.1	Query Match Best Local Similarity 27.0%; Pred. No. 1.2e-11; Matches 85; Conservative 58; Mismatches 124; Indels 48; Gaps 13;	102 GRYFCQLYTDPPQESYTLITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPAT 157	158 TIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGN 212	213 LQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQH 272 :: : : : :	273 AVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTT 324 :	325 TTTTTTTTTILTIIDSRAGEEGTIGAVDHAVIGGVVAVVVRAMLCLLI- 375	376ILGRYPARH 384 : 286 YRRRTFRGDYPAKN 300
RESULT T08732 hypothe C;Date: C;Date: C;Acces R;Acces R;Refer A;Resid	Query Best Match	රු සි	රු සි	čo d	දු පු	è 8	& g

RESULT 2 120992 hypothetical protein F15G9.4a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T20992; T24733

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148
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R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: 219355

A;Accession: T20992

A;Accession: T20992

A;Accession: T20992

A;Accession: T20992

A;Molecule type: DNA

A;Residues: 1-5175 <WILL)

A;Cross-references: UNIPROT:Q8I0L3; EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F1

A;Experimental source: clone F15G9

R;Kershaw, J.

Submitted to the EMBL Data Library, December 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 3
1443290
hemicentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: L1-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C;Accession: T433290; T20993; T24734
R;Vogel, B.E.; Hedgecock, E.M.
S;Description: Hemice EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-A;Reference number: Z22396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 269/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4468/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2409 VYARP-PAKITWLKAGKPLQSDKFVKTSANGQKLYLFKLRETDSSKYTCIATWEAGTDKR 2467
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CESP:F15G9.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2310 CPA-TGKPEPDITWFKDGEAIHIENIADIIPNGELNG-------NQLKITRIK 2354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIOKD-TAVEGEEIEVN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTAMASKPATTIRWFKG------NKELKGKSEVEEWSDMYTVTSQLMLKVHK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVH---IQMTYPLQGLTREGDAFELTCE 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 AIGKPQPVMVTWVRVDDEMPQHAVL----SGPNLFINNLNKTDNGTYRCEASNIVGKAHS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 VTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPL----KDSRFQLLNFSSSEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.9%; Score 261.5; DB 2; Length 5175; 24.6%; Pred. No. 1.2e-09; ive 65; Mismatches 130; Indels 71;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>A;Residues: 1-5198 <VOG>A;Cross-references: UNIPROT:O76518; EMBL:AF074901; PIDN:AAC26792.1
R;Aulston, J.
B;Aulston, Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993
                                                                                                                                                                                                                                                                                    A;Reference number: Z19929
A;Accession: T24133
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 24.6
Matches 87; Conservative
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HIMSP3
poliovirus receptor homolog precursor - mouse
c;Species: Mus muscalus domesticus (western European house mouse)
c;Species: Muscalus domesticus (western European house mouse)
c;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: A38211
R;Morrison, M.E.; Racaniello, V.R.
A;Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus re-A;Reference number: A38211; MUID:92219365; PMID:1560525
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A.Residues: 1-467 <MOR>
A.Residues: 1-467 <MOR>
A.R. Cross-references: UNIPROT: P32507; GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C.Superfamily: poliovitus receptor; immunoglobulin homology
C.Keywords: duplication; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovitus receptor homolog #status predicted <MAT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:7-133/Domain: immunoglobulin homology <IMM1>
F:267-321/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM3>
F:267-322/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: him-4; F15G9.4b
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/.
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                                                          A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Residues: 1-5198 <WIL>
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A;Experimental source: clone F15G9
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
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A;Cross-references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone T09B9
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 KVSLTNVSISDEGRYFCQLYTDPPQESYT-TITVLVPPRNLMIDIQKD-TAVEGEEIEVN 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 AIGKPOPVMVTWVRVDDEMPQHAVL----SGPNLFINNLNKTDNGTYRCEASNIVGKAHS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTAMASKPATTIRWFKG------NKELKGKSEVEEWSDMYTVTSQLMLKVHK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 VTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPL----KDSRFQLLNFSSSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVH---IQMTYPLQGLTREGDAFELTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2468 DFKVSMLVAPSFDEPNIVRRITVNSGNPSTLHCPAKGSPSPIITWLKDGNAIE 2520
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Accession: T24734
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z19929
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A,Cross-references: UNIPROT:P32507; GB:D26107; NID:g475017; FIDN:BAA05103.1; PID:g825507
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R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
d. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with A;Reference number: A53437; MUID:94179228; PMID:8132569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14;
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                                                                     GEARVPGDSGTPMAPVTVISRYRLVPSREAHQOSLACIV-----NYHMDRFKESLTLM 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMASKPATTIRWFKG-NKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIGNIQIQRYLEVQYKPQVHIQMIYPLQGLTREGDAFELICEAIGKPQPVMVTWVRVDDE 268
                                                                                                                                                       GKSEV--EEWSDM--YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRY-----LE 220
                                                                                                                                                                                                                                                                            VQYKPQVHIQ---MTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSG 277
                                                                                                                                                                                                                                                                                                                                    VOYEPEVTIEGFDGNWYLORMD-----VKLTCKADANPPATEYHWTTLNGSLPKGVEAQN 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTIITDSRAGEEG-TIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFA----RH--KGTYF 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Č;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL-----LNFSSSELKVSLTNVSIS
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                                     QESYTTITVLVPPRNLMIDIQKD-TAVEGEEIEV---NCTAMASKPATTIRWFKGNKELK
                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 RTLFFKGPINYSLAGTYICEATNPIGTRSGOVEVNITEFPYTPSPP-------
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A; Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C; Superfamily: poliovirus receptor; immunoglobulin homology
F; 47-133/Domain: immunoglobulin homology < IMP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 22.6%;
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poliovirus receptor mPVR -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-530 < AOK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEGNYTCEFATFPNGTRRGVTWLRVIAQPEN-----HAEAQEVTIGPQSVAVARCV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMASKPATTIRWFKG-NKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPA 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEEPILLPVTLSVRYPPEVSIS-GYDDNWYLGRSEAI-LTCDVRSNPEPTDYDWSTTSGV 293
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A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>F;356-379/Domain: transmembrane #status predicted <TMM>
F;375-467/Domain: intracellular #status predicted <INT>
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                          294 FPASAVAQGSQLLVHSVDRMVNTTFICTATNAVGTGRAEQVILVRDTPQA-----
                                                                                                                                                                                                                                                                                                                                                                       --LNFSSSELKVSLTNVSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTT
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A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
                                                                                                                                                                                                                                                                                              PILPLIPLILL ----LOETG-AQDVRVRVLPEVRGRIGGTVELPCHILPPTTERVSQVT
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                      99;
                                                                                                                                                                                                                                                  PGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEV---ATISCQV----
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                                                                                                                              DB 1; Length 467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCGNDGDRGSYDPKTQVFGNGGPVFWRSASPEPMRPDGREEDEBEEEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             387 TYFTHEAKGADDA------ADADTAIINAEGGQNNSEEKKE
                                                                                                              11.2%; Score 21.0%; 21.6%; Pred. No. 6.5e-10; rive 72; Mismatches 196; Indels -1800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                       -NKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.1%;
25.1%;
                                                                                                                    Query Match
Best Local Similarity 21.6'
Matches 101; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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us-10-622-237-4.rpr

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A, Accession: JE0099
A; Molecule type: mRNA
A; Residues: 1-725 - KUD>
A; Cross-references: UNIPROT:073633; DDBJ:AB008162; NID:g3116226; PIDN:BAA25931.1; PID:g31
A; Experimental source: heart
                                                                                                                                                                                                                                   C;Comment: This protein mediates and regulates various cell-cell interactions through bour c. Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immur F;413-475/Domain: immunoglobulin homology <1MM>F;512-589/Domain: fibronectin type III repeat homology <3FR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: À44194
R;Koike, S.; 1se, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has A;Reference number: A44194; MUID:93059651; PMID:1331508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18;
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                                                                     (N-CAMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 317 DEITLITCEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGK 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            372 TDAGEYFCIASNP-IGVDMQAM-YFEVQYAPKIR----GPVVVYTWEGNPVNITCEVFAH 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57 QLLNPNR-----QTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVS-----ISDEGRY 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EEIEVNCTAMASKPATTIRWFKGNKE-----LKGKSEVEEWSDMYTVTSQLMLKVHKE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                          81
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C,Species: Cercopithecus aethiops (green monkey, grivet)
C,Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32 KDVTVIEGEVATISC---QVN----KSDDSVIQLLN----PNRQTIYFRDFRPLKDSRFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQPVMVTWVRVDDEMPQH-----AVLSGP----NLFINNLNKTDNGTYRCEASNIVGKAHS
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                   R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiokawa, K.
Biochem Biochhys. Res. Commun. 245, 127-132, 1998
A;Title: Molecular cloning of sad-form neural cell adhesion molecules
A;Reference number: JE00099; MUID:98204770; PMID:9535795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80;
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                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 238; DB 2; Length 72
26.2%; Pred. No. 4.5e-09;
ive 61; Mismatches 148; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Superfamily: poliovirus receptor; immunoglobulin homology C;Keywords: transmembrane protein F;259-314/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 26.29
les 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
C; Accession: JE0099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | : | : | : | : | 384 QQRKEQT-----LQGAEEDEDLEGPPSYKPPTPKAKLEAQEMPSQLFTLGASEHSPLKTP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 VPGLYISLVTWQRPDAPANHQNV--AAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 ICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMV 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCKVEHESFEEPALIPVTLSVRYPPEVSIS-GYDDNWYLGRTDA-TLSCDVRSNPEPTGY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIP 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 FARHKGTYFTHEAKGADDAADAD-----TAIINAE-----GGONNSEEKKE 421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19
                                                                                                                                                                                                        C;Species: Homo mapiens (man)
C;Species: Homo mapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 168093
R;Eberle, F; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene A;Reference number: 153960; MUID:95347610; PMID:7622062
A;Accession: 168093
A;Accession: 168093
A;Accession: 168093
A;Accession: 168093
A;Accession: 168093
A;Accession: 168093
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neural cell adhesion molecule 1 - African clawed frog
N:Alternate names: N-CAM 1
C;Species: Xenopus laevis (African clawed frog)
C;Species: 19-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 PTTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAGTVTVTSRFTLVPSGRADGVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 APPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----ELKVSLTNVSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQKDTAVEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-538 <RES>
A;Cross-references: UNIPROT:Q92692; GB:S79172; NID:g1042204; PID:g1042205
A;Cross-references: UNIPROT:Q92692; GB:S79172; NID:g1042204; PID:g1042205
A;Genetics:
A;Genetics: PRR2delta
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 10.9%; Score 238.5; DB 2; Length 538; Best Local Similarity 22.8%; Pred. No. 2.9e-09; Matches 110; Conservative 63; Mismatches 196; Indels 113;
                      TTTTTTTTTLTILTITDSRAGEEGTIGAVDHAVIGGVVAVVV 367
                                                   423
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                                                                                                                                                                                         PRR2 delta - human
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no putat

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A,Molecule type: mRNA
A,Residues: 1-1088 «KRI»
A;Cross-references: UNIPROT:P16170; EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g2146
A;Notes: the authors translated the codon AAA for residue 970 as Leu
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol-
C;Comment: Several forms of NCAM are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Algebriamily: neural cell adhesion molecule; fibronectin type III repeat homology; immuncy. Subperfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immuncy. Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si Fi20-190 Manain: signal sequence #status predicted <2IG.
Fi20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <1D F;20-003,1050-1088/Product: neural cell adhesion molecule, short domain form #status predicted <2IG.
Fi20-1088/Product: neural cell adhesion molecule, short domain form #status predicted <2IG.
Fi20-1088/Product: neural cell adhesion molecule, short domain form #status predicted <2IG.
Fi20-1088/Promain: immunoglobulin homology <IRM1>
Fi20-188/Pomain: immunoglobulin homology <IRM4>
Fi21-381/Pomain: immunoglobulin homology <IRM4>
Fi21-381/Pomain: immunoglobulin homology <IRM5>
Fi31-381/Pomain: immunoglobulin homology <IRM5>
Fi31-485/Pomain: immunoglobulin homology <IRM5>
Fi31-889/Pomain: fibronectin type III repeat homology <FN3B>
Fi31-880/Pomain: fibronectin type III repeat homology <FN3B>
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                                                                                                                                                                                                                                                     cell adhesion molecule long domain form precursor - African clawed frog
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PQPVMVTWVRVDDEMPQH----AVLSGP---NLFINNLNKTDNGTYRCEASNIVGKAHS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDIQVIVNVPPTIQARQLRVNATANMAESVVLSCDADGFPDPEISWLKKGEPIEDGE-EK 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEITLICEA-SGDPIPSITWRTAVRNISSEATTLDGHIVVKEHIRM----SALTLKDIQY 371
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                                                                                                                                                                                                                                                                               N.Alternate names: NCAM-180
N.Contains: neural cell adhesion molecule, short domain form (NCAM-140)
C.Species: Xenopus laevis (African clawed frog)
C.Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
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F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status
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                                        LTIITDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHK
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25.9%; Pred. No. 1.5e-08;
iive 62; Mismatches 148; Indels
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Nucleic Acids Res. 17, 10311-10315, 1989
A;Title: Primary structure and developmental expression
A;Reference number: 809600; MUID:90098871; PMID:2481269
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Best Local Similarity 25.9%
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       337
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B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Residues: DNA
A;Residues: 1-392 < KOLD
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TC-LFVTFPOGSRSVDIWLRVLAKPON-TAEVOK-VOLTGKPVPVARCVSTGGRPPAHIT 178
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SQLTWSRHGESGSMAVFHQTQGPNYSEPKRLEFVAARLGTELRDASLRMFGLRVEDEGNY 121
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                                                                                                                                                                                                                                                            | : : | | : | | : | | : | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 
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C;Superfamily: poliovirus receptor; immunoglobul
F;259-314/Domain: immunoglobulin homology <IMM>
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Best Local Similarity 24.4%;
Matches 100; Conservative 5
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A;MOLECULE type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: UNIPROT:P15151; UNIPROT:Q96BJ1; EMBL:X64116; NID:g35809; PIDN:CAA4547.
A;NOte: 67-Ala was also found
A;NOte: the gamma form has 331-G1y and lacks residues 332-384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Comment: The normal function of this receptor is unknown. Membrane-bound and soluble for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Generacian GDB:PVR; PVS
A;Generaces: GDB:120324; OMIM:173850
A;Generaces: GDB:120324; OMIM:173850
A;Generaces: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Map position: 19q13.2-219q13.2
A;Map position: 19q13.2-219q13.2
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Superfamily: poliovirus receptor alpha #status predicted calg.
F;1-20/Domain: signal sequence #status predicted calg.
F;21-417/Product: poliovirus receptor alpha #status predicted calg.
F;21-33)Domain: extracellular #status predicted calg.
F;21-330-pasin: extracellular monology calmi.
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75:368-411/Domain: intracellular #status predicted <INT>
75:368-411/Domain: intracellular #status predicted
75:361-212,166-221,266-312/Disulfide bonds: #status predicted
7:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S12048; A31496 — R; Xokida, M.; Iizuka, N.; Takeuchi, K.; Takeg R;Koike, S.; Horle, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Takeg REMD J. 9, 3217-3224, 1990 — R;Koike Bpilovirus receptor protein is produced both as membrane-bound and secreted A;Fitle: The poliovirus receptor protein is produced both as membrane-bound and secreted A;Reference number: S12048; MUID:91006015; PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 852-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence,
A;Reference number: A90910; MUID:89168426; PMID:2538245
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                                                                                                                                                                                                                                                                                     poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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                                                                              ---GMSRNAIİFLVLGILVF---LILLGIGIYF 365
343 SRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYF 381
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25.3%; Pred. No. 5.5e-09;
tive 54; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A31496
A;Molcoule type: mRNA
A;Residues: 1-66, A', 68-417 <MEN>
A;Cross-references: GB:M29535
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hes 101; (
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A;Cross-references: GB:M24406
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; CMIM:173850
A;Cross-references: GDB:120324; CMIM:173850
A;Map position: 19413.2-19413.2
A;Map position: 19413.2-19413.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; dupplication; glycoprotein; receptor; transmembrane proce; Keywords: alternative splicing; dupplication; glycoprotein; receptor; poliovirus receptor delta #status predicted <S1G>F;21-392/Product: poliovirus receptor delta #status predicted <S1G>F;21-343/Domain: immunoglobulin homology <IMM2>F;259-314/Domain: immunoglobulin homology <IMM3>F;259-314/Domain: immunoglobul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-392/Domain: intracellular #status predicted <1MT>
F;49-123.166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr
                                                                                                                                                       poliovirus receptor splice form delta precursor - human
N'Alternate names: poliovirus receptor H20B
N'Alternate names: poliovirus receptor H20B
C'Species: Homo sapiens (man)
C'Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C'Accession: A43024; B31496
R'Kokola: A' HOrie, H; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,Title: The poliovirus receptor protein is produced both as membrane-bound and secreted A,Reference number: $12048, MUID:91006015, PMID:2170108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-392 <KOI>
A;Cross-references: UNIPROT:PI5151; EMBL:X64116
A;Cross-references: UNIPROT:PI5151; EMBL:X64116
A;Cross-references: UNIPROT:PI5151; EMBL:X64116
B;Anote: 67-Ala was also found
B;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: B31496
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 TWTRHGESGSMAVFHQTQGPSYSESKRLBFVAARLGAELRNASLRNFGLRVEDEGNYTC- 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 GNKELKGKSEVEEW-SDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLGGMPNTSQVPGFLSGTVTVTSLMILVPSSQVDGKNVTCKVEHESFEKPQLLTVNLTVY 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         223 YKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTT 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -- 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
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25.3%;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A43024
A; Molecule type: DNA
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A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
A;Map position: 2q31-2q31
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A;Residues: 1-344 <RES>
A;Cross-references: UNIPROT:Q62718; EMBL:U16845; NID:9755184; PIDN:AAA67445.1; PID:97551
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      neurotrimin - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C;Accession: 156551
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.
J. Neurosci. 15, 2141-2156, 1995
A;Title: Cloning of neurotrimin defines a new subfamily of differentially expressed neur
A;Reference number: 156551; MUID:95198094; PMID:7891157
A;Accession: 156551
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101
C;Genetics: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clastic titin - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 138346
C;Accession: 138346
C;Accession: 138346
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
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                                                                                       NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TVLVPPRNLMIDIQKDTAV-EGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSD 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 MYTVTSQLMLKVH---KEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQ 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GL-TREGDAFELTCEAIGKPQPVMVTWVRVDDEMPQ------HAVLSGPNLFINNLN 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGVPVGQKGTLQCEASAVPS-AEFQWFKDDKRLVEGKKGVKVENRPFLSRLTFF--NVS 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLLLLLSAAALIPTG----DGQNLFTK---DVTVIEGEVATISCQVNKSDDSVIQLLNPN
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                                                                                                                                                    300 RPVDKPINTTLICHVTNALGARQAELTVQVKE----GPPSEHS-
                                                                                                                                                                                                                                                                                                                     ------GMSRNAIIFLVLGILVF---LILLGGIYF 365
                                                                                                                                                                                                                                                                   SRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYF 381
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
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257 PVMVTWVRVDDEMPQHA-----VLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYML 310
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                                                                                                                                                                                                                                                                                                                     829 VEGTASLEIIRVDMNDAGNFTCRATNSVGSKDSSGALIVQEPPSFVTKPGSKD-VLPGSA 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 GVPVICOVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQ 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   938 SGTYTCKVSN--VAGGVECSANLFVK-EPATFVEKLEPSQ-LLKKGDATQLACKVTGTP- 992
                                                                                                                                                                                                                                                                                                                                                                                                                 144 IEVNCTAMASKPATTIRWFKGNKELKG-----KSEVEEWSDMYTVTSQLMLKVHKEDD 196
                                                                                                                                                                                       35 TVIEGEVATISCQVNKSDDSVIQ---LLN-----PNRQTIYFRDFRPLKDSRFQLLNF
   Length 7962;
Query Match
10.4%; Score 228.5; DB 2; Length
Best Local Similarity 26.1%; Pred. No. 4.4e-07;
Matches 80; Conservative 55; Mismatches 130; Indels
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completed: June 28, 2005, 09:54:47 ne : 26.9399 secs

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Q8k3t6 mus musculu
Q8r5m8 mus musculu
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
                                                                                                   142 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 201
                                                                                                                                                        202 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 261
                                                                                                                                                                                                                                                                     322 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDHAVIG 381
                                                                                                                                                                                                                                                                                                                            382 GVVAVVVPAM.CLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 441
                                                                                                                                                                                                 241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                                                                                                                                                                                                        301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGTIGAVDHAVIG 360
                                                                                                                                                                                                                                                                                                              361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420
                           262 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
 22 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                          181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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99.1%; Score 2176.5; DB 2; Length 456;
Best Local Similarity 97.2%; Pred. No. 1.2e-147;
Matches 422; Conservative 1; Mismatches 0; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Igsf4a; Synonyms=RA175;
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                                                                                                  TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 201
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                           YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                        1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=22192378; PubMed=12202822; DOI=10.1126/science.1072356; Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T., Sudhof T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly."; Science 297:1525-1531(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pujica E., Alkawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF539424; AAN01614.1;
R EMBL; AB183399 BAD30018.1;
R EMBL; AB183399 BAD30018.1;
R GG) GO:0016621; C:integral to membrane; TAS.
R GO; GO:0016221; C:integral to membrane; TAS.
R GO; GO:000551; F:protein binding; IPI.
R GO; GO:000551; F:protein binding; IPI.
R GO; GO:0001538; P:calcium-independent cell-cell adhesion; IDA.
R GO; GO:0007155; P:eall adhesion; IDA.
R GO; GO:0007155; P:eall adhesion; IDA.
R GO; GO:0007155; P:eall adhesion; IDA.
R GO; GO:0007156; P:synaptogenesis; IDA.
R InterPro; IPR003598; Neurexin-like.
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445 AA; 48666 MW; 5B336F23F1877497 CRC64;
                                                                                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Synaptic cell adhesion molecule 1 (RA175 isoform c)
Name=1gsf4a; Synonyms=RA175;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.8%; Score 2193; DB 2;
99.8%; Pred. No. 7.9e-149;
iive 1; Mismatches 0;
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SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
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EYF 444
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Tataubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Rataubberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,

Rataubberg R.L., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,

Diatchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahdy J., Helton E., Ketteman M., Madan A., Rouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

C. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                          300
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                                                                                                                                                                                                                                                                                                    VGKAHSDYMLYVYDPPTTIPPTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAVIG 378
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                         TVLVPPRNLMIDIQRDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 198
                                                                                                       199 YIVISQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                          EGDAPELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                                                                                                       EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                                                                                                                                                                          VGKAHSDYMLYVYDPPTTI PPPTTTTTTTTTTTTTI LTI ITDSRAGEEGTIGAVDHAVIG
                                                                                                                                                                                                                                                                                                                                                                          GVVAVVVFAMLCLL11LGRYFARHKGTYFTHEAKGADDAADADTA11NAEGGONNSEEKK
                                                                                                                                                                                                                                                                                                                                                                                                      GVVAVVVPAMLCLIILGRYFARHKGTYFTHEAKGADDAADDAIINAEGGONNSEEKK
                                                                           YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
Director MGC Project;

Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078966, AH/78966.1;
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig-c2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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SMART; SM00409; IG; 3.
SWART; SM00408; IGc2; 3.
PROSITE; PS50835; IG_LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 29, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.
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                                                                                                                                                                                               TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
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                                                                                                                                                                                                                                 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGANDAADADTAIINA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
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                            22 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCOVNKSDDSVIOLLN
                                                                                                                            PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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                                                                                               PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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AAPPGLRLRLLLLLLLSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou Y., Du G., Chen J., Yuan J., Qiang B., Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF132811, AAF69029.1, -. InterPro; IPR00110; Ig-like. InterPro; IPR003598, Ig_c2. InterPro; IPR003588; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00294; 4.1m; 1.
SMART; SM0408; IGc2;
PROSITE; PS50935; IG LIKE; 3.
SEQUENCE 442 AA; 49537 MW; 68183E3238735062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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Pred. No. 6.7e-147;
2; Mismatches 4;
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(TrEMBLrel. 17, I
(TrEMBLrel. 25, I
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417; Conservative
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01-OCT-2003
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209BY67
209BY7
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Query Match
Best Local Similarity 94.3
Matches 399; Conservative
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                                                                                                                                      PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                    TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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                                                                                            AAPPGERLRIJILILISAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                         PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                                                  YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                          VGKAHSDYMLYVYDPPTTIPPP--TTTTTTTTTTTTTILTIIT-------
                                                                                                                                                                                                                                                                                                                                                    ------DSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYF
                                                                              1 AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fullta E., Alkawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB183400; BAD30019.1;
EMGJ; AB183400; BAD30019.1;
GO; GO:001621; C:isynapse; IDA.
GO; GO:000821; C:synapse; IDA.
GO; GO:000821; C:synaptic vesicle; IDA.
GO; GO:000515; F:protein binding; IPI.
GO; GO:000518; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
GO; GO:007155; P:synaptogenesis; IDA.
                                                         Indels
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SMART; SM00409; IG; 3.
SMART; SM00409; IGC2; 3.
PROSITE; PS50835; IGC 11KE; 3.
SEQUENCE 428 AA; 46903 MW; BIODFF1A2B893573 CRC64;
              476 AA; 51853 MW; 486A43D37082C8FE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                    DB 2;
                                 Score 2138.5; DB 2,
Pred. No. 6.9e-145;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                               THEAKGADDAADADTAIINAEGGQNNSEEKKEYF 423
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InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
                                   97.3%;
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                                                       Matches 419; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
   protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
Hypothetical
SEQUENCE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=RA175
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                                   Query Match
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                                                                                                                         1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                               22 AAPPGLRIRILILILISAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                                                                                                                                          61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                                                                                                                                                                                                                PNRQTIYPRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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STRAIN=C25BL/6; TISSUE=Brain;
STRAIN=C25BL/6; TISSUE=Brain;
STRAIN=22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
"Implications of nectin-like molecule-"JGSP4/RAIJ5/SgIGSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:00045202; C:synapse; IDA.
GO; GO:0008021; C:synaptic vesicle; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0016338; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007155; P:cell adhesion; IDA.
93.2%; Score 2048.5; DB 2; Length 428; 94.3%; Pred. No. 1.7e-138; ive 1; Mismatches 6; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fujita E., Aikawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AY35138 AAQ02381.1;
EMBL; AB181401; BAD30020.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Nectinilike molecule 2 (RA175 isoform d).
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PNRQTIYFRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 138
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last senotation update)
A secretion form of SGIGSF/TSLC1 (RAJT5 isoform e).
Name=Igsf4a; Synonyms=RA175, 8SGIGSF/STSLC1;
Buts mysolus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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SEQUENCE FROM N.A.
Pujita E., Aikawa K., Momoi T.;
Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AB092414; BAC66173.1; -.
R MSD; MGI:189272; Igsf4a.
R MGD; MGI:189272; Igsf4a.
R GO; GO:0016021; C:snrapse; IDA.
R GO; GO:0008021; C:snrapse; IDA.
R GO; GO:0008021; C:synaptic vesicle; IDA.
R GO; GO:000515; F:protein binding; IPI.
R GO; GO:0001538; P:calcium-independent cell-cell adhesion; IDA.
R GO; GO:0007155; P:calcium-independent
R GO; GO:0007165; P:synaptogenesis; IDA.
R GO; GO:0007165; P:synaptogenesis; IDA.
                                                                                                                            1;
                                                                                        443;
                                                                                      DB 2; Length
                                                                                                                            24; Indels
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STRANT-G57BL/6; TISSUE-Spleen cell-derived;
Ito A., Koma Y., Nagano T.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
    SMART; SM00408; IGC2; 1.
PROSITE; PS50835; IG_LIKE; 3.
SEQUENCE 443 AA; 48648 MW; 046B43AA156F6F64 CRC64;
                                                                                  Query Match 92.0%; Score 2020.5; DB 2
Best Local Similarity 92.9%; Pred. No. 1.8e-136;
Matches 394; Conservative 5; Mismatches 24;
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Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii S.
Saito K., Yamamoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugono S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AK075502; BAC11657.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                         Length 417;
                                                                                                                                                                                                                                               0; Indels
                                                                           Pfam; PF00047; ig; 2.
SWART; SM00294; 4.1m; 1.
SWART; SM00408; IGC2: IGC2: IGC2: IGC2: SWS0408; IGC2: IGC2: SEQUENCE 417 AA; 45779 MW; 98500180D37845C2 CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human).
                                                                                                                                                                                                     92.3%; Score 2027; DB 2; 93.4%; Pred. No. 5.7e-137; ive 0; Mismatches 0;
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GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003588; Ig_c2.
InterPro; IPR003585; Neurexin-like.
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InterPro, IPR007110, Ig-like.
InterPro, IPR003598, Ig_c2.
InterPro, IPR003585, Neurexin-like.
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Matches 395; Conservative
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SMART; SM00294; 4.1m; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
library, clone:2800073606 product:immunoglobulin superfamily, member
4, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Functional annotation of a full-length mouse cDNA collection.";
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                                                                                                                                                         Length 336;
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RIKEN FANTOM Consortium;
                                                                                                            9EF3D8B8BE5E8F72 CRC64;
                                                                                                                                                      74.2%; Score 1631; DB 2; 100.0%; Pred. No. 1e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 AA.
                                                                                                                                                                      100.0%; Prec. ...
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                  InterPro, IPR003598; Ig_C2.
Pfam; PR00047; ig; 2.
SMART; SM00408; IGC2.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 336 AA; 37155 MW;
InterPro; IPR007110; Ig-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGKAHSDYMLYVY 313
                                                                                                                                                                           Best Local Similarity 100.
Matches 313; Conservative
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RESTANGENCE FROM N.A.

RAGEDENCE FROM N.A.

RAGENDENCE F. BODO H., CADINICH P., FURUAG S., FURUAG T., HOTT F.,

RAGENDENCE FROM N.A.

RAGENDENCE F., ROTHEN N., HISAMA M., KASUKAWA T., KATO H.,

RAGENDENCE FROM N., KOYA S., KURINARA C.,

RAGENDENCE F., ROHOO H., KONDER R., NUMBAZAKI R., OHNO M.,

RAGENDENCE FROM N., ROHON R., SARAI C., SARAI K.,

RAGENDENCE FROM STANDENCE F., SHIDBARA C., SHIDBAR F.,

RAGENDENCE FROM N., HASABALAKI Y.,

RAGENDENCE FROM N., ROSHIDBAR K., SHIDBAR F., TARARA T.,

RAGENDENCE FROM STANDENCE F., SHIDBAR F., TARARA T.,

RAGENDENCE FROM STANDENCE F., SHIDBAR R., SHIDBAR F., TARARA T.,

RAGENDENCE FROM STANDENCE FROM N., ROSHIDO M.,

RAGENDENCE FROM STANDENCE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120
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STRAIN=CS'BL/6J; TISSUE=Hippocampus; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA lbraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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MEDLINE-CS7BL/G1 TISSUE-Hippocampus;

MEDLINE-CS7BL/G1 TISSUE-Hippocampus;

MEDLINE-CS7BL/G1 TISSUE-Hippocampus;

MEDLINE-CS7BL/G1 TISSUE-Hippocampus;

Konno H., Akiyama J., Nishi K., Kiteunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";
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Best Local Similarity 100.º
Matches 313, Conservative
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PROSITE; PS50835;
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121 EAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYM 180
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EMBL; AB021966; BAA87916.1; -.
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                                                                                                                                                        A Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
EMBL; AF061266; AA067243.1;
R MGD; MG1188272; Igsfaa.
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:000512; F:protein binding; IPI.
R GO; GO:000512; F:protein binding; IPI.
R GO; GO:0001338; P:call adhesion; IDA.
R GO; GO:000715; P:coll adhesion; IDA.
R GO; GO:000715; P:coll adhesion; IDA.
R GO; GO:000715; P:coll adhesion; IDA.
R InterPro; IPR00710; III-1ike.
R InterPro; IPR003588; Neurexin-like.
R Fan; PF00047; ig: 2.
R SMART; SM00408; iGC2; 1.
R SMART; SM00408; iGC2; 1.
R RRASITS; SN00124; 4.1m; 1.
R SMART; SN00125; IGC2; 1.
R PROSITE; PS50835; IGC2; 1.
R SROUNCE 295 AA; 32509 NW; 9DE9D86F6FF6F488 CRC64;
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 1546; DB 2; L 100.0%; Pred. No. 1.1e-102; ive 0; Mismatches 0;
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
Adhesion protein RA175C;
Name=Igsf4a; Synonyms=ra175c;
Name=Igsf4a; Synonyms=Necl2;
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Matches 294; Conservative
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                       (Mouse)
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                                                                                                  NCBI_TaxiD=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVLVPPRNIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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                                                     19 AAPPGLRIKILILILFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLIN 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1to A., Koma, Y., Nagano T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AB094146; BAC661781.; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_c2.
SMART; SM004047; ig; 2.
SMART; SM004043; IG_LIKE; 3.
SMOSITE; PS50835; IG_LIKE; 3.
SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
10-JUNAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1615; DB 2;
Pred. No. 1.4e-107;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                            333 AA.
                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%;
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(TrEMBLrel. 10, I
(TrEMBLrel. 25, I
                                                                                                                                      301 VGKAHSDYMLYVY 313
                                                                                                                                                                       VGKAHSDYMLYVY 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q922H8 PRELIMINARY;
Q922H8;
Q1-MAY-1999 (TrEMBLrel. 1(
Q1-MAY-1999 (TrEMBLrel. 1(
Q1-OCT-2003 (TrEMBLrel. 2:
Nectin-like protein 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 310; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=sTSLC-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Lung;
                                                                             262
                                                                                                                                                                                            322
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086WBB
AC Q86WBB
AC Q86WB
DT 01-JU
DT 
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Q922H8
ID Q9Z2H
AC Q9Z2H
DT 01-MA
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RAJIS, Wahich is the mouse ortholog of TSLC1, a tumor suppressor gene and which is the mouse ortholog of TSLC1, a tumor suppressor gene and the man number of the mouse ortholog of TSLC1, a tumor suppressor gene and the man number of the mouse ortholog of TSLC1, a tumor suppressor gene and the man number of the mouse ortholog of TSLC1, a tumor suppressor gene and the man number of the mouse ortholog of TSLC1, a tumor suppressor gene and the man number of the mouse of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALELTC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 EAIGKPOPUMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 LYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSAGEEGTIGAVDHAVIGGVVAVVVFA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 LYVYDPPTTIPPPPTTTTTTTTTTTTTEPAVHDSRAGEEGTIGAVDHAVIGGVVAVVVFA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 MLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYF 294
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                   Length 295;
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      GO; GO:0007155; P:cell adhesion; IDA.

GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR007110; Ig-like.
InterPro; IPR003589; Neurexin-like.
InterPro; IPR003589; Neurexin-like.
Pfam; PF00047; ig; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM0408; IGC2; 1.
PROSITE; PS0835; IG LIKE; 2.
SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               .,
8
                                                                                                                                                                                                                                                                                                                                             68.0%; Score 1493; DB 2;
96.6%; Pred. No. 6.8e-99;
tive 2; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13. Last sem
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                         Matches 284; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Adhesion protein RA175B.
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Query Match
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Q9QYL5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALELIC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYM 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTTTTTTTTTTLTITT------DSRAGEEGTIGAVDHAV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAAINAEGGQNNSEE 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 IGGVVAVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTC 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 60
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Pujita E., Soyama A., Momoi T.;
"RA175, which is the mouse ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule.";
Exp. Cell Res. 287:75-66(2003).
Exp. AD021964; BAA87914.1; -.
MOD; MGI:1889272; Igsf4a.
GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016021; C:synapsic vesicle; IDA.
GO; GO:001525; F:protein binding; IPI.
GO; GO:0016338; P:calcium-independent cell-cell adhesion; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
R MGD; MGI:1889272; Igsf4a.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0045202; C:synapse: IDA.

R GO; GO:0008512; C:synapse: IDA.

R GO; GO:0008515; F:protein binding; IPI.

R GO; GO:0015318; P:calcium-independent cell-cell adhesion; IDA.

R GO; GO:0007155; P:cell adhesion; IDA.

R GO; GO:0007156; P:synaptcogenesis; IDA.

R GO; GO:0007116; P:synaptcogenesis; IDA.

R InterPro; IPR007110; Ig-like.

R InterPro; IPR003589; Neurexin-like.

R Ffam; PF00047; ig; 1.

R SMART; SM00294; 4.1m; 1.

R SMART; SM00408; IGC2; 1.

R PROSITE; PSS6035; IG LIKE; 2.

SEQUENCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 68.9%; Score 1513.5; DB 2; Length Best Local Similarity 95.4%; Pred. No. 2.4e-100; Matches 291; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13,
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26	27	28.	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1; B7-11; T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response. Mouse lymphoid derived dendritic cell adhesion molecule. 147. .149 /note= "N-Glycosylation site" 286. .288 "N-Glycosylation site" site" site" /note= "N-Glycosylation site" Location/Qualifiers 1. .356 /label= Extracellular_domain 357. .377 /label= Transmembrane domain 378. .423 /label= Cytoplasmic_domain "N-Glycosylation /note= "N-Glycosylation "N-Glycosylation AAY45093 standard; protein; 423 AA. (first entry) . 292 .97 49. .51 /note= " 83. .85 /note= 'note=

21-NOV-2000 (first entry)

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The present amino acid sequence is the mouse lymphoid derived dendritic cell adhesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cyroplasmic region of B7-L1. Mouse LDCAM is found on whole embryo, testes, triple negative cells murine splenic and lymph node CD8+, S49.1 and dendritic cells. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or
                                                                                                                         molecules designated LDCAM are capable of altering or modulating T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or
                                                                                                                                                                                                    Claim 7; Page 46-47; 44pp; English.
  Baum PR, Fanslow WC;
                                                   2000-205712/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells bearing B7L-1
                                                                          N-PSDB; AAZ50883
                                                                                                                         Novel molecule cell function.
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Sequence 423 AA;

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240
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                                                                                                                                PNRQTIYFRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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                                                        AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
                                                                                                                 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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Length 423;
                            Indels
100.0%; Score 2197; DB 3;
100.0%; Pred. No. 2.5e-151;
iive 0; Mismatches 0;
                            423; Conservative
Query Match
Best Local Similarity
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The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606-A80623 encode the 12 secreted protein sequences given in AAA80606-A80623 encode the 12 secreted proteins have various activities of the human secreted proteins have various activities of eppendent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirhematic, dermatchlogical; antiproliferative, antiarthringal activity. The proteins, polypeptides, agonists and antifungal activity. The proteins, polypeptides, agonists and conditions examples of which include: immune disease, disorders and conditions examples of which include: immune disease, Addison's disease and nephritis; dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, crohn's disease and nephritis; hyperproliferative disorders e.g. cronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing proteins and polynucleotide sequences may also be used in wound healing that and protein sequences are represented in sequences AAA80616 and AAB2566 Sequences AAA80677-A80682 represent genes related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer,
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                                                                                                        antirheumatic, dermatological; antiproliferative; antiarteriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antidungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human.
                                                                                      Secreted protein; immunosuppressant; anti-inflammatory; antiarthritic;
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Pred. No. 2.9e-149;
1; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moore PA,
                                         Protein encoded by human secreted protein gene #11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olsen HS, Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wounds, and infectious diseases.
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Matches 418; Conservative
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                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, HCSRP, cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia; Alzheimer's diseases; multiple sclerosis; epilepsy.
                                                                                                                                                                                                              EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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/note= "potential phosphorylation site"
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|Tabel= Immunoglobulin_domain
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/label= Signal_peptide
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label= HCSRP-8
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The present sequence is a novel human cell surface receptor protein (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 312266 from the cDNA library LUNGNOTO2, which was made from Incyte Clone substance. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 3177942. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and melanoma, immune disorders include cancers such as leukaemia and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as a kathesiar's disease, multiple sclerosis and epilepsy.

Polynucleotides encoding HSCRPs may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP antibodies may be used as magnosists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRP and for diagnosis of HCSRP-related disorders. HCSRP and its catalytic or mumunogenic fragments are useful for drug screening using libraries of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human cell surface receptor protein and polynucleotide useful for diagnosis, prevention and treatment of cancer, immune disorders, infection and neuronal disorders
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Pred. No. 2.9e-149;
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), Azimzai Y, Au-Young
                                                                                                                                      /label= Immunoglobulin domain
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/label= Transmembrane_domain
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98US-00206647.
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                                                                                                                                                                                                                                                                                                                                                                                                            VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTILIITDSRAGEEGSIRAVDHAVIG 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lymphoid derived dendritic cell adhesion molecule; LDCAM; human, B7-1; B7-Li; T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response.
                                  YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                              EGDALELICEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
                                                                                        TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
                                                                                                                                                                 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human lymphoid derived dendritic cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Mature_human_LDCAM_polypeptide
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/note= "N-Glycosylation site"
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/note= "N-Glycosylation site"
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/note= "N-Glycosylation site"
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/label= Extracellular_domain
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/label= Transmembrane_domain
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/label= Cytoplasmic_domain
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/label= Leader_peptide
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The present amino acid sequence is the human lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-Li. Human LDCAM is expressed in breast, retina, feetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant rejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecules designated LDCAM are capable of altering or modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 7; Page 42-43; 44pp; English.
98US-0095672P
                                                                                                                                                                                                                        Fanslow WC;
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Gaps .; 0 Length 442; Indels 98.7%; Score 2169; DB 3; 98.8%; Pred. No. 2.9e-149; iive 1; Mismatches 4; Query Match
Best Local Similarity 98.8
Matches 418; Conservative

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240 120 121 TVLVPPRNLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180 198 258 300 420 78 139 TVLVPPRNLMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 199 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 1 AAPPGLRIRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 19 AAPPGLRIRLILLIRSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI PIRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI

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The invention relates to an isolated polynucleotide (I) comprising one of 245 sequences (ABQ93288-ABQ93332). Treating a condition comprising administering to a mammalian subject a composition comprising the protein (II) encoded by (I) (ABP62809-ABP63053) or an antibody (III) to (II).
(I), (II) and (III) are useful for diagnostic evaluation of disorders.
(I) is useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral
                                                                                                                                                                                                                VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTLTILTILTDSRAGEEGTIGAVDHAVIG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide and polypeptides, useful for treatment and diagnosis of Alzheimer's, Parkinson's, Huntington's, amylotrophic lateral sclerosis, immune deficiencies, cancer, autoimmune disorders, multiple
                                                       319 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAVIG
                                                                                                                                                                                                                                                                                                                                       379 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
                                                                                                                       EGDAFELTCEA1GKPQPVMVTWVRVDDEMPQHAVLSGPNLF1NNLNKTDNGTYRCEASN1
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Wehrman T;
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iu C, Drmanac RT,
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Wang D, Liu
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Zhao QA,
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                                                                                                                                                                                                                                                                                         numan; nepatocellular carcinoma; tumour suppressor lung cancer 1; TSLC1;
liver; lung; pancreatic cancer; cell proliferative disorder; cytostatic;
gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Detecting cell proliferative disorder associated with tumor suppressor lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell of subject with reagent detecting TSLC1 and detecting modification in
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                                                                                                                                                                                                                                                            Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
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                                                                                                                  AAE19887 standard; protein; 442 AA.
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Matches 418; Conservative
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EYF
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Ruben SM,
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sclerosis), immune deficiencies, cancer, autoimmune disorders, multiple sclerosis, diabetes and allergies. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTR
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                                                                                                                                                           98.7%; Score 2169; DB 5; Length 442; 98.8%; Pred. No. 2.9e-149;
                                                                                                                                                                                                 4; Indels
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                                                                                                                                                                                               1; Mismatches
                                                                           ftp.wipo.int/pub/published_pct_sequences
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19-APR-2000; 2000US-0198407P.
30-0CT-2000; 2000US-0243792P.
18-APR-2001; 2001US-00836333.
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                                                                                                                    Sequence 442 AA;
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The invention relates to an isolated nucleic molecule that is at least CC 59% identical to 18 human cDNA sequences representing 12 novel genes cended proteins or a polyvucteotide fragment of the cDNA.

Concoding secreted proteins or a polyvucteotide fragment of the cDNA.

CC defined in the specification, its species homologue, a variant or allelic variant of the polyvucteotide having a Dolynucleotide capable of the polyvucteotide to a polymucleotide capable of the polyvucteotide sequence of only A or T residues. Also included are secreted polypeptide (comprising a sequence of only A or T residues 15% correction an uncleated are secreted polypeptide fragment, domain, epitope, full-length corresponding to the only preptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that specifically bind to the polypeptides diagnosing, treating, preventing or amaliorating a medical condition by administering the polyvucteotide corresponding to the cDNA sequence and activity in a biological assay (by expressing the corresponding to the cDNA sequence and activity, in a biological assay (by expressing the cDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay (by expressing the condition, such as cancer, inflammation and other immune diasorders, neurological condition, for preventing, treating, or ameliocating a pathological condition, such as cancer, inflammation and other immune disorders, neurological assay and isolation, such as cancer, inflammation and other immune condition, such as cancer, inflammation and other immune crowners, neurological probes for differential identification of the restriction mapping. The polypeptides and antibodies are useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodical sare also useful for preventing immunological probes for differential identification of the restriction anapping the present is a secreted protein of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Wei Y,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 72; 454pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu D, Crocker PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Kenny JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 98.8
Matches 418; Conservative
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NI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
                                                                                                                                                                                                 WEI Y.
GREENE J M.
                                                                                                                                                                                                                                                                               RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                             CROCKER P
                                                                                                                                                                                                                                                                                                                                                                                                                                           Young PE,
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or human polymucleotides or a polymucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates
                                                                                                                             EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 318
                                                                                                                                                                                       420
                                                                                                                                                                                                                                                   GVVAVVVFAMLCLLIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 438
VGKAHSDYMLYVYDPPTTIPPPFTTTTTTTTTTTTTTTG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                            EGDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                                                                                                                                                                                   GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
                                              YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human, pain, neuronal tissue, gene therapy,
spinal segmental nerve injury, chronic constriction injury, CCI,
spared nerve injury, SNI, Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Costigan M;
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                                                                                                                                                                                                                                                                                                                                                                                                         ADE54238 standard; protein; 442 AA.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-2002; 2002WO-US025765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GEHO ) GEN HOSPITAL CORP.
(FARB ) BAYER AG.
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the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene the rappy). The sequence presented is a human protein (shown in Table 2 of the specification, but was obtained in electronic form directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                             Query Match
98.7%; Score 2169; DB 7;
Best Local Similarity 98.8%; Pred. No. 2.9e-149;
Matches 418; Conservative 1; Mismatches 4;
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The invention traders to identifying (Wil a candidate pay pathway in polypeptide (human orthologue of genes that modify the p53 pathway in polypeptide (human orthologue of genes that modify the p53 pathway in prospectide (human orthologue of genes that modify the p53 pathway in consolidating with a test agent under conditions, where but for the presence of the test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator (CC contacting a cell defective in p53 function with a candidate modulator in a mammalian cell (comprising contacting the cell with an agent that specifically binds on HM polypeptide comprising an HM amino acid contacting an a patient (comprising contacting the cell with an agent that a specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) a from the patient, (b) contacting the sample with a probe for HM contacting the patient, (b) contacting the sample with a probe for HM contacting the results with a control; and (d) determining whether the comparison indicates a likelihood disease). (M1) is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. CM modulators identified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disorder prognosis is related to the p53 function of the cell; so that that contact prognession colliferation of isorders (c) the p53 pathway of a cell, thus restoring the p53 pathway of a cell, thus restoring conditiention of the cell; so that the cell cycle. (M2) and (M3) are also useful for modulating the p53 pathway of a cell, and (M3) are also useful for modulating the p63 pathway such as angiogenic, and colliferation of the cell cycle. (M2) and (M3) are also useful for treating defects in the p53 pathway such as angiogenic, appoptotic or cell proliferation disorders disorders. The p63 pathway such as 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to an isolated nucleic acid sequence, or its albelic variant, a fragment of the DDNA sequence, or its fragment, domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver discorders such as hepatitis or neural discorders such as Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Greene JM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 2169; DB 8;
Pred. No. 2.9e-149;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 136; 380pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Olsen HS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  liver disorders or neural disorders.
                                                                                                                        98US-0105971P.
99WO-US025031.
2000US-0198407P.
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                                                            18-APR-2001; 2001US-00836353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Young PE, Kenny JJ,
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                                                                                                                                                                                                                                                    NI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
GREENE J M.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 442 AA;
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19-APR-2000;
                                                                                                                            28-OCT-1998;
10-JUL-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                  (WEIY/)
(GREE/)
(RUBE/)
                                                                                                                                                                                                                                                        (/CCIN)
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The invention relates to identifying (M1) a candidate p53 pathway

Example 2; Page 469-470; 678pp; English.

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antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                                                                                                                                                                                                                                           Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53 pathway in Drosophila.
                                                                                                                                                                                                                                                                  Funke RP;
                                                                                        Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic;
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                                                                                                                                                                                                                                                                  Belvin M, Francis-Lang H,
                                                                      Human p53 modifying protein, SEQ ID 156.
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                 ABO07196 standard; protein; 442
                                                                                                                                                                                                                     10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
                                                                                                                                                                                           03-JUN-2002; 2002WO-US017382
                                                                                                                                                                                                            05-JUN-2001; 2001US-0296076P
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                                                                                                                                                                                                                                                (EXEL-) EXELIXIS INC
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                                                                                                                                                       WO200299122-A1
                                                                                                                                     Homo sapiens.
                                                    13-AUG-2003
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                                   ABO07196;
RESULT 10
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GVVAVVVFAMLCLLIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 438
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                                                                                                                                                                                                                                                                                                                      Sequence 442 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Human; p53 modifier; cytostatic; cancer; cytostatic; antiangiogenic; antiapoptotic; p53 pathway; breast cancer; colon cancer; kidney cancer; lung cancer; ovarian cancer; angiogenesis; cell cycle; apoptotic disorder; cell proliferation disorder.
                                                                                                                                                                                          EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
                                                                          YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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                               Length 442;
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represents a human p53 pathway modifying protein
                                6; DB 6;
4.8e-149;
                               Score 2166; DE Fred. No. 4.8e-2; Mismatches
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                               98.68;
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10-OCT-2001; 2001US-0328605P.
15-FEB-2002; 2002US-0357253P.
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                                               Conservative
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                                      al Similarity
417; Conserv
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                Sequence 442 AA;
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The invention relates to identifying (M1) a candidate p53 pathway condulating agent, by contacting an assay system comprising a purified HM collypeptide (human orthologue of ganes that modify the p53 pathway in Drosophila) or nucleic acid with a test agent under conditions, where but correct the presence of the test agent. The system provides a reference activity, and detecting a test agent-biased activity of the assay system. Also included are modulating (M2) a p53 pathway of a cell (comprising contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting a cell defective in p53 function with a candidate modulator contacting the cell with an agent that specifically binds to a HM polypeptide comprising an HM amino acid sequence, where p53 function is restored, modulating (M3) a p53 pathway in a mammalian cell (comprising contacting the cell with an agent that specifically binds an HM polypeptide or nucleic acid) and diagnosing (M4) contacting the patient; (b) contacting the sample with a probe for HM expression; (c) comparison indicates a likelihood disease). (M1) is useful contacting modulators of the p53 pathway. A probe for HM expression is useful for diagnosing breast, colon, kidney, lung and ovarian cancer, in a patient, where the cancer has greater than 25 % expression level. (c) in a patient, where the cancer has greater than 25 % expression level. (c) confidentified by (M1) are useful in a variety of diagnostic and therapeutic applications, where disease or disease or disease or cell conditating the p53 pathway of a cell, thus restoring the p53 function of the cell, so that the cell undergoes normal condition of the cell, so that the cell undergoes normal condition or prograssion the p53 pathway of a cell, thus restoring the p53 pathway such as angiogenic, also useful for treating defects in the p53 pathway such as angiogenic, also useful sor treating defects in the p53 pathway such as angiogenic, represents a hum
Identifying modulators of the p53 pathway for use in treating apoptotic or cell proliferation disorders, comprises screening for agents that modulate activity of a human ortholog of genes that modify the p53
                                                                                                                                                                                                                                                                                                                             Example 2; Page 557-559; 678pp; English.
                                                                                                                                                                                                 pathway in Drosophila.
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ö Length 442; Match 98.6%; Score 2166; DB 6; Local Similarity 98.6%; Pred. No. 4.8e-149; les 417; Conservative 2; Mismatches 4;

120 360 138 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180 TVLVPPRNLMIDIQRDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 198 240 258 300 318 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTDSRAGEEGGIRAVDHAVIG 378 9 78 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 199 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTGAVDHAVIG 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR EGDAFELTCEA1GKPQPVMVTWVRVDDEMPQHAVLSGPNLF1NNLNKTDNGTYRCEASN1 **EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI**

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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also claimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially expressed in neuronal tissue of a first animal expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates the expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polymetides or their antibodies. The polynucleotide or the compound that activity is useful for preparing a medicament for treating pain and a pharmaceutical composition comprising the one or more polymetides or their antibodies. The polymucleotide or the compound that in usual segmental nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed the specification) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed the prin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                         chronic constriction injury; CCI;
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                                                                                                                                                                                                                                                                                       Human Protein AAF69029, SEQ ID NO 7525.
                                                                                                                                                      ADE61605 standard; protein; 442 AA.
                                                                                                                                                                                                                                                                                                                                                         spinal segmental nerve injury; c
spared nerve injury; SNI; Chung.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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spinal segmental nerve injury; chronic constriction injury; CCI;
spared nerve injury; SNI; Chung.
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    Length 442;
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Query Match
98.6%; Score 2166; DB 7;
Best Local Similarity 98.6%; Pred. No. 4.8e-149;
Matches 417; Conservative 2; Mismatches 4;
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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preparing a medicament for treating pain in an animal
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98.6%; Pred. No. 4.8e-149;
live 2; Mismatches 4;
                            invention discloses a composition comprising
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              Claim 1; Page; 1017pp; English.
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Matches 417; Conservative
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                                                                                       EGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 318
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                  YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                                EGDAFELTCEA I GKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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RESULT. 14 AAY17830

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The present invention describes nucleic acids encoding PRO secreted and transmembrane proteins used therapeutically. The PRO proteins have cytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polymucleotides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a RRO protein having homology to complement proteins may be used in inflammatory responses
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 AAPPG--LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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                                                                                                                       Human; PRO protein; tumour necrosis factor family; TNF; cytokine;
secreted protein; transmembrane protein; inflammation disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding PRO secreted and transmembrane proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2149; DB 2;
Pred. No. 8.2e-148;
1; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney AL, Yuan J,
standard; protein; 440 AA.
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970S-0069334P-
970S-0069425P-
970S-0069694P-
970S-006969P-
970S-0069870P-
970S-0069870P-
970S-0069873P-
                                                                                          Human PRO355 protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GETH ) GENENTECH INC
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16-DEC-1997;
16-DEC-1997;
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(GETH ) GENENTECH INC.
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N-PSDB; AAA49563.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO71; PRO323; PRO519; PRO315; PRO341; PRO345; PRO345; PRO345; PRO345; PRO345; PRO345; PRO345; PRO345; PRO345; PRO346; 
                                                                                                                     VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTGAVDHAVIG
                 GVVAVVV FAMLCLI I I I GRY FARHKGTY FTHEAKGADDAADADIAI I NAEGGONNSEEKK
 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
                                                            EGDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
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/note= "Tyrosine kinase phosphorylation site"
365. 371
/note= "N-myristoylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Tyrosine kinase phosphorylation site"

    .15
    'note= "N-myristoylation site"

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/note= "N-glycosylation site"
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/note= "N-glycosylation site"
306. .310
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233. .240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .36
/label= Signal peptide
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/label= Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                       standard; protein; 440
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99. .103
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic
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HB, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
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98.3%; Pred. No. 8.2e-148;
iive 1; Mismatches 4;
     "N~myristoylation site"
/note= "N-myristoylation s: 428. .432
/note= "N-myristoylation s: 430. .434
/note= "N-glycosylation sit
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98US-0112850P.
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Matches 416; Conservative
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Hillan KJ, Kljavin IJ,
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377 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 436

421 EYF 423 |||| 437 EYF 439

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Search completed: June 28, 2005, 09:50:07 Job time: 114.452 secs

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Sequence 111, App Sequence 262, App Sequence 2, Appli Sequence 110, App Sequence 61, App Se

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PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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FION: Molecules Designated B7L1
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Fatent No. US20020164686A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR FILING DATE: 1999-08-05
FRIOR APPLICATION NUMBER: 60/095,663
FRIOR FILING DATE: 1999-08-07
FRIOR FILING DATE: 1998-08-07
SEQ ID NOS:
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                                                                      Query Match
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Matches 423; Conservative
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; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22
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                                                                                                                                                                                                  June 28, 2005, 09:53:58; Search time 108.073 Seconds (without alignments) 1505.131 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

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                                   GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-10-622-237-4
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	SULT 3 -10-302-041-22 Sequence 22, Application US/10302041 Publication Wo. US20030144478A1 GENERAL INFORMATION: APPLICANT: Baum, Peter TITLE OF INVENTION: Molecules Designated B7L1 FILE OF INVENTION: Molecules Designated B7L1 FILE OF INVENTION: MUMBER: US/10/302,041 CURRENT APPLICATION NUMBER: US/09/778,510 PRIOR FILING DATE: 2001-02-07 PRIOR FILING DATE: 1099-08-05 PRIOR FILING DATE: 1099-08-05 PRIOR FILING DATE: 1099-08-06 PRIOR FILING DATE: 1099-08-06 PRIOR FILING DATE: 1099-08-06 PRIOR FILING DATE: 1099-08-07 PRIOR FILING DATE: 1090-08-07 VINDER OF SEQ ID NOS: 22 SOFTWARE: PAT TYPE: PRT ONCANIEM: Mus musculus 100.0%; Score 2197; DB 14; Length 423; Matches 423; Conservative 0; Mismatches 0; Indels 0; Gaps	DD I AAPPGLELELELELSAAALIPIGUSQUEFIKUVIVIEGEVAIISCQUNKSDUSVIQUELN 60 QY 61 PURQTIYPRDFRPLKDSRFQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120	OY 121 TVLVPPRNLMIDIQKOTAVEGEBIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180 121 TVLVPPRNLMIDIQKOTAVEGEBIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180 OY 181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240	241 EGDAFELTCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNI	Qy 301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Oy 361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEGGONNSEEKK 420 	Qy 421 EYF 423
121 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRNFKGNKELKGKSEVEEWSDM 180	301 VGKAHSDYMLVYVDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	EQ ID NO 4 LENGTH: 423 TYPE: PRT ORGANISM: mus musculus	<pre>uery Match</pre>		121 TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRMFKGNKELKGKSEVEEMSDM 180 	181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240 	241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300

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PRIOR APPLICATION NUMBER: 60/490,027
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 423
                                                                                               TYPE: PRT
CORGANISM: mus musculus
US-10-898-408-4
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Publication No. US20050058642A1
GENERAL INFORMATION:
APPLICANT: GALIBERT, Laurent J.
APPLICANT: YAN, Wei
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-4
CURRENT APPLICATION NUMBER: US/10/898,408
CURRENT FILING DATE: 2004-07-23
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                       Sequence 4, Application US/1062237

Sequence 4, Application US/1062237

Publication No. US2004020456811

GENERAL INPORMATION:

APPLICANT: Banni, Peter R.

APPLICANT: Fanniow III, William C.

TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REFERENCE: 2873-US

CURRENT APPLICATION NUMBER: US/10/622,237

CURRENT APPLICATION NUMBER: US/09/778,187B

PRIOR APPLICATION NUMBER: US/09/778,187B

PRIOR FILING DATE: 1999-08-05

PRIOR FILING DATE: 1999-08-05

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.1

SEQ ID NO 4

LENGTH: 423
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ORGANISM: mus musculus
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Best Local Similarity
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                                                                                                                           1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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Query Match 100.0%; Score 2197; DB 17; Length 423; Best Local Similarity 100.0%; Pred. No. 1.2e-153; Matches 423; Conservative 0; Mismatches 0; Indels 0;
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FILE SPERENCE: 21402-21
FILE OF INVENTION NUMBER: US/10/015,115
CURRENT APPLICATION NUMBER: 60/248,153
PRIOR PILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR FILING DATE: 2000-11-17
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Publication No. US20030207800A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Patturajan, Meera
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TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of TITLE OF INVENTION: Using the Same; FILE REFERENCE: 21402-211 CURRENT APPLICATION NUMBER: US/10/115,115 CURRENT PELING DATE: 2002-09-23; PRIOR PELICATION NUMBER: 60/249,598 PRIOR FILING DATE: 2000-11-17 PRIOR APPLICATION NUMBER: 60/249,598 PRIOR FILING DATE: 2001-01-26; PRIOR PELICATION NUMBER: 60/264,240 PRIOR FILING DATE: 2001-01-26; PRIOR PELICATION NUMBER: 60/264,240 PRIOR FILING DATE: 2001-02-02; PRIOR PELICATION NUMBER: 60/269,562 PRIOR PELICATION NUMBER: 60/269,562 PRIOR PELICATION NUMBER: 60/304,348 PRIOR PELICATION NUMBER: 60/304,348 PRIOR FILING DATE: 2001-07-10; PRIOR PELICATION NUMBER: 60/313,283 PRIOR PELICATION NUMBER: 60/304,348 PRIOR FILING DATE: 2001-08-17; PRIOR PELICATION NUMBER: 60/304,348 PRIOR PELICATION NUMBE
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US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. US20020164686A1
; GENERAL INFORMATION:
; APPLICANT:
Baum, Peter
            Padigaru, Muralidhara
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; ORGANISM: Mus musculus
US-10-015-115-113
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100.0%; Pred. No. 1.3e-153;
ive 0; Mismatches 0;
PRIOR APPLICATION NUMBER: 60/264,240
PRIOR FILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR APPLICATION NUMBER: 60/269,562
PRIOR APPLICATION NUMBER: 60/304,348
PRIOR PILING DATE: 2001-07-10
PRIOR PELING DATE: 2001-07-13
PRIOR PELING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
PRIOR PILING DATE: 2001-08-17
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Publication No. US20030207800A1
GENERAL INFORMATION:
APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Servinsen, Bryan D
APPLICANT: Servinsen, Bryan D
APPLICANT: Patturajan, Meera
APPLICANT: Guo, Xiaojia
APPLICANT: Gangolli, Esha A
APPLICANT: Shimkets, Richard A
APPLICANT: Shimkets, Richard A
APPLICANT: Li, Li
APPLICANT: Li, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 423; Conservative
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US-10-015-115-112
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Best Local Similarity
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EYF 444
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79 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 138
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Pred. No. 1.5e-151;
1; Mismatches 4;
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Pred. No. 1.5e-151;
1; Mismatches 4;
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| Sequence 136, Application US/09984130
| Publication No. US20030055231A1
| GENERAL INFORMATION:
| APPLICAMY: Ni et al.
| TITLE OF INVENTION: 12 Human Secreted Proteins
| FILE REPRENCE: PF489P2
| CURRENT APPLICATION NUMBER: US/09/984,130
| CURRENT FILING DATE: 2001-10-29
| PRIOR FILING DATE: 2001-10-39
| PRIOR FILING DATE: 2000-10-30
| PRIOR FILING DATE: 2000-04-19
| PRIOR FILING DATE: 2000-04-19
| PRIOR PELICATION NUMBER: 60/198,407
| PRIOR FILING DATE: 1999-10-27
| PRIOR FILING DATE: 1999-10-27
| PRIOR FILING DATE: 1999-10-27
| PRIOR FILING DATE: 1998-10-28
| NUMBER OF SEQ ID NOS: 149
| SOFTWARE: ParentIn Ver: 2.0
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Best Local Similarity 98.8%;
Matches 418; Conservative
                                                                                                   Query Match
Best Local Similarity 98.8%;
Matches 418; Conservative
   ; ORGANISM: homo sapiens
US-09-778-1878-2
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Pred. No. 1.5e-151;
1; Mismatches 4;
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Fatent No. US20020168712A1
GENERAL INPORMATION:
APPLICANT: Baum, Peter R.
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE REFERENCE: 2873-US
CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 1999-08-05
FRIOR APPLICATION NUMBER: US 60/095,672
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1998-08-05
FRIOR FILING DATE: 1998-08-05
FRIOR FILING DATE: 1998-08-05
FRIOR FILING DATE: 1998-08-05
FRIOR FILING DATE: 1998-08-07
   Molecules Designated B7L1
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR APPLICATION NUMBER: PCT/US99/17906
FRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-05
FRIOR APPLICATION NUMBER: 60/095,663
FRIOR FILING DATE: 1998-08-07
FRIOR PILING DATE: 1998-08-07
FRIOR PILING DATE: 1988-08-07
FRIOR FILING DATE: 1989-08-07
FRIOR FILING DATE: 1988-08-07
FRIO
                                                                                                                       3R: PCT/US99/17906
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Best Local Similarity 98.8%;
Matches 418; Conservative
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ORGANISM: Homo sapien
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US-09-778-187B-2
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TYPE: PRT
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llarity 98.8%; Pred. No. 1.5e-151;
Conservative 1; Mismatches 4;
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Publication No. US2003014478A1

GRNERAL INFORMATION:

APPLICAMT: Baum, Peter

TITLE OF INVENTION: Molecules Designated B7L1

FILE REFERENCE: 2844-08,

CURRENT APPLICATION NUMBER: US/10/302,041

CURRENT APPLICATION NUMBER: US/9/778,510

PRIOR PELING DATE: 2001-02-07

PRIOR FILING DATE: 1999-08-05

PRIOR PELING DATE: 1998-08-05

PRIOR PELING DATE: 1998-08-05

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 20

LENGTH: 442
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US-10-302-041-20
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Best Local Similarity
Matches 418; Conserv
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TITLE OF INVENTION: 12 Human Secreted Protein FILE REPERENCE: PF489P1
CURRENT APPLICATION NUMBER: US/09/036,353A
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR APPLICATION NUMBER: CO105,971
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ' Sequence 136, Application US/09836353A
' Publication No. US20030129685A1
' GENERAL INFORMATION:
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US-09-836-353A-136
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US-09-836-353A-136
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### PEPLICANT: Shillmete, Alterator A PEPLICANT: Shillmete, Alterator A PEPLICANT: Taupier, Raymond J APPLICANT: Li Li Li Muralidhara E PULCANT: Padigaru, Muralidhara TITLE OF INVENTION: Using the Same FILE REPRENCE: 21402-21 CURRENT APPLICATION NUMBER: 60/248,153 PRIOR PELICATION NUMBER: 60/249,58 PRIOR APPLICATION NUMBER: 60/249,58 PRIOR PELING DATE: 2001-01-26 PRIOR FILING DATE: 2001-01-26 PRIOR FILING DATE: 2001-02-02 PRIOR PELICATION NUMBER: 60/269,262 PRIOR PELING DATE: 2001-02-02 PRIOR FILING DATE: 2001-02-02 PRIOR FILING DATE: 2001-02-02 PRIOR FILING DATE: 2001-02-02 PRIOR FILING DATE: 2001-02-03 PRIOR FILING DATE: 2001-02-04 PRIOR FILING DATE: 2001-03-04 PRIOR FILING DATE: 2001-04-05 PRIOR FILING DATE: 2001-04-05 PRIOR FILING DATE: 2001-04-05 PRIOR FILING DATE: 2001-04-05 PRIOR FILING DATE: 2001-07-31 PRIOR FILING DATE: 2001-08-17 PRIOR FILING DATE: 2001-07-31 PRIOR FILING DATE: 2001-08-17 PRIOR FILING DATE: 2001-07-31 PRIOR FILING DATE: 2001-08-17 PRIOR FIL
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     Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
                                                                                                                                                   Gangolli, Esha A
Shimkets, Richard
                                                                                                       Guo, Xiaojia
Kekuda, Ramesha
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Matches 418; Conservative
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
APPLICANT: YOSHINORI, Muxamaki
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JHU1770-1
CURRENT APPLICATION NUMBER: US/10/403,107
PRIOR APPLICATION NUMBER: US/09/930,803
PRIOR FILING DATE: 2001-08-15
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                                                                                                                                                                                      RESULT 13
US-10-403-107-1
Sequence 1, Application US/10403107
Publication No. US20030165974A1
GENERAL INFORMATION:
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Matches 418; Conservative
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ORGANISM: Homo sapiens
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US-10-015-115-111
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                                                                             US-10-363-616-262

Sequence 262, Application US/10363616

Sequence 262, Application US/10363616

Publication No. US20040044181A1

GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

FILE REFERENCE: 21272-113 (793)

CURRENT APPLICATION NUMBER: US/10/363,616

CURRENT APPLICATION NUMBER: 09/654,935

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 490

SEQ ID NO 262

LENGTH: 442
                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
US-10-363-616-262
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439 EYF 441
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Sequence 20, Appl
Sequence 1, Appli
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Sequence 61, P
Sequence 5, Ap
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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Copyright (c) 1993 - 2005 Compugen Ltd.
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S-09-904-920A-84
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US-09-30-80-80-31
US-09-930-80-80-11
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US-09-930-91
US-08-659-914A-5
US-08-659-914A-5
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US-08-778-510-6
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Sequence 9 Sequence 1 Sequence 4 Sequence 2 Sequence 6 Sequence 6

09-949-016-11380

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Sequence 2, Appli Sequence 754, Ap Sequence 6278, Ap Sequence 6215, Ap Sequence 6515, Ap Sequence 3, Appli Sequence 1, Appli Sequence 4, Appli Sequence 2, Appli Sequence 6, Appli Sequence 46, Appli Sequence 46, Appli Sequence 2, Appli			4; Length 423;	APPGLERELLILLISAAALIPTGGGONETKOVTVIEGEVATISCOVNKSDDSVIQLEN 60	AAPPGLRIERLILLILISAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLIN 60 PRRQTIYFRDFRPLKDSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120	18	YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240 	GDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300 	VGKAHSDYMLXVXDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
US-08-429-742-2 US-09-949-016-7564 US-09-723-368-2 US-09-949-016-6518 US-09-949-016-6515 US-09-949-016-6515 US-09-0397-3 US-09-700-397-4 US-09-700-397-4 US-09-700-397-4 US-09-49-016-6728 US-09-49-016-6728 US-09-49-016-6728 US-09-44-657D-46 US-08-414-657D-41 US-08-414-657D-41 US-09-135-080-2 US-09-315-080-2 US-09-316-0576-41	ALIGNMENTS	69 / 7 / 7 / 05 / 05 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 / 0 0 /	Score 2197; DB	AALIPTGGONLFTKDVTVIE	AALIPTGDGQNLFTKDVTVIE RFQLLNFSSSELKVSLTNVSI	AVEGEEI EVNCTAMASKPATT	VPVI CQVEHPAVTGNLQTQRY VPVI CQVEHPAVTGNLQTQRY	VMVTWVRVDDEMPQHAVLSGE 	11 PPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
100.55 100.33	22 Application US/0	, Peter Mol. 284 Mol. 2848 Wol. 2001-1999 UMBER: 1999 UMBER: 1998 S: 2.	23 Mus musculus -22 100.0* Similarity 100.08	APPECERTIFIED AND A STREET OF THE STREET APPECERTATION APPECERTATION AND A STREET A	AAPPGLRLRLLLLLSA PNRQTIYFRDFRPLKDS	TVLVPPRNLMIDIQKOT.	YTVTSQLMLKVHKEDDG YTVTSQLMLKVHKEDDG	EGDAFELTCEAIGKPOP EGDAFELTCEAIGKPOP	VGKAHSDYMLYVYDPPT
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US-09-866-028-61
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APPLICANT:
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GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK
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Pred. No. 1.7e-184;
1; Mismatches 4;
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                                                                                                                                                                                                                                                                       Sequence 20, Application US/09778510
FREERL NO. 6512095
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
FITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION NUMBER:
CURRENT FILING DATE:
FRIOR FILING DATE:

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US-09-930-803-1
'Sequence 1, Application US/09930803
'Patent No. 6596493
'GENERAL INFORMATION:
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Best Local Similarity 98.8
Matches 418; Conservative
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EYF 441
                                                                                                    EYF 423
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LENGTH: 442
TYPE: PRT
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US-09-778-510-20
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APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                  APPLICANT: REEVES, ROGET
TITLE OF INVENTION DIAGNOSIS AND TREATMENT
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin version 3.0
SEQ ID NO 1
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Grimaldi, Christopher
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 98.8
Matches 418; Conservative
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APPLICANT: Botstein, David
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Hillan, Kenneth
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Tumas, Daniel
Wood, William
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Napier, Mary
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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; Patent No. 6642360
; GENERAL INFORMATION:
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APPLICANT:
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FILING DATE: February
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PRIOR
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                                                                                                                                                                                                                                                                                                                                  19 AAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 76
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/866,028 CURRENT FILING DATE: 2001-05-25 PIOT application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                          TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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                                                                                                                                                                                                                                                                2;
                                                                                                                                                                                                                                Length 440;
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                                                                                                                                                                                                                            Score 2149; DB 4;
Pred. No. 9.9e-183;
1; Mismatches 4;
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Patent No. 6734288
GENERAL INFORMAȚION:
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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Best Local Similarity 98.3
Matches 416; Conservative
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APPLICANT: Botstein, David
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Tumas, Daniel
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                                                                                                                                                        TYPE: PRT
CRGANISM: Homo Sapien
US-09-866-028-61
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EYF 439
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US-09-944-457-61
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FILING DATE: NO. 6734288ember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
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APPLICATION WUMBER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
                               CURRENT FILING DATE: 2011-09-26
PRIOR APPLICATION NUMBER: 60/06/318
PRIOR PILING DATE: 2001-05-25
PRIOR PELING DATE: 2001-05-25
PRIOR PELING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/06/9335
PRIOR APPLICATION NUMBER: 60/06/9335
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/06/9, 696
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 16, 1998
PRIOR PELING DATE: PEDEUARY 9, 1998
PRIOR PELING DATE: PEDEUARY 10, 1999
PRIOR PELING DATE: PEDEUARY 10, 1999
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CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
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FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
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PILLING.DATE: March 30, 2000
APPLICATION NUMBER: PCT/USOO/14042
FILING DATE: May 22, 2000
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APPLICATION NUMBER: PCT/US00/03565
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APPLICATION NUMBER: PCT/US00/04414
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FILING DATE: March 2, 2000
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70 DFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNL 129
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; Sequence 5, Application US/08660531
; Patent No. 6221645
; Patent No. 6221645
; Patent Edward Chrysler, Susanna M.S.
APPLICANT: Chrysler, Sukanto
; APPLICANT: Sinha, Sukanto
; APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
от 18/08/659, 984A 07-US/08/659, 984A 07-UUN-1996 N: 436
                                                  APPLICATION NUMBER: US/08/659,984A
CLASSIPICATION NUMBER: US/08/659,984A
CLASSIPICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-07N-1995
ATTORNEY/AGENT INFORMATION:
NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-00281
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
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430 EGSQVNAEEKKEYF 443
                         CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TVLVPPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGDALELTCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNI 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19 AAPPG--LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 76
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APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATE SYSTEM: PC-DOS/MS-DOS
SOFTWARRE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2149; DB 4;
Pred. No. 9.9e-183;
1; Mismatches 4;
              PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
SEQ ID NO 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08659984A Patent No. 5942400 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 98.33
Matches 416; Conservative
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                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CORGANISM: Homo Sapien
US-09-944-457-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
ZIP: 94111-3834
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US-08-659-984A-5
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 LMLKVHKEDDGVPVICQVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELICEAIGKPOPVMVTWVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGK 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 904; DB 3; Length 444;
Pred. No. 5.8e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Mismatches 136; Indels
                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         304 AHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIT
                                                                                                                                                                                                                                                                                                                            15270-002210US
Two Embarcadero Ctr., 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.1%; Score 904;
                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
                                                           ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                         NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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EGSQVNAEEKKEYF 443
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Matches 194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
               San Francisco
California
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                                                                                                                                                                                           FILING DATE:
                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-660-531-5
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RESULT 8 US-08-659-984A-1 ; Sequence 1, Application US/08659984A

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86 SSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIE 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 WVRVDDEM--PQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 WIKDGGELPDPDRMVVSGRELNILFILNKTDNGTYRCEATWIIGQSSAEYVLIVHDVPWTL 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 GQFPLTQNVTVVEGGTAILITCRVDQNDNTSLQWSNPAQQTLYFDDKKALRDNRIELVRAS
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APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
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APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/POCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
40.7%; Score 893.5; DB 2;
Best Local Similarity 45.0%; Pred. No. 4.6e-71;
Matches 188; Conservative 73; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                              ZIP: 94111-3834
COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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STRANDEDNESS: si
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  -DSRAGEEGTIGAVDHAVIGGVVAV 365
                               307 LPTIIPSLTTATVTTTVAITTSPTTSATTSSIRDPNALAGONGP----DHALIGGIVAV 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 YFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 YFGEKRALRDNRIQLVSSTPHELSISISNVALADEGEYTCSIFTMPVRTAKSLVTVLGIP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 RNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKG-KSEVEEWSD--MYTV 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 299 NIVGKAHSDYMLYVYDPPTTIPPPPTTTTTTTTTTTTTILTIITDSRAGEEGTIGAVDHAV 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 IGGIVAFIVFLLILILIFLGHYLIRHKGTYLTHEAKGSDDAPDADTAIINAEGGGGGGDD 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70
                                                                                            36 VVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYF 423
                                                                                                                    11 LLLLLLACSWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        184 TSQLMLKVHKEDDGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTREG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        303 SNMGSYTAYFILNVNDPS---PVPSSSSTY--------HAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         359 IGGVVAVVVFAMLCLLILIGRYFARHKGTYFTHBAKGADDAADADTAIINAEGGONNSEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                       APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REPERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.6%; Score 738.5; DB 4;
38.8%; Pred. No. 2.6e-57;
iive 73; Mismatches 136;
                                                                                                                                                                                                                                                     Sequence 4, Application US/09778510
Patent No. 6512095
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US-09-778-510-6
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320 PPPTTTTTTTTILLIIT
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Best Local Similarity 38.8
Matches 165; Conservative
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                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Baum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
SEQ ID NO 4
LENGTH: 398
                                                                                                                                                                                                            RESULT 10
US-09-778-510-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         146 VNCTAMASKPATTIRWFKGNKELKGKSEVEEWS---DMYTVTSQLMLKVHKEDDGVPVIC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 203 QVEHPAVTGNLQ-TQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVT 261
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363 VVFVTLCSIFLLGRYLARHKGTYLTNEAKGAEDAPDADTAIINAEGSOVNAEEKKEYF 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 GQFPLTQNVTVVEGGTAILTCRVDQNDNTSLQMSNPAQQTLYFDDKKALRDNRIELVRAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27;
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45.0%; Pred. No. 4.6e-71;
Live 73; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Ctr., 8th Floor CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION:
TELEPHONE: 415-326-2400
                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                               Sequence 1, Application US/08660531
Patent No. 6221645
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INFORMATION FOR SEQ ID NO: 1:
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IYPE: amino acid
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Matches 188; Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                    RESULT 9
US-08-660-531-1
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Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
                                                                                                                                Stewart, Timothy A. Tumas, Daniel
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Best Local Similarity 38.3
Matches 162; Conservative
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------HAIIG 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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                                                                                                                                                                                                                                                                                                                                                                                                      LLLLLLLLEACCWAPGGANLSQDDSQPWTSDETVVAGGTVVLKCQVKDHEDSSLQWSNPAQQ 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LLLLLLSAAALIPTG-----DGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQ
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                          DB 4; Length 398;
                                                                                                                                                                                                                                                                                                       33.3%; Score 732.5; DB 4; Length 38.3%; Pred. No. 9e-57; ive 74; Mismatches 144; Indels
Baum, Peter
rTON: Molecules Designated B7L1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             305 MGSYKAYYTLNVNDPS---PVPSSSSTY-----
                                 FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 200-02-07
PRIOR APPLICATION NUMBER: ECT/US99/17906
PRIOR PILING DATE: 1999-08-05
PRIOR PLING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PAtentin Ver. 2.0
                                                                                           PCT/US99/17906
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Patent No. 6635468
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Grimaldi, Christopher J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Firvaroff, Ellen
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
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Best Local Similarity 38.33
Matches 162; Conservative
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                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapien
                         TLE OF INVENTION:
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                                                                                                                                                                                                                    LENGTH: 398
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                                                                                                                                                                                                  SEQ ID NO 6
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65 TIYPRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLV 124
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                                                                                 and Transmembrane Polypeptides and Nucleic
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38.3%; Pred. No. 9e-57;
tive 74; Mismatches 144;
                                                                                                                                     TILLE REPERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT APPLICATION NUMBER: US/09/907,794A

PRIOR PILING DATE: 2000-02-22

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR PLING DATE: 1999-07-08

PRIOR PLING DATE: 1999-07-28

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-08

PRIOR PELING DATE: 1999-09-13

PRIOR PELING DATE: 1999-09-15

PPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PRILING DATE: 1999-11-00
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-30
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NOS: 423
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125 PPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 732.5; DB Pred. No. 9e-57;
              PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-30
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
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Patent No. 6686451
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APPLICANT: Genentech, Inc.,
APPLICANT: Achkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Bernoyers, Luc
APPLICANT: Estrara, Napoleone
APPLICANT: Filvaroff, Ellen
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38.3%;
  FILING DATE: 1999-10-05
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Best Local Similarity 38.3
Matches 162; Conservative
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FILE SPERENEE: 10466-14
CURRENT PAPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09-15
PRIOR PILING DATE: 1999-09-15
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TVTSQLMLKVHKEDDGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTR 240
                                                                               241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
                                                                                                    GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420
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APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
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; Patent No. 6664376
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Grimaldi, Christopher J.
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Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Pan, James
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Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
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Filvaroff, Ellen
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Gerber, Hanspeter
Gerritsen, Mary E.
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APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
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Eaton, Dan L.
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182
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305 MGSYKAYYTLNVNDPS---PVPSSSSTY----
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CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
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Grimaldi, Christopher
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Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Hillan, Kenneth, J
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Gerritsen, Mary E
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Mather, Jennie P.
Pan, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR PELICATION NUMBER: US 60/143, 048
PRIOR PELING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PELING DATE: 1999-07-28
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-09
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PELING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PELING DATE: 1999-09-15
PRIOR PELING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-10-05
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR PELING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30991
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PELING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR PELING DATE: 1999-12-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Acids Encoding the Sar
FILE REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
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PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-07
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
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PRIOR PILING DATE: 1999-07-28
                                                                            Godowski, Paul J.
Grimaldi, Christopher
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Stewart, Timothy A.
Tumas, Daniel
Gerber, Hanspeter
Gerritsen, Mary E
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Mather, Jennie P.
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Best Local Similarity 38.3
Matches 162; Conservative
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SEQ ID NO 84
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84
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65 TIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLV 124

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PPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
                                                                                                                                                                                                                                                                                        246 EGÜKLLIHCEGRGNPVPQQYLWEK-EGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSN 304
                                                                                                                                                                                                                                                                                                                                                                          361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------HAIIG 334
                                             129 IPQKPIITGYKSSLREKDTATINCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTF
                                                                                                                        182 TVTSQLMLKVHKEDDGVPVICQVEHPAVTG-NLQTQRYLEVQYKPQVHIQMTYPLQGLTR
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PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
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125 PPRNLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGK-SEVEEWSD--MY 181
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RESULT 1

probable WRKY-type DNA binding protein At2g38470 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T19C21.4 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date. Os-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T02498; D84805 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,

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TZ6880
hypothetical protein Y43FBC.9 - Caenorhabditis elegans
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C;Accession: T2680
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
A;Reference number: Z20279
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A;Accession: T26880
A;Status: prediminary; translated from GB/EMBL/DDBJ
A;Accession: T26880
A;Status: prediminary; translated from GB/EMBL/DDBJ
A;Residues: 1-108 < WIL>
A;Coss-references: UNIPROT:09xWN0; EMBL:AL032637; PIDN:CAA21621.1; CESP:Y43FBC.9
A;Gene: CESP:Y43FBC.9
A;Gene: CESP:Y43FBC.9
A;Introns: 40/3
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promastigote surface antigen P2 (clone 4.6) precursor - Leishmania major (fragment)
C.Species: Leishmania major
C.Species: Leishmania surface antigen derived from a multigenic family.
J. Biol. Chem. 266, 24477-24484, 1991
A.Title: Variants of a Leishmania surface antigen derived from a multigenic family.
A.Reference number: A41710; MUID:92105105; PMID:1761547
A.Reference number: A41710; MUID:92105105; PMID:1761547
A.Residues: L-327 - AMURA
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A.Residues: L-327 - AMURA
A.Residues: Diocked carboxyl end; glycoprotein; lipoprotein; phosphatidylinositol linkage
F;1-299/Product: promastigote surface antigen P2 (fragment) #status predicted <PSA>
F;300-327/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;000-327/Domain: carboxyl-terminal propeptide #status predicted <CTP>F;000-327/Domain: carboxyl-terminal propeptide amidated carboxyl end (Asp) (in mature form).
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C.Species: Caenorhabditis
R.Chissoe, S.
Submitted to the EMBL Data Library, July 1995
S.Submitted to the EMBL Data Library, July 1995
A.Description: The sequence of C. elegans cosmid EEED8.
A.Reference number: Z18428
A.Reference number: Z18428
A.Reference number: Z1822
A.Reference number: A.Reference of C. elegans cosmid EEED8.
A.Reference number: A.Reference of C. elegans cosmid EEED8.
A.Reference number: Z1842
A.Reference number: Z1842
A.Reference number: Statis Bristol N2
A.Residues: 1-304 ccHI>
A.Residues: 1-304 ccHI>
A.Residues: UND:g733507; PID:g733608; PIDN:AAC46771
A.Resperimental source: strain Bristol N2
C.Genetics:
A.Reference CESP:EEED8.11
A.Herons: Z7/1; Z42/2
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100.0%; Pred. No. 6.9e-05;
iive 0; Mismatches 0; Indels
                                                                 Indels
                        Pred. No. 3.4e-06; 
; Mismatches 0;
100.08; Pre-
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Best Local Similarity 100.
Matches 14; Conservative
                        Best Local Similarity 100.
Matches 15; Conservative
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A;Molecule type: mRNA
A;Residues: 1-518 <MIC>
A;Cross-references: UNIPROT:Q43753; EMBL:Z18952; NID:g18319; PIDN:CAA79477.1; PID:g18320
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A;Molecule type: DNA
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V 100.0%; Pred. No. v...
O; Mismatches
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A;Reference number: S15811
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, Residues: 1-141, I', 143-780, E', 782-885, 'GY'
, Cross-references: EMBL:X51478
Slade, M.B.
                                                                                                                                                                                                                                                                                         459 TTTTTTTTTTI 472
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Best Local Similarity 100.0
Matches 14; Conservative
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                                                                                                                                                                     Query Match
Best Local Similarity
Matches 14; Conserv
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Molecule type: DNA
Residues: 1-889 <LEI>
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C;Species: Dianthus caryophyllus (clove pink)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: 81925
R;Park, K.Y.; Drory, A.; Woodson, W.R.
Bjant Mol. Biol. 18, 377-386, 1992
A;Title: Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase from senesci
A;Reference number: 819252; MUID:92119258; PMID:1731995
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C;Species: Dianthus caryophyllus (clove pink)
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 0.2-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S31442
R;Michael, M.Z.
R;Michael, M.Z.
A;Description: Isolation of petal senescence-associated cDNA clones encoding 1-aminocycl
A;Reference number: S31442
A;Accession: S31442
A, Cross-references: UNIPROT:P27486; EMBL:M66619
C.Superfamally: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F;276/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                              A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: D84805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: At2g38470; T19C21.4
A;Map position: 2
A;Introns: 74/3; 143/3; 321/2; 375/2
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A.Molecule type: DNA
A.Residues: 1-512 <STO>
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A;Residues: 1-516 <PAR>
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A; Status: preliminary
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Richting, B.; Lindher, I.J.; Noegel, A.A.
Richting, B.; Lindher, I.J.; Noegel, A.A.
Mol. Cell. Biol. 10, 3727-3736, 1990
A;Title: The extrachromosomal replication of Dictyostelium plasmid Ddp2 requires a cis-ark A;Reference number: A35679; MUID:90287164; PMID:2192261
A;Accession: A35679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cross-references: UNIPROT:Q23895; GB:MS5298; NID:g167727; PIDN:AAA33191.1; PID:g167728; Slade, M.B.; Chang, A.C.M.; Williams, K.L. Banid 24, 195-207, 1990.
;Title: The sequence and organization of Ddp2, a high-copy-number nuclear plasmid of Di;Reference number: S14202; MUID:91172902; PMID:2077544
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A;Title: A novel multi-domain mucin-like glycoprotein of Cryptosporidium parvum mediates A;Reference number: Z20989; MUID:99066935; PMID:9851610
A;Rccession: T31113
C;Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph-
F;278/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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C;Species: Cryptosporidium parvum
C;Date: 22-0cc-1999 #sequence_revision 22-0ct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rep protein - slime mold (Dictyostelium discoideum) plasmid Ddp2
C;Species: Dictyostelium discoideum
C;Date: 28-Sep-1990 #sequence revision 28-Sep-1990 #text_change 09-Jul-2004
C;Accession: A35679; S14202; $15811
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A;Residues: 1-141,'I',143-353,'A',355-780,'E',782-885,'GY' <SLA2>
A;Cross-references: EMBL:X51478; NID:g7307; PIDN:CAA35843.1; PID:g7308
C;Genetics:
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                                                                                                                                                           Length 518;
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100.0%; Pred. No. 0.00011;
ative 0; Mismatches 0; Indels
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Merczoite surface antigen - malaria parasite (Plasmodium falciparum)
C,Species: Plasmodium falciparum
C,Species: S3310
R,Ramasamy, R.; Ranasinghe, C.
submitted to the BMBL Bata Library, November 1993
A,Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood
A,Reference number: S39310
A,Reference number: S39310
A,Status: preliminary
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-278 *RAM>
A,Residues: 1-278 *RAM>
A,Residues: 1-278 *RAM>
A,Residues: UNIPROT:Q25862; EMBL:X76087; NID:g434996; PID:g836639
C,Superfamily: Epstein-Barr virus nuclear antigen
C,Superfamily: Epstein-Barr virus nuclear antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C.Accession: A45632
A.Fitle: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A.Riachen: R1916
A.Contente: KR1916
A.Contents: KR1916
A.Accession: A45632
                                                                                                                                                                                  A/Accession: T2686
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Accession: T2686
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Status: 1-245 <WIL>
A/Residues: 1-245 <WIL>
A/Cross-references: UNIPROT:Q9XWP2; EMBL:AL032637; PIDN:CAA21609.1; CESP:Y43F8C.5
A/Experimental source: clone Y43F8C
C/Genetics: CESP:Y43F8C.5
A/Introns: 69/3; 163/2
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26868
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
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Best Local Similarity 100.0
Matches 13; Conservative
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                                                                                                                                                         A; Reference number: Z20279
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Best Local Similarity
Matches 13; Conserv
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A;Molecule type: DNA
A;Residues: 1-274 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                              alkaline phosphatase (EC 3.1.3.1), intestinal type II - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004
C;Accession: B56888
R;Engle, M.J.; Alpers, D.H.
Cin. Chem. 38, 2506-2509, 1992
A;Title: The two mRNAs encoding rat intestinal alkaline phosphatase represent two distint A;Reference number: A56888; MUID:93092310; PMID:1458592
A;Accession: B5688
      A;Cross-references: UNIPROT:096503; EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAC9
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S01358
salivary glue protein sgs-3 precursor - fruit fly (Drosophila simulans)
C;Species: Drosophila simulans
C;Species: Drosophila simulans
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01358, A29888
A;Marrin, C;H:; Mayeda, C;A:; Meyerowitz, E.M.
J. Mol. Biol. 201, 273-287, 1988
A;Ritle: Evolution and expression of the Sgs-3 glue gene of Drosophila.
A;Reference number: S01358; MUID:88332966; PMID:3138416
A;Accession: S01358
A;Stetus: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Experimental source: duodenal mucosa
A.Note: sequence extracted from NCBI backbone (NCBIN:121249, NCBIP:121252)
C.Superfamily: Alkaline phosphatase
C.Keywords: intestine; membrane protein; phosphoric monoester hydrolase
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0
                                                              Query Match 3.2%; Score 14; DB 2; Length 1832; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 14; Conservative 0; Mismatches 0; Indels
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A/Cross-references: FlyBase:FBgn0012853
A/Cross-references: PlyBase:FBgn0012853
C/Superfamily: salivary glue protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-217/Product: salivary glue protein sgs-3 #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ?.9%; Score 13; DB 2; Length 67; Local Similarity 100.0%; Pred. No. 0.00016; les 13; Conservative 0; Mismatches 0; Indele
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A,Residues: 1-217 <MAR>
A,Cross-references: UNIPROT:P13729
                                                                                                                                                                                                                        373 PTTTTTTTTT 386
                                                                                                                                                                                         340 PTTTTTTTTT 353
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A,Molecule type: mRNA
A,Residues: 1-67 <ENG>
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A;Cross-references: UNIPROT:Q19269; EMBL:Z73896; PIDN:CAA98057.1; GSPDB:GN00022; CESP:FO<sup>*</sup>
A;Experimental source: clone F09E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-519 <WIL>
A;Cross-references: UNIPROT:Q09592; EMBL:Z46935; PIDN:CAA87049.1; GSPDB:GN00020; CESP:Ml(
A;Experimental source: clone M106
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C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: 818408; 817576
C;Accession: 818408; 817576
Biochim. Biophys. Acta 1090, 299-304, 1991
A;Title: isolation of a mRNA that encodes a putative intestinal alkaline phosphatase reg A;Reference number: $18408; MUID:92062729; PMID:1954251
A;Accession: $18408
A;Status: preliminary
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A;Cross-references: UNIPROT:P51740
A;Note: the correct sequence of residues 144-160 is shown in Fig. 2; the corresponding c R;Yang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
Biochim. Biophys. Acta 1075, 75-82, 1991
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23739
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A;Introns: 47/2; 110/3; 185/2; 231/2; 270/2; 321/2; 347/3; 411/3; 452/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M106.2
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A;Introns: 40/1; 110/3; 141/2; 219/3; 393/1
C;Superfamily: probable zinc metalloproteinase T04G9.2
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.9%; Score 13; DB 2; Le Best Local Similarity 100.0%; Pred. No. 0.00091; Matches 13; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 0.00091;
                                                                         A;Accession: T20658
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
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     R;Percy, C.
submitted to the EMBL Data Library, May 1996
A;Reference number: Z19307
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Matches 13; Conservative
                                                                                                                                                                          A; Residues: 1-517 <WIL>
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A; Residues: 1-551 <STR>
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A;Accession: T22023
A;Accession: T22023
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Restdues: 1-284 <WILD.
A;Restdues: 1-284 <WILD.
A;Cross-references: UNIPROT:Q20202; EMBL:Z69792; PIDN:CAA93666.1; GSPDB:GN00028; CESP:F4
A;Experimental source: clone F40E10
C;Genetics:
C;Genetics:
A;Gene: CESP:F40E10.5
A;Map position: X
A;Introns: 34/3; 76/2; 141/3; 183/3; 240/3
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A;Cross-references: EMBL:AF045635; PIDN:AAC02556.1; GSPDB:GN00022; CESP:C05G6.3
A;Experimental source: strain Bristol N2; clone C05G6
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C;Species: T32949
R;Kemp, K.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid C05G6.
A;Reference number: Z21252
A;Recession: T32949
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA.
                                                                                                                                                                                                                                                                                hypothetical protein F40E10.5 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004
C.Accession: T22023
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20658
                                   Gaps
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                                   0; Indels
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  100.0%; Pred. No. 0.00054; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, Pebruary 1996
                                                                                                                  101 TTTTTTTTT 113
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                                13; Conservative
Best Local Similarity
Matches 13; Conserva
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A;Gene: CESP:C05G6.3
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A, Gene: CESP: F55D12.5
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A;Reference number: 219385
A;Reference number: 219385
A;Accession: T21175
A;Accession: T21175
A;Molecule type: DNA
A;Residues: 1-651 <WIL>
A;Residues: 1-651 <WIL>
A;Cross-references: UNIPROT:019659; EMBL:275538; PIDN:CAA99842.1; GSPDB:GN00019; CESP:F5
A;Experimental source: clone F20G4
R;McMurray, A.
A; Title: Purification and characterization of phytase from rat intestinal mucosa. A; Reference number: $17576; MUD: 91370007; PMID: 1654110
A; Accession: $17576; MUD: 91370007; PMID: 1654110
A; Accession: $17576
A; Molecule type: protein
A; Residues: 20-29 < YAN>
A; Residues: 20-29 < YAN>
A; Note: 10-Val was also found
C; Superfamily: alkaline phosphatase
C; Keywords: phosphoric monoester hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession: T32661
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-560 cHEN>
A;Cross-references: EMBL:AF039047; PIDN:AAB94223.1; GSPDB:GN00023; CESP:K11D12.1
A;Experimental source: strain Bristol N2; clone K11D12
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A;Reference number: Z19606
A;Accession: T22735
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-651 <W12>
A;Residues: 1-651 <W12>
A;Cross-references: EMBL:Z75542; PIDN:CAA99864.1; GSPDB:GN00019; CESP:F55D12.5
A;Experimental source: clone F55D12
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein K11D12.1 - Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: Caenorhabditis elegans Cispecies: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 Cistecssion: T32661 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 Ribenkhaus, 7.; Wohldmann, P.; Gillam, B. Rubmitted to the EMBL Data Library, December 1997 A;Description: The sequence of C. elegans cosmid K11D12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: CESP:K11D12.1
A;Map position: 5
A;Introns: 5/3; 48/3; 90/3; 127/3; 149/3; 190/1; 207/1; 233/3; 264/1; 480/1
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2.9%; Score 13; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00096;
Matches 13; Conservative 0; Mismatches 0;
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Matches 13; Conservative
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Cispecies: Ruminococcus flavefaciens
Cibate: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
Cibacession: S51592
Mol. Gen. S51592
Mol. Gen. Genet. 245, 260-264, 1994
A;Title: Identification of non-catalytic conserved regions in xylanases encoded by the xy, A;Reference number: S51592; MUID:95115675; PMID:7816035
A;Accession: S51592
A;Status: preliminary
A;Molecule type: DMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:052753; EMBL:235226; NID:9516273; PIDN:CAA84537.1; PID:951627; F;42-239/Domain: endo-1,4-beta-xylanase homology <XYL>F;258-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein phosphatase 2C-like protein Spalten - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: T08606
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A;Accession: T08611
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Restidues: L-831 <AUB>
A;Residues: 1-831 <AUB>
A;Coss.references: UNIPROT:015756; EMBL:AF020409; NID:g2425146; PID:g2425147
C;Genetics:
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C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                            Gaps
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A;Map position: 1
A;Introns: 29/2; 54/3; 93/3; 180/2; 236/1; 264/2; 471/3; 486/3; 583/3
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                                                                                      Length 651;
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                                                                                Query Match 2.9%; Score 13; DB 2; Les
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 13; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                          513 TTTTTTTTTT 525
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Best Local S
Matches 13
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В

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phospholipase C - yeast (Candida albicans)
C;Species: Candida albicans
C;Species: Candida albicans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18257
R;Bennett, D.E.; Mccreary, C.E.; Coleman, D.C.
Ricobiology 144, 55-72, 1998
A;Title: Genetic characterization of a phospholipase C gene from Candida albicans: presentiation: T18257
A;Reference number: Z18844; MUID:9812901; PMID:9467900
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AjMolecule type: DNA
AjResidues: 1-1099 - GBEN>
AjCross-references: UNIPROT:013433; EMBL:Y13975; NID:g2462981; PIDN:CAA74308.1; PID:g246
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C.Species: Mus musculus (house mouse)
C.Jate: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
C.Jate: 02-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
C.Jacession: JE0120
R.Haidaris, C.G.; Medzihradsky, O.F.; Gigliotti, F.; Simpson-haidaris, P.J.
A.Hitle: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A
A.Reference number: JE0120; MUID:98344138; PMID:9679195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;566-726/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
                                                                                                                                                                                                                                                                                                                                               R;Wada, M.; Nakamura, Y.
DNA Res. 1, 163-168, 1994
A;Title: NGG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
A;Accession: JC2300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-1083 <WAD>
A;Cross-references: UNIPROT:Q12075; GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06705.1;
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C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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C;Keywords: glycoprotein
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A;Residues: 1-1282 <HAI>
A;Crons-references: GB:AF143102
C;Coment: This protein is a surface antigen of pneumonia.
                                                                                                                                                                                         glycoprotein MSG100 - Pneumocystis carinii
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.00.0%; Pred. No. 0.0017;
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                                                                                                                                                                                    cell surface
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JU2217
major surface glycoprotein 5 - Pneumocystis carinii
C.Species: Pneumocystis carinii
C.Species: Pneumocystis carinii
C.Species: Pneumocystis carinii
C.Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C.Accession: JC2217
R.Kitada, K.; Wada, M.; Nakamura, Y.
DNA Res. 1, 57-66, 1994
A.Title: Multi-gene family of major surface glycoproteins of Pneumocystis carinii: full-A;Recession: JC2217; MUID:96051981; PMID:7584029
A.Accession: JC2217
A;Molecule type: mRNA
A;Residues: 1-1076 <KIT>
A;Cession: JC2217
A;Residues: 1-1076 <KIT>
A;Cession: JC2217
A;Residues: 1-1076 <KIT>
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Reywords: glycoprotein
C;Superfamily: Pneumocystis carinii major surface glycoprotein #status predicted
F;245,471,574,804,837/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S12519

Glutactin - fruit fly (Drosophila melanogaster)

C;Species Drosophila melanogaster

C;Species Drosophila melanogaster

C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C;Accession: S12519

E;Olson, P. F.; Fessler, L. I.; Nelson, R.E.; Sterne, R.E.; Campbell, A.G.; Fessler, J.H.

EMBO J. 9, 1219-1227, 1990

A;Title: Glutactin, a novel Drosophila basement membrane-related glycoprotein with seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-1023 -OLS>
A;Cross-references: UNIPROT:P33438; EMBL:X53286; NID:G297084; PIDN:CAA37380.1; PID:G2970
C;Genetics:
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R;Aubry, L.; Firtel, R.A.
submitted to the EMBL Data Library, August 1997

**Reference number: Z16454

**A;Reference number: Z16454

**A;Reference number: T08606

**A;Reference number: T08606

**A;Reference type: mRMA

**A;Molecule type: mRMA

**A;Molecule type: mRMA

**A;Residues: 1-975 *AUB>

**A;Cross-references: UNIPROT:015743; EMBL:AF019985; NID:g2425120; PID:g2425121

**A;Genetics: A;Genetics:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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100.0%; Pred. No. 0.0016;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0017;
iive 0; Mismatches 0; Indels
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Matches 13; Conservative
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Matches 13; Conservative
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A; Status: preliminary
A; Molecule type: DNA
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C;Species: Dictyostelium discoideum)
C;Species: Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71628; S78068
R;Schuster, S. C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
E;MED J. 15, 3880-3889, 1996
A;Title: The hybrid histidine kinase DokA is part of the osmotic response system of Dicty, A;Reference number: S71628; MUID:96324396; PMID:8670893
A;Accession: S71628
A;Accession: S71628
A;Accession: S71628
A;Kesidues: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Moscule type: DNA
A;Molecule type: DNA
A;Mole
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C;Keywords: phosphoprotein; signal transduction
F;1520-1629/Domain: response regulator homology <RRH2>
F;1568/Binding site: phosphate (Asp) (covalent) #status predicted
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C;Bate: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Date: 19-80235
R;Geissler, H.; Schwarz, E.C.; Soldati, T.
submitted to GenBank, September 1998
A;Description: Identification of two novel and highly divergent myosins in DictyOstellum
A;Reference number: A59235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 2 - slime mold (Dictyostelium discoideum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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A;Molecule type: DNA
A;Residues: 1-149, E',151-219, TRVLKLIQSTNNWIYWY',238-1671 <SCW>
A;Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; PID:g1237202
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.9%; Score 13; DB 2; Length 1737;
100.0%; Pred. No. 0.0025;
tive 0; Mismatches 0; Indels
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F;62-874/Domain: myosin motor domain homology #status atypical
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Best Local Similarity 100.0
Matches 13; Conservative
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T17456
T17456
T27456
T2745
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Molecule type: DNA
A,Residues: 1-1635 <DBL>
A,Cross-references: UNIPROT:017412; EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AABB
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Thirdors

Chitinase (EC 3.2.1.14) - yellow fever mosquito

C;Species: Aedes aegypti (yellow fever mosquito)

C;Date: 20.5ep-1999 #sequence_revision 20.5ep-1999 #text_change 09-Jul-2004

C;Accession: T14075

R;de la Vega, H; Specht, C.A.; Liu, Y.; Robbins, P.W.

Insect Mol. Biol. 7, 233-239, 1997

A;Title: Chitinases are a multi-gene family in Aedes, Anopheles, and Drosophila.

A;Reference number: Z17872

A;Accession: T14075
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2.9%; Score 13; DB 2; Length 1402;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 13; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                           Length 1282;
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A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
                                                                                                                                                                                                                                                                                  0; Indels
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A;Gene: dffA
C;Function:
A;Description: involved in the cell adhesion and cell sorting
                                                                                                                                                                                       Score 13; DB 2; I
Pred. No. 0.0019;
                                                                                                                                                                                  Query Match 2.9%; Score 13; DB 2
Best Local Similarity 100.0%; Pred. No. 0.00
Matches 13; Conservative 0; Mismatches
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Matches 13; Conservative
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C,Accession: A54843
R;Choi, K.W.; Benzer, S.
Cell 78, 125-136, 1994
A;Title: Rotation of photoreceptor clusters in the developing Drosophila eye requires th A;Reference number: A54843; MUID:94306509; PMID:8033204
A;Accession: A54843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolox (Xeywordss: alternative splicing; ATP F;Xeywords: alternative splicing; ATP F;38-301/Domain: protein kinase homoloyy «KIN» F;46-54/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q23993; GB:U12009; NID:g515669; PIDN:AAA21124.1; PID:g532558
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C;Species: Schistosoma mansoni
C;Dete: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: S33640; S27841
R;Webster, P.J.; Mansour, T.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nemo, form I - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 477;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-458 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, September 1999
A;Reference number: 221048
A;Accession: T31631
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone Y57A10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C,Genetics:
A,Gene: CESP:Y57A10A.i
A,Introns: 8/3; 54/3; 112/3; 151/1
                                                                                            134 rrrrrrrrrrr 145
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Best Local Similarity 100.
Matches 12; Conservative
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A;Molecule type: mRNA
A;Residues: 1-477 <CHO>
                                                  340
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                                                                 C. Accession: T18273

R. Zhou, K.; Takegawa, K.; Emr, S. D.; Firtel, R.A.

R. Zhou, K.; Takegawa, K.; Emr, S. D.; Firtel, R.A.

R. Zhou, K.; Takegawa, K.; Emr, S. D.; Firtel, R.A.

R. Zhou, K.; Takegawa, K.; Emr, S. D.; Firtel, R.A.

R. Zhou, K.; Takegawa, K.; Emr, S. D.; Firtel, R.A.

A. Reference number: 206411

A. A. Accession: T18273

A. A. Accession: T18273

A. Status: preliminary; translated from GB/EMBL/DDBJ

A. Molecule type: mRNA

A. Residues: 1-1858 < ZHO>

A. Cross-references: UNIPROT.P54674; EMBL:U23477; NID:g733521; PID:g733522; PIDN:AAA85722
C; Genetics:

A. Gene: PIK2

C; Keywords: phosphotransferase
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S05358
Substitute of the part of
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A;Molecule type: DNA
A;Residues: 1-342 <GAT>
A;Kesidues: 1-342 <GAT>
A;Cross-references: UNIPROF:Q22902; EMBL:U64858; PIDN:AAB18288.1; GSPDB:GN00023; CESP:C1
A;Experimental source: strain Bristol N2; clone C16D9
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C.Species: Dictyostelium discoideum
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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100.0%; Pred. No. 0.0027;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0054;
tive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0032;
ive 0; Mismatches 0; Indels
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R,Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C16D9.
A;Accession: T29557
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Best Local Similarity 100.
Matches 13; Conservative
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Best Local Similarity
Matches 12; Conserv
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Matches 12; Conserv
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A; Residues: 1-183 < SHA>
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A;Introns: 59/2; 316/3
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A;Gene: CESP:C16D9.1
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Indels

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A;Cross-references: UNIPROT:Q9NA83; EMBL:AL117195; NID:e1549729; PIDN:CAB55014.1; CESP:Y.
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                                                C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004 C;Accession: T31631
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hypothetical protein Y57A10A.i - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
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0.0069;
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RESULT 43
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                       A;Title: Conserved classes of homeodomains in Schistosoma mansoni, an early bilateral me A;Reference number: 833640; MUD: 92399260; PMID: 1356008
A;Accession: 833640
A;Molecule type: mRNA
A;Residues: 1-524 <WEB>
A;Residues: 1-524 <WEB>
C;Conserved: WID: 1026601; EMBL: 844191; EMBL: M85305; NID: 9161103; PIDN: AAA29929
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C;Superfamily: Alkaline phosphatase
C;Keywords: intestine; phosphoprotein; phosphoric monoester hydrolase
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A;Molecule type: DNA
A;Residues: 1-530 cGAT>
A;Residues: 1-530 cGAT>
A;Cross-references: UNIPROT:O61209; EMBL:AF040646; PIDN:AAB94986.1; GSPDB:GN00020; CESP:A;Experimental source: strain Bristol N2; clone H17B01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alkaline phosphatase (EC 3.1.3.1), intestinal - mouse
C;Species: Mus musculus (house mouse)
C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 16-Aug-2004
C;Accession: B36307 K.; Ziomek, C.A.; Millan, J.L.
Genomics 8, 541-554, 1990
A;Title: Genomics structure and comparison of mouse tissue-specific alkaline phosphatase
A;Reference number: A36307; MUID:91139124; PMID:2286375
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32812
R;Gattung, S.; Maggi, L.
R;Gattung, S.; Maggi, L.
A;Bestription: The sequence of C. elegans cosmid H17B01.
A;Reference number: Z21227
A;Reference number: Z21227
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                                                                                                                                                                                                                    A,Gene: smox-2
C,Superfamily: homeobox homology
C,Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;424-480/Domain: homeobox homology <HOX>
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A;Map position: 2
A;Introns: 42/3; 58/1; 173/3; 268/2; 308/2; 340/1; 364/2; 387/3
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100.0%; Pred. No. 0.0077;
iive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.0078;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 12; Conservative
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ses 12; Conservative
Dev. 38, 25-32, 1992
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A; Residues: 1-559 < MAN>
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Matches
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Gaps

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A;Reference number: Z19200
A;Accession: T19339
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-680 < WILL>
A;Cross-references: UNIPROY: 093374; EMBL: Z79598; PIDN: CAB01865.1; GSPDB: GN00028; CESP: C44
A;Experimental source: clone C44H4
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A;Reference number: Z19743
A;Accession: T219743
A;Accession: T219754
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-681 - WIL>
A;Crossi-references: UNIPROT:Q9XUS9; EMBL:Z81568; PIDN:CAB04593.1; GSPDB:GN00021; CESP:K06
A;Experimental source: clone K08E3
C;Genetics:
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regulatory protein CRAC - slime mold (Dictyostelium discoideum)
c;Species: Dictyostelium discoideum
c;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
C;Accession: A54795
C;Accession: A54795
A; Kuspa, A.; Lilly, P.J.; Shaulsky, G.; Levin, L.R.; Loomis, W.F.; Devreotes, J. Cell Biol: 126, 1537-1545, 1994
A;Title: CRAC, a cytosolic protein containing a pleckstrin homology domain, is required f
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                                                                                                                                                                                                                               hypothetical protein C44H4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein K08B3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23454
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A;Introns: 26/3; 74/3; 122/3; 216/3; 364/3; 589/3
                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data Library, August 1996
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A;Introns: 36/1; 73/2; 237/3; 361/3; 612/3
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259 TTTTTTTTTT 270
341 TTTTTTTTT 352
                               341 TTTTTTTTT 352
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C;Accession: T30546
R;Mel, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Rifet. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari. A;Reference number: Z17905; MUD:98380374; PMID:9712777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)

[Species in Drosophila melanogaster

C; Species in Drosophila melanogaster

C; Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004

C; Accession: $28399; $18353

R; Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.

R; Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.

A; Title: Laminin A chain: expression during Drosophila development and genomic sequence.

A; Reference number: $28399; MUID:93049203; PMID:1425586
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.Residues: 1-3712 <KUS>
.Cross-references: UNIPROT:Q00174; GB:M96388; NID:g157799; PIDN:AAA28662.1; PID:g157800
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Biol. Chem. 266, 22893-22904, 1991
Filtle: Drosphila laminin A chain sequence, interspecies comparison, and domain struct: Reference number: S18253; MUID:92078147; PMID:1744083
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Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h. Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular; 233-330/Domain: laminin-type EGF-like homology <LEG>.333-400/Domain: laminin-type EGF-like homology <LEG>.
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A;Experimental source: f.sp. hominis
                                                                                                                                                                                                                              major surface glycoprotein - Pneumocystis carinii (fragment)
C;Species: Pneumocystis carinii
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
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:Residues: 1762-3712 <GAR>
:Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
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100.0%; Pred. No. 0.013;
.ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 12; Conservative
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A; Residues: 1-1002 <MEI>
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C;Species: Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A56910
J. Bacteriol. A57: 2943-2951, 1993
A.Filint, H.J.; Martin, J.; McPherson, C.A.; Daniel, A.S.; Zhang, J.X.
J. Bacteriol. 175, 2943-2951, 1993
A.Fitle: A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase domai A;Reference number: A36910
A;Reference number: A36910
A;Status: preliminary
                    A; Accession: A54706
A; Status: preliminary
A; Status: preliminary
A; Residues: 1-698 < NIS>
A; Cross-references: UNIPROT: P35401; GB: U06228; NID: G641960; PIDN: AAA61782.1; PID: G456398
A; Cross-references: UNIPROT: P3341
C; Superfamily: Dictyostelium regulatory protein CRAC
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A;Residues: 1-825 <NHA.
A;Cross-references: UNIPROT:Q17921; EMBL:U51998; PIDN:AAA96080.1; GSPDB:GN00028; CESP:C1
A;Experimental source: strain Bristol N2; clone C12D12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9S310; GB:S61204; NID:g385910; PIDN:AAB26620.1; PID:g385911
A;Note: sequence extracted from NCBI backbone (NCBIN:131871, NCBIP:131872)
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A;Introns: 48/1; 86/3; 137/1; 172/3; 224/3; 253/1; 287/3; 328/2; 454/1; 487/3; 692/1
C;Superfamily: Epstein-Barr virus membrane antigen gp350
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F;259-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
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Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
Cibacesion: T28634
R;Nhan, M.; Hawkins, J.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C12D12.
A;Reference number: Z20656
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100.0%; Pred. No. 0.011;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                            Query Match 2.7%; Score 12; DB 2; Length 698; Best Local Similarity 100.0%; Pred. No. 0.0098; Matches 12; Conservative 0; Mismatches 0; Indels
A;Reference number: A54796; MUID:94375528; PMID:8089184
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A, Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local Similarity 100.
Matches 12; Conservative
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A; Residues: 1-802 <FLI>
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probable auxin-induced protein, 50455-50036 [imported] - Arabidopsis thaliana (Grobable auxin-induced protein, 50455-50036 [imported] - Arabidopsis thaliana (Grouse-ear cress)
C; Date: 0.2-Var-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C; Accession: D86417
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chun, C.W.; Conn, L.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I A; Title: Sequence and analysis of chromsome lof the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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Cypothetical protein SA2097 [imported] - Staphylococcus aureus (strain N315)

Cypecies: Staphylococcus aureus

Cypecies: Staphylococcus aureus

Cypecies: Staphylococcus aureus

Cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

Cypeciesion: C90029

Cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

Cypecies: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

Cypecies: 10-May-2002

Cypecies: 10-May-2002

Cypecies: 10-May-2003

Cypecies: 10-May-2004

Cypecies: 10-May
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T26561
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C;Superfamily: Caenorhabditis elegans hypothetical protein Y9DIA.2
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100.0%; Pred. No. 0.021;
ive 0; Mismatches 0; Indels
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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submitted to the EMBL Data Library, September 1999
A;Reference number: 220233
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A,Experimental source: clone Y24F12A
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Matches 11, Conservative
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Best Local Similarity 100.
Matches 11, Conservative
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A;Molecule type: DNA
A;Residues: 1-139 <STO>
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                     F;2698-3712/Domain: G < DOMG>
F;2698-2863/Domain: repeat G1 < RG1>
F;2698-2863/Domain: repeat G2 < RG2>
F;2864-3048/Domain: repeat G3 < RG3>
F;3049-3223/Domain: repeat G3 < RG3>
F;3049-32200/Domain: repeat G4 < RG3>
F;3334-3528/Domain: repeat G4 < RG4>
F;3529-3712/Domain: repeat G5 < RG5>
F;3529-3712/Domain: repeat G5 < RG5>
F;3629-3712/Domain: repeat G5 < RG5>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ankyrin 3, long splice form - human
NyAlternate names: ankyrin G
Sypecies: Home sapiens (man)
C;Species: Home sapiens (man)
C;Species: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55575
B;Kordeli, B.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A;Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax A;Reference number: A55575; MUID:95138209; PMID:7836469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: mRNA
A,Residues: 1-4377 <KOR>
A,Cross-references: UNIPROT:Q12955; GB:U13616; NID:g608024; PIDN:AAA64834.1; PID:g608025
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C,Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
C,Keywords: alternative splicing; peripheral membrane protein
F;73-105/Domain: ankyrin repeat homology <ANO1.
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.00.0%; Pred. No. 0.04;
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Fil39-171/Domain: ankyrin repeat homology «ANO3»
Fil20-200/Domain: ankyrin repeat homology «ANO3»
Fil20-233/Domain: ankyrin repeat homology «ANO5»
Fil20-233/Domain: ankyrin repeat homology «ANO5»
Fil20-323/Domain: ankyrin repeat homology «ANO5»
Fil20-323/Domain: ankyrin repeat homology «ANO8»
Fil30-333-365/Domain: ankyrin repeat homology «ANO8»
Fil36-398/Domain: ankyrin repeat homology «ANO9»
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F;2116-2697/Domain: I/II, heptad repeats <DOM2>
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A;Cross-references: GDB:424503; OMIM:600465
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F;762-794/Domain: ankyrin repeat homology
F;795-827/Domain: ankyrin repeat homology
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F;465-497/Domain: ankyrin repeat
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A;Residues: 1-373 <AND>
A;Cross-references: EMBL:U55854; PIDN:AAA98013.1; GSPDB:GN00020; CESP:C04G6.2
A;Experimental source: strain Bristol N2; clone C04G6
                                                                                                                                                                                                                                                          CiSpecies: Drosophila yakuba
CiSpecies: Drosophila yakuba
CiSpecies: Drosophila yakuba
CiSpecies: Drosophila yakuba
CiSpecies: Drosophila yakuba
CiSpecies: Drosophila Sequence revision 30-Sep-1989 #text_change 09-Jul-2004
CiAccession: S01360; CiB.; Meyerowitz, E.M.
Mol. Biol. 201, 273-287, 1988
A;Title: Evolution and expression of the Sgs-3 glue gene of Drosophila.
A;Reference number: S01358; MUID:88332966; PMID:3138416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C04G6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T2956
R;Anderson, K; Chissoe, S.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C04G6.
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C;Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: FlyBase:FBgn0013172
C;Superfamily: salivary glue protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-263/Product: salivary glue protein sgs-3 #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.5%; Score 11; DB 2; Length 263; 100.0%; Pred. No. 0.036; ative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels
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A;Introns: 33/3; 85/3; 143/1; 179/1; 226/2; 263/1; 310/2
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A;Residues: 1-263 <MAR>
A;Cross-references: UNIPROT:P13728
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RAD 23B protein - channel catfish
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z20648
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les 11; Conserv
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Best Local
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Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C90029
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-166 <KUR>
A;Cross-references: UNIPROT:Q99RW9; GB:BA000018; PID:g13702104; PIDN:BAB43396.1; GSPDB:GCGenetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T46896

merozoite surface antigen 2 [imported] - malaria parasite (Plasmodium falciparum) (fragm merozoites Plasmodium falciparum) (fragm C;Species Plasmodium falciparum)
C;Species Plasmodium falciparum
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T46896
C;Accession: T46896
Mol. Biochem. Parasitol. 63, 203-212, 1994
Mol. Biochem. Parasitol. 63, 203-212, 1994
A;Title: Plasmodium falciparum genetic diversity can be characterized using the polymorp A;Reference number: Z24128; MUID:94277144; PMID:8008018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-208 <PRE>
A;Cross-references: UNIPROT:Q25949; EMBL:L19048; NID:g438839; PIDN:AAC37195.1; PID:g4388
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C;Species: Caenorhabditis elegans
C;Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T26560
R;Lennard, N.
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A;Introns: 12/2; 55/1; 200/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y9D1A.2
                                                                                                                                                                                                                                                                                                                                                                                  2.5%; Score 11; DB 2; Length 166; 100.0%; Pred. No. 0.025; ive 0; Mismatches 0; Indels
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A,Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-234 <WIL>
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A,Reference number: Z20233
A,Accession: T26560
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A,Map position: 2
C,Superfamily: Epstein-Barr virus nuclear antigen
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Best Local Similarity 100.
Matches 11; Conservative
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Matches 11; Conserv
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A; Molecule type: mRNA
A; Residues: 1-525 <STA>
A; Cross-references: UNIPROT: P17955; GB:X52583; NID: 957640; PIDN: CAA36813.1; PID: 957641
A; Cross-references: UNIPROT: P17955; GB:X52583; NID: 957640; PIDN: CAA36813.1; PID: 957641
Proc. Natl. Acad. Sci. U.S.A. 85, 9595-9599, 1988
A; Title: Partial CDNA sequence encoding a nuclear pore protein modified by O-linked N-ace
A; Reference number: A31762; MUID: 89071743; PMID: 3200844
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R;Cordes, V.; Waizenegger, I.; Krohne, G.
Eur. J. Cell Biol. 55, 31-47, 1991
A;Title: Nuclear pore complex glycoprotein p62 of Xenopus laevis and mouse: cDNA cloning A;Reference number: A56573; MUID:92007945; PMID:1915419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nuclear pore glycoprotein p62.
         A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992 C;Superfamily: octopamine receptor type I
C;Keywords: G protein-coupled receptor
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C;Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 09-Jul-2004
C;Accession: A35596; A31762; Ī55336; S11666
R;Starr, C.M.; D'Onofrio, M.; Park, M.K.; Hanover, J.A.
J. Cell Biol. 110, 1861-1871, 1990
A;Title: Primary sequence and heterologous expression of nuclear pore glycop A;Reference number: A35596; MUID:90277705; PMID:2190987
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C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
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J. Biol. Chem. 266, 11980-11985, 1991
A;Title: The gene encoding rat nuclear pore glycoprotein p62 is intronless.
A;Reference number: ISS336; MUID:91268076; PMID:2050692
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A;Residues: 370,'FR',373-525 <DON>
A;Cross-references: GB:J04143; NID:g623564; PIDN:AAA60741.1; PID:g623565
A;Experimental source: hepatic
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100.0%; Pred. No. 0.065;
ive 0; Mismatches 0; Indels
                                                                                                                                 Length 484
                                                                                                                              DB 2;
0.061;
                                                                                                                              2.5%; Score 11; DB 100.0%; Pred. No. 0.0 tive 0; Mismatches
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A;Molecule type: DNA
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C;Keywords: coiled coil; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear pore glycoprotein p62 - rat
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                                                                                                                                 Query Match
Best Local Similarity
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les 11; Conserv
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S58868
G protein-coupled receptor GCR1 - migratory locust
C.Species: Locusta migratoria (migratory locust)
C.Accession: S58868; S58869
R; Vanden Broeck, J.; Vulsteke.
J. Neurochem. 64, 2387-2395, 1995
A; Title: Characterization of a cloned locust tyramine receptor cDNA by functional expres
A; Recence number: S58868; MUID:95279966; PMID:7760020
A; Roccession: S58868
A; Residues: 1-484 < VANA
A; Residues: 1-484 < VANA
A; Residues: 1-484 < VANA
A; Residues: preliminary, nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-307, 'D', 309-338,'K', 340-484 < VAZ>
A; Cross-references: EMBL:X69521; NID:g871406; PIDN:CAA49269.1; PID:g871407
Riliu, Z.; Li, P.; Kocabas, A.; Karsi, A.; Ju, Z.
Biochem. Biophys. Res. Commun. 289, 317-324, 2001
A;Title: Microsatellite-containing genes from the channel catfish brain: Evidence of tri
A;Reference number: JC7783
A;Contents: Brain
A;Accession: JC7783
A;Alolecule type: mRNA
A;Residues: 1-385 <LIU>A;Cross-references: UNIPROT:Q7LZR8
C;Comment: This protein with a polythreonine tract, has importance in the nucleotide exc
C;Genetics ad33b
A;Introns: 76/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:09GZH9; EMBL:AF026212; PIDN:AAB71300.1; GSPDB:GN00028; CESP:
A;Experimental source: strain Bristol N2; clone F52G3
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C'Jaces 20-Ct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C'Accession: T32467
R'Blanchard, M.; Gattung, S.; Sansone, J.
submitted to the EMBL Data Library, September 1997
A'Description: The sequence of C. elegans cosmid F52G3.
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A;Introns: 31/1; 49/1; 104/1; 117/1; 220/1; 241/2; 307/1; 370/3
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                                                                                                                                                                                                                                                                                                                                                                                                                         2.5%; Score 11; DB 2; Length 385; 100.0%; Pred. No. 0.05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein F52G3.5 - Caenorhabditis elegans
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A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Molecule type: DA
A;Residues: 1-415 <BLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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es 11; Conserv
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A;Residues: 1-649 <WIL>
A;Cross-references: UNIPROT:Q22225; EMBL:Z66500; PIDN:CAA91305.1; GSPDB:GN00020; CESP:T0
A;Experimental source: clone T05C12
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R;Hauser, F.; Hoffmann, W.
J. Biol. Chem. 257, 24620-24624, 1992
A;Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1 A;Reference number: A45155; MUID:93077556; PMID:1447205
A;Accession: A45155
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A;Residues: 1-662 <HAU>
A;Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q83183; EMBL:X77798; NID:g535195; PIDN:CAA54825.1; PID:g5351
C;Superfamily: murine cytomegalovirus gp88 protein
                                                                     gp88 protein - murine cytomegalovirus
C;Species: murine cytomegalovirus
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Accession: 6-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: 847277
R;Thaele, R.; Lucin, P.; Schneider, K.; Koszinowski, U.
Submitted to the EMBL Data Library, Pebruary 1994
A;Reference number: 847277
A;Reference number: 847277
A;Reference preliminary
A;Reference DNA
A;Residues: 1-569 <THA>
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
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A;Introns: 28/3; 48/3; 103/3; 156/3; 192/3; 249/3; 408/3; 495/3; 623
C;Superfamily: Caenorhabditis elegans hypothetical protein T05C12.4
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100.0%; Pred. No. 0.078;
ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein T05C12.4 - Caenorhabditis elegans
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A;Molecule type: DNA
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F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF3>
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translocated intimin receptor Tir [imported] - Escherichia coli (strain O157:H7, substra C; Species: Escherichia coli (5. Spacession: A98199)

R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G. Gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001

A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc A; Reference number: A99629; MUID:21156231; PMID:11258796

A; Accession: A98199

A; Status: preliminary

A; Molecule type: DNA

A; Residues: 1-558 < HAY>
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
                                A;Cross-references: UNIPROT:Q63850; GB:S59342; NID:g236260; PIDN:AAB19953.1; PID:g236261
A;Note: sequence extracted from NCBI backbone (NCBIN:59342, NCBIP:59343)
C;Comment: The amino end of this protein contains O-linked N-acetylglucosamine additions
C;Keywords: glycoprotein; nuclear membrane; peripheral membrane protein
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Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 11; Conservative 0; Mismatches 0
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100.0%; Pred. No. 0.068;
iive 0; Mismatches 0
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Pred. No. 0.068;
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Best Local Similarity
Matches 11; Conserv
A;Residues: 1-526
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Cispecies: Archaeoglobus fulgidus
Cispecies: Archaeoglobus fulgidus
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Cispecies: Archaeoglobus fulgidus
Cispecies: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cispecies: Os-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
Cispecies: Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, S.F.; Steischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N.
Smith, H.O.; Wosser, V. Venter, J.C.
A;Authors: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor
A;Reference number: A69250; MUID:98049343; PMID:9389475
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C;Species: Dictyostelium discoideum
C;Date: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 09-Jul-2004
C;Accession: T1875
R;Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Tile: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Biol A;Reference number: Z06411
A;Accession: T18275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-1093 <ZHO>
A;Cresidues: 1-1693 <ZHO>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-816 <KLE>
A;Cross-references: UNIPROT:028331; GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB89306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U20864; NID:g669026; PID:g669033; PIDN:AAC46666.1; CESP:F32A5.2
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Genetics:
A;Gene: CESP:F32A5.2
A;Introns: 23/1; 58/3; 102/3; 136/2; 277/2; 380/2; 422/1; 502/1; 580/2; 648/1; 935/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Accession: C69493
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Caenorhabditis elegans
C.Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C.Accession: T16232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribauley, A. submitted to the EMBL Data Library, July 1995
submitted to the EMBL Data Library, July 1995
A;Description: The sequence of C. elegans cosmid F32A5.
A;Reference number: Z18482
A;Recession: T16232
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein F32A5.2 - Caenorhabditis elegans
                                                   hypothetical protein AF1948 - Archaeoglobus fulgidus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  338 PPPTTTTTT 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      357 peptitititi 367
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A; Residues: 1-977 < PAU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein 2C13.3 - Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispecies: Caenorhabditis elegans
Cispacies: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
Ciscession: T25937
Ribradshaw, H.
Submitted to the EMBL Data Library, August 1996
A.Poscription: The sequence of C. elegans cosmid ZC13.
A.Reference number: Z20113
A.Reference number: Z20113
A.Reference number: J2937
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-732 - GRA>
A.Residues: 1-732 - 
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A,Gene: CESP:ZC13.3
A,Map position: X
A;Introns: 19/3; 52/2; 86/1; 169/1; 301/1; 365/1; 401/3; 506/2; 528/2; 553/1; 639/1; 683
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A;Cross-references: UNIPROT:Q20908; EMBL:Z74473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F56H9
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hypothetical protein F56H9.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22808
R;Burton, J
R;Burton, J
R;Reference number: 219618
A;Reference number: 219618
A;Reference number: T2808
A;Recession: T2808
A;Recession: T2808
A;Recession: T2808
A;Recession: T2808
A;Cocosion T2808
A;Cocosion T2808
A;Cocosion T2808
A;Cocosion T2808
A;Cocosion T2808
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                                                                                                                                                             Score 11; DB 2; Length 662;
Pred. No. 0.079;
0; Mismatches 0; Indels
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A;Gene: CESP:F56H9.1
A;Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
                                                                                                                                                                 Query Match
2.5%; Score 11; DB 3
Best Local Similarity 100.0%; Pred. No. 0.07
Matches 11; Conservative 0; Mismatches
F;526-566/Domain: trafoil homology <TRF4>
F;573-613/Domain: trafoil homology <TRF5>
F;621-661/Domain: trafoil homology <TRF6>
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Best Local Similarity
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RESULT 68

Gaps

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C;Species: Gallus gallus (chicken)
C;Date: 13.Sep-1996 #text_change 09-Jul-2004
C;Accession: IS1382
C;Accession: IS1382
B;Agsoni, C.L.; Walker, M.B.; Norris, M.D.; Reh, T.A.
Development 120, 769-783, 1994
A;Title: A chicken achaete-scute homolog (CASH-1) is expressed in a temporally and spati:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60095, E;S50126; S44060
R;Swida, U; Lucka, L; Kress, H.
Development 108, 269-280, 1990
A;Title: Glue protein genes in Drosophila virilis: their organization, developmental con-A;Reference number: A60095; MUID:90276249; PMID:2351069
A;Accession: A60095
A;Molecule type: DNA
A;Reference number: A60095; MUID:90276249; PMID:333481; PIDN:CAA53796.1; PID:g433482
A;Cross-reference: UNIPROT:027423; GB:X76203; NID:g433481; PIDN:CAA53796.1; PID:g433482
B;Canio, W.; Swida, U.; Kress, H.
B;Chim: Biophya. Acta 1219, S76-580, 1994
A;Title: Molecular cloning of the Drosophila virilis larval glue protein gene Lgp-3 and A;Reference number: S50125; MUID:95002181; PMID:7918662
A;Reference number: S50125; MUID:95002181; PMID:7918662
                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q90575; EMBL:U01339; NID:g401726; PIDN:AAC59658.1; PID:g4017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Status: preliminary; nucleic acid sequence not shown; translation not shown; Molecule type: DNA
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C;Species: Drosophila melanogaster
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Superfamily: salivary glue protein
C;Keywords: glycoprotein; salivary gland; tandem repeat
C;Reywords: glycoprotein; salivary gland; tandem cspeat
F;1-23/0main: slignal sequence #status predicted csIG-
F;43-86;94-104/Region: 1.residue repeats (T-T-T-T-T-C-P-T-T-T)
F;105-160/Region: 8-residue repeats (T-T-T-T-T-T-P)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 219;
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A;Molecule type: mRNA
A;Residues: 1-219 <JAS>
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100.0%; Pred. No. 0.26;
trive 0; Mismatches
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100.0%; Pred. No. 0.27;
tive 0; Mismatches
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A;Cross-references: FlyBase:FBgn0010305
A;Map position: X16A
                                       chaete-scute homolog - chicken
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Best Local Similarity 100.º
Matches 10, Conservative
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Matches 10; Conservative
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b04327

hypothetical protein MG338 - Mycoplasma genitalium
C;Species: Mycoplasma gentalium
C;Species: Mycoplasma gentalium
C;Species: Mycoplasma gentalium
C;Species: Mycoplasma gentalium
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: D64237
R;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
R;Fraser, C.M.; Venter, J.C.
Science 270, 397-403,
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Title: The minimal gene complement of sequence not shown; translation not shown
A;Recession: D64237
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residuca: 1-1271 cTTGR>
A;Cross-references: UNIPROT:P47580; GB:U39716; GB:L43967; NID:g1046037; PID:g1046042; TI
C;Genetics:
A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics
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submitted to the Protein Sequence Database, August 2000
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N;Alternate names: protein T20K14_210
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51538
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100.0%; Pred. No. 0.14;
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A;Experimental source: cultivar Columbia; BAC clone T20K14
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100.0%; Pre
                                    C;Keywords: phosphotransferase
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A;Introns: 97/3
A;Note: T20K14_210
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A; Note: PIK4
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RESULT 73

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C; Accession: A03329
R; Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
J. Mol. Biol. 168, 765-789, 1983
A; Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila A; Reference number: A92904; MUID:83294545; PMID:6411930
A; Molecule type: DNA
A; Residues: 1-307 cGAR>
A; Molecule type: DNA
A; Residues: 1-307 cGAR>
A; Cross-references: UNIPROT:P02840; GB:X01918; NID:g8581; PIDN:CAA25994.1; PID:g603989
C; Comment: This protein is produced by third-instar larvae.
C; Genetics:
A; Gene: sgs-3
A; Cross-references: FlyBase:FBgn0003373
A; Map position: 3L (88C)
A; Introns: 10/1
C; Superfamily: salivary glue protein
C; Keywords: salivary gland; tandem repeat
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Search completed: June 28, 2005, 10:21:26 Job time : 32.5711 secs

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32 15 3.4 139 2 P90601 33 15 3.4 139 2 Q6WAZ8 34 15 3.4 140 2 Q96ZW5 35 15 3.4 143 2 O15776 36 15 3.4 148 2 O16019	15 3.4 148 2	15 3.4 648 2 1 15 3.4 1015 2 1 14 3.2 1 1015 2 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	14 3.2 107 2 14 3.2 216 2 14 3.2 304 1 14 3.2 341 2	14 3.2 350 2 14 3.2 356 2 14 3.2 364 2	14 3.2 365 2 14 3.2 445 2	14 3.2 512 1	14 3.2 667 2	14 3.2 746 2 14 3.2 746 2 14 3.2 860 2	14 3.2 872 2 14 3.2 874 2	14 3.2 887 2 14 3.2 889 2 14 3.2 895 2	14 3.2 937 2	14 3.2 1728 2 14 3.2 1832 2 14 3.2 1832 2	14 3.2 1893 2	14 3.2 2208 2	14 3.2 3550 2 13 2.9 56 2	13 2.9 67 2	13 2.9 67 2 13 2.9 67 2	13 2.9 71 2 13 2.9 71 2	13 2.9 72 2	13 2.9 106 2	13 2.9 106 2	13 2.9 107 2 13 2.9 107 2	13 2.9 107 2	13 2.9 109 2	13 2.9 115 2 13 2.9 116 2	13 2.9 118 2	13 2.9 119 2 13 2.9 119 2	13 2.9 120 2	13 2.9 123 2	13 2.9 128 2	99 13 2.9 130 2 00 13 2.9 131 2	13 2.9 132 2 13 2.9 139 2	03 13 2.9 143 2 04 13 2.9 150 2	
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lon 5.1.6 05 Compugen Ltd.	14	Search time 113.949 Seconds (without alignments) 1986.316 Million cell updates/	AIINAEGGQNNSEEKKEYFI 442		1612378 segs, 512079187 residues		parameters: 1612378	length: 0 length: 200000000	i Ļistin			results predicted by chance to have a . to the score of the result being printed of the total score distribution.		ALES.	Description		HOH HOH	mus mus	mus	QBK3t6 mus mu		rati	mus	mus mus	mus		עע	061033 trypar	061046 trypar	COWALZ LIYPAL 015774 trypar	O61025 trypar Q962w4 trypar	061021 trypar 061056 trypar	P90603 trypar 061037 trypar	
GenCore version Copyright (c) 1993 - 2005	protein search, using sw model	June 28, 2005, 09:55:58 ;	US-10-622-237-2 442 1 MASVVLPSGSQCAAAAAAA	OLIGO Gapop 60.0 , Gapext 60.0		ο·	hits satisfying chosen			Б	: uniproc_sproc : uniproc_tremb	No. is the number of results p greater than or equal to the s derived by analysis of the to	wiis	SUMMAKIE	Query Match Length DB ID	77.1 442 2	75.1 443 74.9 333	33.9 336 2 33.9 336 2	33.9 417 2	33.9 445 2	33.9 456 2	33.9 476 2 28.7 278 2	28.7 289 2	28.7 306 2	23.5 295 2 19.0 84 2	3.4 74 2	3.4 86 2	3.4 102	3.4 115 2	3.4 122 2	3.4 125 2 3.4 125 2	3.4 126 2 0	3.4 128 2 3.4 139 2	
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C TISSUE=Whole embryo;
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C TISSUE=Whole embryo;
C TISSUE=Whole embryo;
C Saito K., Negama T., Nakamatsu A., Nagai T., Nakamura Y.,
C Saito K., Sugano S., Isogai T.;
C Submitted (NAR-2002) to the EMBL/GenBank/DDBJ databases.
C REMBL; AKO7550; BAC7116; 19-1; 1-1.
C REMPL; SM00259; 19-1; 1-1.
C REMPL; SM00294; 4.1m; 1.
C SMART; SM00294; 107.2; 1...
C SMART; SM00294; 107.2; 1...
C SMART; SM02894; 107.2; 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NNLNKTDNGTYRCEASNI VGKAHSDYMLYVYDPPTTI PPPTTTTTTTTTTTTLTI LTI ITD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                 .
0
                                                                                                                  Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 443;
                                                                                                                                                               Indels
SMART; SM00294; 4.1m; 1.
SMART; SM0408; IGG2; IG LILE;
PROSITE; PS50835; IG LILE; 3.
SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 046B43AA156F6F64 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OMAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein PSEC0200.
Homo sapiens (Human)
                                                                                                               Score 341; DB 2; L
Pred. No. 1.3e-310;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  443 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.1%; Score 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        442
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SEQUENCE 443 AA; 48648 MW;
                                                                                                                  77.1%;
99.8%;
                                                                                                             Query Match 77.1
Best Local Similarity 99.8
Matches 441; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                           121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QBN2F4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBN2F4
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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
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                                 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project.

1. Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

2. Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

2. RMBL; AB092414; BAC66173.1; ---

2. EMBL; AB183402; BAD30021.1; ---

2. EMBL; AB183402; Lggffa.

2. EMBL; AB183402; Lggffa.

2. GO: 0016021; C:integral to membrane; TAS.

3. GO: 00100121; C:integral to wemicle; IDA.

4. GO: GO: 000021; C:synaptic vesicle; IDA.

5. GO: GO: 0016338; P:crotein binding; IPI.

6. GO: 0016338; P:crotein binding; IPI.

7. GO: GO: 0016338; P:crotein binding; IPA.

8. GO: GO: 0016338; P:crotein adhesion; IDA.

8. GO: GO: 0007155; P:crotein adhesion; IDA.

8. GO: GO: 0007155; P:crotein adhesion; IDA.

8. InterPro; IPR007110; III-like.

8. InterPro; IPR007310; III-like.

8. InterPro; IPR007359; Ig-C2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUB=Spleen cell-derived;
Ito A., Koma Y., Nagano T.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interro;

Pfam; PP00047; ig; 2.
SWART; SMO408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 3.
PROSITE; PS50835; IG LIKE; 3.
                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
02-OCT-2004 (TrEMBLrel. 28, Last annotation update)
A secretion form of SgIGSF/TSLC1 (RA175 isoform e).
Name=Igsf4a; Synonyms=RA175, sSgIGSF/STSLC1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 33.9%; Score 150; DB 2; Le Best Local Similarity 100.0%; Pred. No. 1.1e-131; Matches 150; Conservative 0; Mismatches 0;
                                                                                                                                                                           301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
                                                                                                                                      NNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
                                                                                                                                                                                                                                                                                                                                336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DTAVEGEEIEVNCTAMASKPATTIRWFKGN 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090
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01-JUN-2001 (
01-JUN-2001 (
01-OCT-2003 (
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Q9D6E7
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ID 09
AC 09
DT 01
DT 01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
                                                                                                                                                                                                                        TISCQVNKSDDSVIQLLNDNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
                                                                                                                                                                                                                                                                                                                                   RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
                                                                                                                                                                                                                                                                                                                                                                                                            KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
                                                                                                                                                                                                                                                                                                                                                                                                                                           241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
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                                                                                                                                                                                         TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
                                                                                                                                                                                                                                                                                                 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
                                                                                                                   1 MASVVLPSGSQCAAAAAAAAPGLRIRILLILESAAALIPTGGGQNLFTKDVTVIEGEVA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MASVVLPSGSQCAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                                                              1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1to A., Koma Y., Nagano T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
BMBL, AB094146; BAC66179.1; -
InterPro; IPR007110; Ig-1ike.
InterPro; IPR007110; Ig-2.
SMART; SM004009; Ig-2.
SMART; SM004009; IG-2: 1
PROSITE, PS0035; IG LIKE; 3.
SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
100.0%; Pred. No. 3.5e-302; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYD 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        333
                         Matches 332; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 331; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=sTSLC-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Lung;
                                                                                                                                                                                            61
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Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carnincib P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Sogabe Y., Suzuki A., Nishi K., Shinaqawa A., Shiraki T.,
Sano H., Saaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagawi A., Tayawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.;
B Wumantsu M., Hayashizaki Y.;
B Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AK013775; BAB289881; -
B MGD; MGI:189372; Igsfal to membrane; TAS.
GO; GO:0016021; C:integral to membrane; TAS.
RO; GO:0016021; C:synaptic vesicle; IDA.
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C STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=C57BL/6J; TISSUE=Hippocampus;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
A Shibata K., Itoh M., Aizawa K., Kitsunai T., Tashiro H., Itoh M.,
A Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watchiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
A Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
TRIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
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STRANT=CESTBL/6J; TISSUE=Hippocampus;
MEDLINE=CSTBL/6J; TISSUE=Hippocampus;
MEDLINE=CSTBL/6J; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Komo H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team, "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573(2002).
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
MEDLINE=9579253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
  CDNA, RIKEN full-length enriched
                     library, clone:2900073G06 product:immunoglobulin superfamily, member 4, full insert sequence.
                                                                        Mus mušculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musimus; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                             RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE-Hippocampus;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Hippocampus;
The FANTOM Consortium,
musculus adult male hippocampus
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94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
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STRAIN=CS7BL/6; TISSUB=Brain;
STRAIN=CS7BL/6; TISSUB=Brain;
MEDLINE=22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
MEDLINE=22841094; PubMed=12826663; DOI=10.1074/jbc.M305387200;
Shingai T., Ikeda W., Meden S., Morimoto K., Takekuni K., Itoh S., Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.;
"Implications of nectin-like molecule-
2/IGSFARAIN-SSIGSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells.";
J. Biol. Chem. 278:35421-35427(2003).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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GO; GO:0005515; F:protein binding; IPI.
GO; GO:0016338; P:calcium-independent cell-cell adhesion; IDA.
GO; GO:0007415; P:cell adhesion; IDA.
GO; GO:0007416; P:synaptogenesis; IDA.
InterPro; IPR00310; Ig-1ike.
InterPro; IPR0047; ig; 2.
SMART; SM00409; IGC2; 1.
PROSITE; PSSO835; IG LIKE; 3.
SROUBNCE 336 AA; 37157 MW; FF887FAF4EFDF120 CRC64;
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60; 60:0045202; C:synapse; IDA.
60; 60:0008021; C:synapse; IDA.
60; 60:0005515; F:protein binding; IPI.
60; 60:0005515; P:cell adhesion; IDA.
60; 60:0007155; P:cell adhesion; IDA.
60; 60:0007155; P:cell adhesion; IDA.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Nectin-like molecule 2 (RA175 isoform d).
                                                                                                                                                                                                                                                                                                                                                                                                                                           33.9%; Score 150; DB 2; Le
100.0%; Pred. No. 1.1e-131;
iive 0; Mismatches 0;
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InterPro; IPR003598; Ig c2.
InterPro; IPR003585; Neurexin-like.
Pfam; PR00047; Ig; 2.
SWART; SM00294; 4.1m; 1.
SWART; SM00408; IGC2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 417 AA; 45779 WW; 985001;
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Best Local Similarity
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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A FUJITA E. Aikawa K., Momoi T.;

Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

E RMBL; AB183400 BAD2019.1;

R GO; GO: 0016521; C: Synapse; IDA.

R GO; GO: 0008221; C: Synapse; IDA.

R GO; GO: 0005215; F: protein binding; IPI.

R GO; GO: 0005515; F: protein binding; IPI.

R GO; GO: 000515; P: protein binding; IPI.

R GO; GO: 000715; P: protein binding; IDA.

R GO; GO: 000716; P: protein binding; IDA.

R GO; GO: 000716; P: protein binding; IDA.

R GO; GO: 000716; P: protein desion; IDA.

R GO; GO: 000716; P: prodein adhesion; IDA.

R InterPro; IRR00710; Ig-like.

R InterPro; IRR00710; Ig-like.
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33.9%; Score 150; DB 2; Length 417; 100.0%; Pred. No. 1.3e-131; ive 0; Mismatches 0; Indels
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SWART; SM00409; IG; 3.
SWART; SM00409; IGC2; 3.
SWART; PS00369; IGC2; 3.
SROAITE; PS03635; IG LIKE; 3.
SEQUENCE 428 AA; 46903 MW; B10DFF1A2B893573 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                   DTAVEGEEIEVNCTAMASKPATTIRWFKGN 186
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25-OCT-2004 (TrEMBLrel. 28,
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                      Matches 150; Conservative
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Matches 150; Conservative
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           Similarity
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Name=RA175;
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 Query Match
Best Local 8
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445 AA

08K3T6; 01-OCT-2002 (TrEMBLrel. 22, Created)

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97 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 156
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Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu X., Kavalali E.T.,
Sudhof T.C.;
                                                                                                                                                                                                                                                                                                                                                            "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly."; Science 297:1525-1531(2002).
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MEDLINE=22226620; PubMed=12242005; DOI=10.1016/S0378-1119(02)00835-1;
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                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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A Fujita E., Alkawa K., Momoi T.;

L Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.

L SUBMISS AF539424; AANOIG14.1; -..

R EMBL; AB183399; BAD30018.1; -..

R MGD; MG1188272.2; Igsf4a.

GO; GO:00045202; C:synaptic vesicle; IDA.

GO; GO:000512; F:protein binding; IPI.

R GO; GO:000515; P:coll adhesion; IDA.

R GO; GO:0007155; P:graptogenesis; IDA.

R InterPro; IPR00310; Ig-like.

R InterPro; IPR003598; Neurexin-like.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEGNI, PF00047; 19; 2.
SMART; SW00294; 4.lm; 1.
SMART; SW00409; 1GC.2; 1.
SMART; SW00409; 1GC.2; 1.
SEQUENCE 445 AA; 48666 MW; 5B336F23F1877497 CRC64;
01-OCT-2002 (TrEMBLrel. 22, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Synaptic cell adhesion molecule 1 (RA175 isoform c)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tumor suprressor in lung cancer 1.
                                                                           Name=Igsf4a; Synonyms=RA175;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.9%;
Best Local Similarity 100.0%
Matches 150; Conservative
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                               NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                STRAIN=C57BL
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SEQUENCE FROM N.A.
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                    88 BB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 156
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Fukami T., Satoh H., Fujita E., Maruyama T., Fukuhara H., Kuramochi M., Takamoto S., Momoi T., Murakami Y.; "Identification of the Tslc1 gene, a mouse orthologue of the human tumor suppressor TSLC1 gene.";
                                                                                                                                                          Gene 295;7-12(2002).

R MGD; MGI:1889272; 19814a.

R MGD; MGI:1889272; 19814a.

R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0008021; C:integral to weaicle; IDA.

R GO; GO:0008021; C:synapse; IDA.

R GO; GO:0008021; F:protein binding; IPI.

R GO; GO:000715; F:protein adhesion; IDA.

R GO; GO:000715; P:cell adhesion; IDA.

R GO; GO:000716; P:synaptogenesis; IDA.

R InterPro; IPR007110; IQ-1ike.

R InterPro; IPR003598; IQ-2.

R InterPro; IPR003598; Neurexin-like.
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Eukaryota, Metacos, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.9%; Score 150; DB 2; Length 445; 100.0%; Pred. No. 1.4e-131; ive 0; Mismatches 0; Indels
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SMART; SM00408; 1GC2; 1.
PROSITE; PS50835; IG LIKE; 3.
REOUENCE 445 AA; 48664 MW; C5DSA070DAF70E55 CRC64;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.9%;
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Best Local Similarity
Matches 150; Conserv
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08RSM
AC 08RSM
AC 08RSM
AC 08RSM
AC 08RSM
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DE RA175
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TISSUB_TENEINS.

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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                  Length 456;
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Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC078966; AAH78966.1;
InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003598; Ig_C2.
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SWART; SM00409; IG; 3.
SWART; SM00408; IGc2; 3.
PROSITE; PS50835; IG_LIKE; 3.
Hypothetical protein.
SEQUENCE 476 AA; 51853 MW; 486A43D37082C8FE CRC64;
SMART; SM00294; 4.1m; 1.
SMART; SM0408; IG-2; IG-2;
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 456 AA; 49787 MW; 3226E866A4BCIC7F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Rattus norvegicus (Rat).
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                                                                                                                                                                                                                                             33.9%; Score 150; DB 2; L4 100.0%; Pred. No. 1.4e-131; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 186
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Best Local Similarity 100.0
Matches 150; Conservative
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SEQUENCE FROM N.A.
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                                    Q9QYL5
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RESULT 13
Q9QYL5
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                                                                                                                                                             DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
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                                                                                       34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
                                                                                                                  37 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 96
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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             33.9%; Score 150; DB 2; Length 476; 100.0%; Pred. No. 1.5e-131; ive 0; Mismatches 0; Indels
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Pfam, PP00017, ig; 1.

SMART; SM00294; 4.lm; 1.

SMART; SM00408; IGC2; 1.

PROSITE; PS50835; IG_LIKE; 2.

PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 13, Last sequence update) (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 127; DB 2; Le
Pred. No. 3.4e-110;
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100.0%; Pred. No....
0; Mismatches
                                                                                                                                                                                                                                                            DIAVEGEEIEVNCTAMASKPATTIRWFKGN 186
                                                                                                                                                                                                                                                                                                                                                                         278 AA
                                                                                                                                                                                                                                       DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR003585; Neurexin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adhesion protein RA175N.
Name=1gsf4a; Synonyms=ra175n;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                150; Conservative
                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KTDNGTY 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTDNGTY 164
                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000
01-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127;
             Query Match
Best Local S:
Matches 150
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                                                                                                                                                                                                                                                                          157
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Best Local 8
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Matches
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244
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"RA175, which is the mouse ortholog of TSLC1, a tumor suppressor gene
in human lung cancer, is a cell adhesion molecule.";

Exp. Call Res. 287:57-66 (2003).

Exp. Call Res. 287:57-66 (2003).

Exp. Call Res. 287:57-66 (2003).

RMGD; MGI: 1889272; Igst4a.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:000821; C:synaptic vesicle; IDA.

GO; GO:0005515; Piprotein binding; IPI.

RGO; GO:0005515; Piprotein binding; IPI.

RGO; GO:000155; Piprotein binding; IDA.

GO; GO:000155; Piprotein binding; IDA.

GO; GO:0007416; P:synaptogenesis; IDA.

RGO; GO:0007416; P:synaptogenesis; IDA.

RICHEPPO; IPR001598; Ig.22.

RICHEPPO; IPR001598; Neurexin-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQ
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MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8;
Fujita E., Soyama A., Momoi T.;
"RAJTS, which is the mouse ortholog of TSLC1, a tumor suppressor gene
                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00047; ig; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2, 1.
PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 289 AA; 31811 MW; 8D1B836D0565AEA4 CRC64;
                                        OJ-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175B.
Name=Igsf4s, Synonyms=ra175b;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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  PRT;
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Name=Igsf4a; Synonyms=ra175a;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.0
Matches 127; Conservative
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PRELIMINARY;
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                                                                                                                                                                                               Mus musculus (Mouse)
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264 ELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAH 323
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                                                                                                                                                                                                                                                                                                                 245 VHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLN 304
                                                                                                                                                                                                                         38 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ 97
                                                                                                                                                                                         185 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ
                                                                                                                           Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Lsubmitted (APR.1998) to the EMBL/GenBank/DDBJ databases.
Lsubmitted (APR.1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF061266; AA.667243.1; -.
R GO; GO:0016621; C:integral; omembrane; TAS.
R GO; GO:0016222; C:integral; omembrane; TAS.
R GO; GO:0016221; C:integral; omembrane; TAS.
R GO; GO:0016212; C:integral; DA.
GO; GO:0016318; P:protein binding; IPI.
R GO; GO:000115; P:protein binding; IPI.
R GO; GO:0007115; P:protein binding; IPI.
R GO; GO:0007116; P:synaptogenesis; IDA.
R InterPro; IPR00710; III-1ike.
R InterPro; IPR003588; Neurexin-like.
R Pfam; PF00047; ig; 2.
R SMART; SW00294; 4 1m; 1.
R SMART; SW00408; IGC2; 1.
R PROSITE; PSS6835; IGLIKE; 2.
C SEQUENCE 295 AA; 32509 MW; 9DE9D86F6FF6F488 CRC64;
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                                                          Length 306;
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306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                          Query Match 28.7%; Score 127; DB 2; Le Best Local Similarity 100.0%; Pred. No. 3.7e-110; Matches 127; Conservative 0; Mismatches 0;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Mus musculus (Mouse).
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SEQUENCE
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Q6MZK6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     185 ELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 VHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLN 304
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                      Exp. Cell Res. 287:57-66(2003).

R MGD; MGI:1889272; 198f4a.; -
R GO; GO:0016021; C:integral to membrane; TAS.
R GO; GO:0008021; C:integral to membrane; TAS.
R GO; GO:0008021; C:integral to wesicle; IDA.
R GO; GO:0008021; C:inynaptic vesicle; IDA.
R GO; GO:000515; F:protein binding; IPI.
R GO; GO:000155; P:protein binding; IPI.
R GO; GO:0007155; P:cell adhesion; IDA.
R GO; GO:000716; P:synaptogenesis; IDA.
R InterPro; IRR00310; Ig-like.
R InterPro; IRR003598; Neurexin-like.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS06395; IGC2; 2.
SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
in human lung cancer, is a cell adhesion molecule.";
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RAI75C.
Name=158f4a; Synonyms=ral75C;
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.0
Matches 127; Conservative
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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nes 15; Conservative
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Nes 15; Conservative
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                                                                                                                                                   SEQUENCE FROM N.A.
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                                              Name=EMUCe-12;
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Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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EMBL. AR034411, AAC14222.1; -..

InterPro; IPR00458; Tryp_mucin.

Pfam; PF01456; Mucin; 1.
                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                    TISSUE-Human retina;
The German Human cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BX641042; CAE46024.1; -..
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Pred. No. 1.1e-05;
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
                   Hypothetical protein DKFZp686F1789 (Fragment)
Name=DKFZp686F1789;
Homo sapiens (Human).
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100.0%; Pred. No. 1...
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
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SEQUENCE
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Q9TVF2
ID Q9TVF
AC Q9TVF
DT 01-MA
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061023
AC 06102
AC 06102
DT 01-AU
DT 0
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                                     Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBL_TaxID=5693;
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.W., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.W., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).
EMBL, AP036465; AAC14259.1; -.
InterPro; IPR000458; Tryp_mucin.
Pfam, PF01456; Mucin. 1.
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01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
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100.0%; Pred. No. 1.2e-05;
tive 0; Mismatches 0;
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Mucin-like protein (Fragment)
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Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAINCI-Prenner;
MEDLINE-98225151, PubMed-9556557; DOI=10.1074/jbc.273.18.10843;
MEDLINE-98225151, PubMed-955657; DOI=10.1074/jbc.273.18.10843;
MEDLINE-98225151, PubMed-955657; DOI=10.1074/jbc.2773.18.10843;
MINOIA J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of J. Biol. Cham. 273:10843-10850(1998).

EMBL, AF034550, AAC14247.1; -..

EMBL, AF034650, AAC14247.1; -..

PIGMT. PRO10456, Mucin; 1.

SEQUENCE 115 AA; 11729 MW; 321826F0FDEDEFOE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.4%; Score 15; DB 2; Length 115;
100.0%; Pred. No. 1.6e-05;
iive 0; Mismatches 0; Indels
01-MAR-2004 (TrEMBLrel. 07, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Name.emiske protein.
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Query Match
Best Local Similarity 100.0%
Matches 15; Conservative
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Matches 15; Conservative
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                                                                                               Name=EMUCt-7;
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                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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Rhabditidae; Peloderinae; Caenorhabditis.
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Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 15; DB 2; Length 102;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 108;
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Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL AL032637; CAA21621.1; -
PIR; T26880; T26880.
                                                                                                                                                                                                                                                                                                                                                                                    102 AA; 10605 MW; E55212A8D1297E5A CRC64;
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WormDep; Y43FBC.9; CE1907.
Wprobhetical protein.
SEQUENCE 108 AA; 11733 MW; F72D37C2B7432602 CRC64;
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Last annotation update)
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3.4%; Score 15; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 1.5e-05;
Matches 15; Conservative 0; Mismatches 0;
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100.0%; Pred. No.
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MEDLINE=99069613; PubMed=9851916;
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01-NOV-1999 (TrEMBLrel. 12, La
01-JUN-2003 (TrEMBLrel. 24, La
Hypochetical protein Y43F8C.9.
ORFNames=Y43F8C.9;
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006;
Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O.,
Frasch A.C.C.;
"Differential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of
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100.0%; Pred. No. 1.6e-05;
iive 0; Mismatches 0; Indels
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                                                       05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Mol. Biochem. Parasitol. 133:81-91(2004).
EMBL; AY298908; AAQ74639.1; -.
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Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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STRAIN=C1-Brenner;
MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
                                                                                                                                                                            Length 125;
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  Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF398553; AAK64016.1; -. InterPro: IPR000458; Tryp_mucin. Pfam; PF01456; Mucin; 1. Pfam; PF01456; Mucin; 1. SEQUENCE 125 AA; 12870 MW; 2188F87FA6C71F07 CRC64;
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Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AF036409; AAC14220.2; -.
InterPro; IFP00458; Tryp_mucin.
Pfam; PF0456; Mucin; 1.
SEQUENCE 126 AA; 13023 MW; F3858008D3C768A1 CRC64;
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J. Biol. Chem. 273:10843-10850(1998).
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"Two distinct groups of mucin-like genes are differentially expressed in the developmental stages of Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 93:01-114(1998).

EMBL, AF027872; AAC48350.1; -
InterPro; IRR000458; Tryp_mucin.
Pfam; PF01456; Mucin. 1.2.

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NCBI_TaxID=5693;
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MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'Oroso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.M., D'Oroso I., Aslund L., Sanchez D.O., Frasch A.C.;
Genes having hypervariable regions.";
J. Bail. Chem. 273.10843.10850(1998).
Briol. Arc14224.1;
InterPro; IPR00458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.7
SEQUENCE 125 AA; 12894 MW; 2DF1A14AA29A8604 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein MUC-loc6.
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Pred. No. 1.7e-05;
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Di Noia J.M., Frasch A.C.C.;
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nes 15; Conservative
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Name=EMUCe-9;
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                                                          FROM N.A.
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                                                                                    STRAIN-Berkeley;
NCBI_TaxID=5693;
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PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O., Frrasch A.C.C.; Prasch A.C.C.; "Differential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trypanosoma cruzi.
Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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STRAIN=Berkeley;
MEDLINE=97113006; PubMed=8943259; DOI=10.1074/jbc.271.50.32078;
Di Noia J.M., Pollevick G.D., Kavier M.T., Previato J.O.,
Mendoca-Previato L., Sanchez D.O., Frasch A.C.;
"High diversity in mucin genes and mucin molecules in Trypanosoma cruzi.";
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100.0%; Pred. No. 1.9e-05;
Live 0; Mismatches 0; Indels
                                           J. Biol. Chem. 273:10843-10850(1998).

EMBL; AF036427; AAC14349.1; -.

Interpro; IPRO00458; TYP_mucin.

Pfam; PF01456; Mucin; 1.

SEQUENCE 139 AA; 14311 MW; 9236BB31B85992B7 CRC64;
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InterPro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 139 AA; 14395 WW, D7DCECEE2FF8A26B CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MUC. Y-1 protein.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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Mol. Biochem. Parasitol. 133:81-91(2004).
EMBL; AY298908; AAQ74640.1; -.
InterPro; IPR000458; Tryp_mucin.
                         genes having hypervariable regions.";
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Matches 15; Conservative
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Matches 15; Conservative
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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NCBI_TaxID=5693;
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MEDLINE=9825151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of
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                                                                                                          D'Orso I., Di Noia J.M.;
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF036463; AAC14257.2; -.
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EMBL; U62550; AAC47402.1; -.

InterPro; IPRO00458; Tryp_mucin.

Pfam; PF01456; Mucin; 1.

SEQUENCE 128 AA; 13207 MW; 30ACB7C3F8E633B4 CRC64;
                                                                                                                                                                           Interpro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 126 AA; 13049 MW; F399BC78D3C768A1 CRC64;
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J. Biol. Chem. 273:10843-10850(1998)
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01-AUG-1998 (TrEMBLrel. 07,
01-MAR-2004 (TrEMBLrel. 26,
Mucin-like protein.
Name=EMUCe-37p20;
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Best Local Similarity 100.(
Matches 15; Conservative
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01-MAY-1997 (TrEMBLrel.
                                                                                       STRAIN=Cl-Brenner;
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Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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                                                                                                                                                                                                                                    MEDLINE-98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
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SEQUENCE 148 AA; 15212 MW; ABF2E02CF13EA059 CRC64;
                                                                                         Created)
Last sequence update)
Last annotation update)
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Pred. No. 2e-05;
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J. Biol. Chem. 273:10843-10850(1998).
EMBL; AF036407; AAC14218.1; -.
InterPro; IPR00458; Tryp_mucin.
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01-AUG-1998 (TrEMBLrel. 07,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trypanosoma cruzi."
                                                                                                                                Mucin-like protein.
Name=EMUCe-1;
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nes 15; Conserv
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                         STRAIN=Cl-Brenner
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                                                                  061019
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Matches
                                        RESULT 36
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                                                    0610190
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MEDLINE-98324409; PubMed-9662032; DOI=10.1016/S0166-6851(98)00025-5;
Freitzes-Uunior L.H., Briones M.R., Schenkman S.;
"Two distinct groups of mucin-like genes are differentially expressed in the developmental stages of Trypanosoma cruzi.";
MOI. Biochem. Parasitol. 93:101-114(1998).
EMBL; AF027874; AAC48352.1;
InterPro: IPR000458; Tryp_mucin.
                                                                                                                                                                                                                                                            Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5693;
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.larity 100.0%; Pred. No. 1.9e-05;
Conservative 0; Mismatches 0; Indels
                                    3.4%; Score 15; DB 2; Length 139;
100.0%; Pred. No. 1.9e-05;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 15; DB 2; Length 143;
Pred. No. 1.9e-05;
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                                                                                                                                                                                                                                                                                                                         STRAIN-C1-Brenner;
Di Noia J.M., Frasch A.C.C.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF398552; AAK94015.1;
InterPro; IPR00458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 139 AA; 14277 MW; 79A799908014DD21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                      AMERICAN PF01456; Mucin; 1. SEQUENCE 140 AA; 14343 MW; 5CC154418F2A58CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 AA; 14610 MW; 6AB6E7B7FA85F58B CRC64;
                                                                                                                                                                                                        01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein MUC-locs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein (Fragment).
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100.0%; Pred. No. 1...
0; Mismatches
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                                                                                       339 PPTTTTTTTTT 353
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                                                                                                              71 PPTTTTTTTTT 85
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Best Local Similarity 100.8
Matches 15, Conservative
                                                  Local Similarity 100.
18s 15; Conservative
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NON TER 143
SEQUENCE 143 AA: 1461
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Matches 15, Conserv
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                                    Query Match
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Matches
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Q962W5
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Gaps

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0; Indels

Length 148;

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PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006;
Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O.,
Frasch A.C.C.;
"Differential accumulation of mutations localized in particular
domains of the mucin genes expressed in the vertebrate host stage of
                                                                                                                                                   Trypanosoma cruzi.
Bukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Biochem. Parasitol. 133:81-91(2004).

EMBL; A7298908; AAQ74638.1; -.

Interpro; IPRO00458; TryP_mucin.

Pfan; PF01456; Mucin; 1.

SEQUENCE 148 AA; 15203 MW; C7F2E02CF13554E6 CRC64;
                                                         05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
         148 AA.
PRT;
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RESULT 38 Q25334

Pred. No. 6.9e-05;

100.08;

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Best Local Similarity
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Mus musculus (Mouse). 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000008H23 product:hypothetical Acyl-COA dehydrogenase/Glutamic acid-rich region containing protein, full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.P., Giligo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
                                                                     Surface antigen P2 (Fragment).
Leishmania major.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
NCBI_TaxID=5664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                         Murray P.J., Spithill T.W.; "Variants of a Leishmania surface antigen derived from a multigenic
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                                                                                                                                                                                                                                                                                                                                                                                                               3.4%; Score 15; DB 2; Length 327;
100.0%; Pred. No. 3.8e-05;
iive 0; Mismatches 0; Indels
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Baumgart C.;
Bunmgart C.;
BuncyBase; DDB0168226; JC2V2_0_00892.
InterPro; IPR008654; IWS1_C.
InterPro; IPR08654; IWS1_C.
Bypothatical protein.
SEQUENCE 648 AA; 73372 MW; 2879FE40FCD76D3E CRC64;
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SEQUENCE 327 AA, 34229 MW; 2571B35B6577E715 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insert sequence.
Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 327 AA.
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                                                                                                                                                                                                                                                                                 InterPro, IPR009030, Grow fac_recept.
InterPro, IPR006210, IEGF.
InterPro, IPR001611; LRR.
                                                                                                                                                                                                                        family.";
J. Biol. Chem. 266:24477-24484(1991)
EMBL, X57135; CAA40414.1; --
PIR; S20074; S20074.
 PRT;
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                                                                                                                                                            STRAIN=V121;
MEDLINE=92105105; PubMed=1761547;
                                                                                                                                                                                                                                                                                                                         InterPro; IPR007090; LRR plant.
Pfam; PF00560; LRR 1; 3.
SMART; SM00181; EGF; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPTTTTTTTTTTT 197
                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Conservative
PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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08648
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AC 08648
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DT 01-JU
DT 01-JU
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RA SIGNI
RA LICHMA
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RA SEQUE
RA SUBMI
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3.4%; Score 15; DB 2; Length 648;

Query Match

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Ebkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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  Gaps
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Histidine kinase
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Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC115594; AAO51537.1; -.
GO; GO:0016301; F:kinase activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                             Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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  Mismatches
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                                                                                                       130 PPPTTTTTTTTT 144
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15; Conservative
                                                   338 PPPTTTTTTTTTTT
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ઠ 셤 RESULT 42
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D01050
AC 06105
AC 06105
DT 01-AU
DT 01-

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
                                                                                                                                  Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                          "Genome sequence of the nematode C. elegans: a platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein EEED8.11.
Poly-Thr.
; 60C223B88F534151 CRC64;
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100.0%; Pred. No. 0.00031;
                              01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein EEED8.11 in chromosome II precursor.
ORFNames-EEED8.11;
Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
-!- SIMILARITY: Some, to C.elegans R13F6.2 and R13F6.8.
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Last annotation update)
304 AA.
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                                                                                                                                                                                                                      STRAIN=Bristol N2;
MEDLINE=99069613; PubMed=9851916;
The C. elegans sequencing consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; T15922; T15922.
Wormbase; Washeneolou(7139; EEEDB.11.
WormPep; EEEDB.11; CE01884.
InterPro; IPR001304; Lectin_C.
SMART; SM00034; CLECT; 1.
Hypothetical protein; Signal.
SIGNAL.
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304 AA; 32982 MW;
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Matches 14; Conservative
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STANDARD;
                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                      NCBI_TaxID=6239;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
                                                                                                                                                                                                                                                                      Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma
NCBI_TaxID=5693;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.2%; Score 14; DB 2; Length 216;
100.0%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CL-Brenner;
DI Noia J.M., Frasch A.C.C.;
Di Noia J.M., Frasch A.C.C.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF798551; AAK94014.1;
InterPro; IPR000458; Tryp_mucin.
Pfam. PP01456; Mucin; 1.
SEQUENCE 216 AA; 21815 MW; 01C85738541BB6C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0962W6;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mucin-like protein MUC-loc2.
                                                                                                                                                                                  01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                    107 AA
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                                                                                                                                                                      Created)
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              341 TTTTTTTTTTT 354
                                34 TTTTTTTTTT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                    Name=EMUCt-9;
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YOOB_CAEEL
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Matches

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RESULT 43
0962W
10 0962W
AC 0962W
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DE MUCIN
OX NCEI
CX NCEI
RN (1)
RN (1)
RN (1)
RN SEQUE
RC STRAI
RA SIN
RA SUMMI
DR EMBL;
DR EMBL;
SO SEQUE
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Matches

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Gaps

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A Ballew R.M., Agadyan A., An H.J., Andrews Frannkoon C., Beadley B.M., Beeson K.Y., Beand A., Baxendale J., Bayraktarogu L., Beaaley B.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Bucker J., Bordet B., Botchan M.R., Bouck J., Broteter A., Chandra I., Beartis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Raburtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Raber B., Delher A., Deng Z., Mays A.D., Dew I., Dietz S.M., A Dodson K., Doup L.E., Downes M., Digan-Rocha S., Dunkov B.C., Dunn P., Burbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., Rolodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M., Glasser K., Andrei B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Allal M., Kalush F., Karpen G.H., Re Z., Kennison J.A., Ketchum K.A., Allali M., Marphy B., Marryby L., Morberson D., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B.E., McIntosh T.C., McLeod M.P., McPherson D.L., Raben D.L., Rabin M., Nelson D.L., Mobarry C., Morris J., Moshrefi A., Raington K.A., Nixon K., Nusny D.M., Nelson D.L., Raington K.J., Nixon K., Scheeler F., Shen H., Raington K., Saunders R.D., Scheeler F., Shen H., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Strakman D.A., Wainspon M., Strong R., Sun E., Strakman D.A., Wainspon M., Strong R., Sun E., Strakman D.A., Wainspon M., Strong R., Sun K., Waissarman D.A., Wainspon M., Strong S., Tao, X., Nakon S., Rain M., Strong S., Zhu X., Smith H.O., RW Zheng X.H., Zaveri J.S., Zhong F.N., Zhong W., Zhan M., Zhan G., Zhan G., Zhan G., Zhan G., Zhan G., Zhan S., Zhu X., Smith H.O., R., Fering E.W., Rubin G.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=2242605; PubMed=12537568; MEDLINE=2242605, PubMed=12537568; MEDLINE=2242605, PubMed=12537568; MEDLINE=2242605, PubMed=12537568; Medline=1 D.A., Kronmiller B., Frise B., Hodgson A., Patel S., Adams M., Champe M., Dugan S.P., Frise B., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Park S., Peiffer B.D., Richards S., Sodergren B.J., Neinstas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaminker J.S., Bergman C.M., Kromiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
  Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Annotation of the Drosophila melanogaster euchromatic genome: a
Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22426070; PubMed=12537573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 287:2185-2195(2000).
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Submitted (SEP-2002)
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Gaps
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Name=agCGS2059; ORFVAmes=ENSANGC0000015451;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AgCP8129 (Fragment).
Name=agCGS119; ORFNames=ENSANGG00000007781;
Anopheles gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TAXID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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Pred. No. 0.00035;
            EMBL, AE003751; ANN14054.1; --
EMBL, AE003751; ANN14054.1; --
ENBL, AE003751; Castracellular; IEA.
GO; GO:0008051; F:chitin binding; IEA.
GO; GO:0008061; F:chitin binding; IEA.
InterPro; IPR002557; Chitin bind PerA.
InterPro; IPR002025; GMP/Cyt_deam.
Ffam; PF01607; CBM 14; 1.
SNART; SM00494; ChEBD2; 1.
PROSITE; PS09040; CHIT BIND II; 1.
PROSITE; PS09040; CHIT BIND II; 1.
EROSITE; PS09040; CHIT BIND II; 1.
EROSITE; PS09031; CYT GMP DEAMINASES; UNKNOWN 1.
SEQUENCE 341 AA; 38627 Mv; A935A06377885A15 CRC64;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            350 AA; 37565 MW; F4765CEF710FA9A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                       350 AA.
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GO; GO:0016020; C:membrane; IEA.
Interpro; IPR002000; Lamp.
PRINTS; PR00336; LYSASSOCTDMP.
PROSITE; PS00310; LAMP_1; UNKNOWN_1.
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01-MAR-2004 (TrEMBLrel. 26, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last anno
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Matches 14; Conservative
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Best Local Similarity 100.0'
                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Man G.J., Nielsen C.B., Butler J., Rehman B.,
Blkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endizzi M.,
A Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
Roy A., Foley K., Naylor J., Thomann N., Barrett R., Greenberg D.,
A Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
A Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S.,
A Farden O., Plamann M., Seller S., Dunlap J., Nedford A., Aramayo R.,
A Yarden O., Plamann M., Seller S., Dunlap J., Radford A., Aramayo R.,
A Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
Nature O.O. 0.000 (2003).
                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                    Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
                                                                                                                                                                                                                                                                             Length 356;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 364;
                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                              356 356
356 AA; 39404 MW; C51B095A700DEC22 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .l protein.
364 AA; 40946 MW; ECIDF588FE543738 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                         Query Match
3.2%; Score 14; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 14; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 14; DB 2; Le
Pred. No. 0.00036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AABX01000420; EAA29686.1; -.
InterPro; IPR008547; DUF829.
Pfam; PF05705; DUF829; 1.
                                                                                                                                                                          EMBL; AAAB01008986; EAA00798.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.2%; Scc.
100.0%; Pred
0; M
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                                                                                                                                                                                                                                                                                                                                                                                           316 Prirrirririr 329
                                                                                                                                                                                                                                                                                                                                                      340 PTTTTTTTTTT 353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTTTTTTTTTT 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein.
Name=NCU09343.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
tes 14; Conserv
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5141;
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                                                            STRAIN=PEST
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NON TER
SEQUENCE
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RESULT 48

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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckrer G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A. "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 which is
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                Q869R5;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.2%; Score 14; DB 2; Length 365;
100.0%; Pred. No. 0.00037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family Si.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry win preliminary data.

EMBL; AAABO1008905; EAA09700.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AA; 39409 MW; 132DEB0383959196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0004263; F:chymotrypsin activity; IEA.
GO; GO:0008233; F:chymotrypsin activity; IEA.
GO; GO:0004295; F:trypsin activity; IEA.
GO; GO:0006508; F:trypsin activity; IEA.
INTERPRO; IPR001254; Peptidase SI.
InterPro; IPR001314; Peptidase SIA.
InterPro; IPR001014; Peptidase SIA.
InterPro; IPR00100903; Pept Ser Cys.
                                                                                                                                                                   Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
365 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=agCG50324; ORFNames=ENSANGG0000010153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AC116957; AAO52509.1; -. GO; GO:0016301; F:kinase activity; IEA.
                                                                                                                                                     Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00722; CHYMOTRYPSIN
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DNA_BIND
DOMAIN
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                                         SEQUENCE
                                                                                                                                                                                                                1A1C_DIACA

ID 1A1C_DIA

AC P274\overline{8}6;
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SH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUNCTION: Transcription factor. Interacts specifically with the W box (5'-(T)TGAC(C/T)-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).
SUBCELLUIAR LOCATION: Nuclear (Probable).
SIMILARITY: Belongs to the WRKY group I family.
SIMILARITY: Contains 2 WRKY domains.
                                                                                                                                                                                                                                            10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 44, Last sequence update)
10-0CT-2004 (Rel. 44, Last annotation update)
05-JUL_2004 (Rel. 44, Last annotation update)
Probable WRXY transcription factor 33 (WRXY DNA-binding protein 33).
Name=WRXX33 OrderedLocusNames=At2g38470; ORFNames=T19C21.4;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. Columbia;
MEDLINE-20083487; PubMed=10617197; DOI=10.1038/45471;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shean T.P., Benito M.-I., Town C.D.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA-binding; Nuclear protein; Repeat; Transcription regulation.
DOMAIN 123 135 Thr-rich.
                                                                                                                 .;
0
                                                                                 3.2%; Score 14; DB 2; Length 445; 100.0%; Pred. No. 0.00043; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Arabidopsis thaliana transcription factor WRKY33.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                       445 AA; 48897 MW; 48A34474F5414364 CRC64;
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                          Hydrolase; Protease; Serine protease.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Columbia, TISSUE=Flower;
Lippok B., Somssich I.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF509499; AAM34736.1; -. EMBL; AC004683; AAM14994.1; -.
                                                                                                                                          340 PITITITITIT 353
                                                                                                                                                                      Prirrirririr 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003657; WRKY. Pfam; PF03106; WRKY; 2.
                                                                                                Best Local Similarity 100. Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50811; WRKY; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 402:761-768(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; T02498; T02498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            thaliana.";
                                        NON TER
SEQUENCE
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                                                                                   Query Match
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                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1-carboxylate + methylthioadenosine.
-!- COFACTOR: Pyridoxal phosphate.
-!- PATHMAY: Ethylene biosynthesis; first (rate-limiting) step.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent aminotransferase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-AUG-1992 (Rel. 23, Last sequence update)
05-UTL-2004 (Rel. 44, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) (ACC
1-aminocyclopropane-1-carboxylate synthase) (S-adenosyl-L-methionine methylthioadenosine-1yase).
Name=ACS2; Synonyms=CARACC;
Caryophyla; eudicotyledons; core eudicots;
Caryophyllaceae; Dianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyridoxal phosphate (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P18485; IIAX.
InterPro; IPR001176; ACC synthase.
InterPro; IPR004839; Aminotrans I/II.
InterPro; IPR004839; NHtrans I I/II.
InterPro; IPR004839; NHtrans I I I I.
Pfam; PF00155; Aminotran I 2; I.
PRINTS, PR00753; ACCSVNTRĀSE.
PROSITE; PS00105; AA TRANSERE CLASS I; I.
Ethylene biosynthesië; Fruit Tipening; Lyase; Multigene family;
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100.0%; Pred. No. 0.00049;
ive 0; Mismatches 0; Indels
                                                                                                                           DB 1; Length 512; 0.00049;
                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Poly-Thr.
C31BA10732E940AE CRC64;
                                               481 Asn-rich.
56457 MW; 8F19CBE41BC18662 CRC64;
                                                                                                                                                                             0
                                                                                                           3.2%; Scot.
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                            517 AA.
WRKY 1.
WRKY 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92119258; PubMed=1731995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                517 AA; 58057 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1992 (Rel. 23, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.04;
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                                                                                                                                                                                                                                                      122 PITITITITI 135
                                                                                                                                                                                                                                 340 PITITITITIT 353
                                                                                                                        Query Match
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.
Les 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
  235
414
481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S19252; S19252.
  171 2
349 4
461 4
512 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyridoxal phosphate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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Gaps

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043753

RESULT 53

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Archaea; Buryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S. Buburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:000453; F:hydrolase activity, hydrolyzing O-glycosyl .
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
Pfam; PF00553; CBM 2; 1.
Pfam; PF005704; Glyco.hydro_18; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidaa; Drosophilidae; Drosophila.
                                      Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 717;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 14; DB 2; Length /1./; Pred. No. 0.00065;
                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-VC1 / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AE010231; 1LG2.
73337 MW; 92F583112C839992 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete proteome. SEQUENCE 717 AA; 78635 MW; PBCB55B9C850E38B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                        DB 2; Le
0.00061;
                                                                                                                                                                                                                                                        717 AA.
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                                Query Match 3.2%; Score 14; UD Best Local Similarity . 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                Created)
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                                                                                                                    340 PITITITITIT 353
                                                                                                                                         PTTTTTTTT 353
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                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=PF1233;
                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
667 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=2261;
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  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query. Match
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Matches
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                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
1-aminocyclopropane 1-carboxylate synthase (EC 4.4.1.14).
Dianthus caryophyllus (Carnation) (Clove pink)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Caryophyllaceae; Dianthus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Michael M.Z.;
Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.
EMBL; Z18952; CAA79477.1; -.
PIR; S31442; S31442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Alveolata, Apicomplexa, Coccidia, Eimeriida,
Cryptosporidiidae, Cryptosporidium.
CCBI_TaxID=5807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 518 AA; 58003 MW; EF8B8BC8F03A493E CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00753; ACCSYNTHASE.
PROSITE; PS00105; AA_TRANSFER_CLASS_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0016829; F:Lyase correctivit GO; GO:0008483; F:transaminase activit GO; GO:0009688; F:biosynthesis; IEA. InterPro; IPR001176; ACC_synthase. InterPro; IPR004839; Aminotrans I_II. InterPro; IPR004838; NHtransf_1ES.
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InterPro; IPR000458; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, 01-0CT-2003 (TrEMBLrel. 25, Hypotheical protein. 0RFNames=1MB.826;
                  341 TTTTTTTTTT 354
                                                     458 TTTTTTTTTTT 471
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Genome Res. 0:0-0(2003).
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                                                                                                                                                       PRELIMINARY;
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ses 14; Conserv
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RESULT 54 Q7YYY0

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Matches

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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases

FlyBase;

SHRES

EMBL, AE003835; AAF59007.1; -. FlyBase; FBgn0033361; CG8181. SEQUENCE 746 AA; 78593 WW; FB6F9F8DA3027334 CRC64;

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Ballew R.M., Basua A., Baxendale J., Baytaktaroglu L., Beasley E.M.,
Beeson K.Y., Bennos P.V., Bernan B.P., Bhandara D., Bolshakov S.,
RA Beeson K.Y., Bennos P.V., Bernan B.P., Bradktaroglu L., Beasley E.M.,
RA Bertis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley C., Perraz C., Ferraz S., Pleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferratera S., Pleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
Alali M., Kalush F., Karpen G.H., We Z., Kennison J.B.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
R., Mattei B., McIntcosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Pacher F., Shen H.,
RA Balazzolo M., Fittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,
RA Reington D.R., Nalson K.A., Nixon K., Nuskern D.R., Puri V., Ranker B.C., Siden-Kiandon S., Pollard J., Puri V., Smith T.,
RA Shier B.C., Siden-Kiandon S., Simpson M., Skupski M.P., Smith T.,
RA Palazzolo M., Pittman G.S., Pan S., Capeler F., Shen H.,
Rayersa B., Tector C., Turner R., Venter B., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhong S., Yao Q.A., Yeh R.,
Rayers B.W., Rubin G.M., Venter J.C.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong S., Yao Q.A., Yeh S.,
Rayers G., Siden-Graden G., Scheeler F., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

MEDLINE=22446065; PubMed=12537568;

MEDLINE=22446065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Painskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

Weinstock G., Scherer S.E., Myers B.W., Gibbs R.A., Rubin G.M.,

"Finishing a whole-genome shotgun: Release 3 of the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; The transposable elements of the Drosophila melanogaster euchromatin:
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MEDILINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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to the EMBL/GenBank/DDBJ databases

Submitted (SEP-2002)

FlyBase;

[6] SEQUENCE FROM N.A.

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BEDLINE-297140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260;
Shaulsky G., Escalante R., Loomis W.F.;
"Developmental signal transduction pathways uncovered by genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DICTORNES; DEBGLISTITY) MAKA.

GO; GO:0005524; F: PTF binding; IEA.

GO; GO:0004674; F: PTCtein serine/threonine kinase activity; IEA.

GO; GO:0004713; F: PTCtein serine/threonine kinase activity; IEA.

GO; GO:0016740; F: PTCTEINE SERINE kinase activity; IEA.

GO; GO:0016468; P: PTCTEIN amino acid phosphorylation; IEA.

InterPro; IPR0011009; Kinase like.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR002290; Ser_thr_pkinase.

InterPro; IPR001245; Tyr_pkinase.

PEGM; PF00069; Pkinase; 1.
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100.0%; Pred. No. 0.00076;
   Length 746;
                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRODOSO TYRKINASE.

PRODOM; PRODOSOUS, TYRKINASE.

PRODOM; PRODOSOUS, ETKC; L.

PROSITE; PSOULOS; PROTEIN KINASE ATP; UNKNOWN 1.

PROSITE; PSOULOS; PROTEIN KINASE DOM; 1.

PROSITE; PSOULOS; PROTEIN KINASE ST; UNKNOWN 1.

ATP-binding; Hypothetical protein; Kinase; Transferase.

SEQUENCE 860 AA; 97812 MW; 20AEDBC81826DC21 CRC64;
                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).
   DB 2; Le
                                                                                                                                                                             860 AA.
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   3.2%; Score 14; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches
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01-NOV-1998 (TrEMBLrel. 08,
01-MAR-2004 (TrEMBLrel. 26,
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Query Match 3.2% Best Local Similarity 100.0° Matches 14; Conservative
                                                                                                                                                                                                                                                         Hypothetical protein mkcA.
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Length 874;

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Mol. Cell. Biol. 10:3727-3736(1990).
EMBL; M55298; AAA33191.1; -.
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3.2%; Scu-
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SEQUENCE FROM N.A.
STRAIN=WS380B;
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                                                                                                                                                                   STRAIN=DG61;
MEDLINE=98139494; PubMed=9472083;
Shammat I.M., Gonzales C., Welker D.L.;
"Dictyostelium discoideum nuclear plasmid Ddp6 is a new member of the Ddp2 plasmid family.";
                                                                                                                                                                                                                                                                                                                                             MEDLINE=99169343; PubMed=10087212; DOI=10.1006/plas.1998.1385; Gonzales C.M., Spencer T.D., Pendley S.S., Welker D.L.; "Dgpl and Dfpl are closely related plasmids in the Dictyostelium Ddp2 plasmidy."; Plasmily."; Plasmid #41:89-96(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=DG61;
MEDLINE=92390516;
Yin Y., Welker D.L.;
"Dictyostelium giganteum plasmid Dgpl is a member of the Ddp2 plasmid
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MEDLINE=99189343; PubMed=10087212; DOI=10.1006/plas.1998.1385;
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                                                                           Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=5787;
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NCBI_TaxID=79012;
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PIR, P00444; P00444
InterPro; IPR007778; Dict REP.
Pfam, PF05086; Dicty_REP; 1.
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Plasmid Dfp1.
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                                                 Dictyostelium giganteum.
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Plasmid 28:37-45(1992)
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STRAIN=WS380B;
MEDLINE=91172902; PubMed=2077544;
Slade M.B., Chang A.C.M., Williams K.L.;
"The sequence and organisation of Ddp2, a high copy number plasmid of Dictyostelium discoideum.";
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MEDLINE=91172003; PubMed=2077545;
MEDLINE=91172003; PubMed=2077545;
Chang A.C.M., Slade M.B., Williams K.L.;
Identification of the origin of replication of the eukaryote Dictyostelium discoideum nuclear plasmid Ddp2.";
Plasmid 24:208-217(1990).
EmBL; X51478; CAA35843.1 j.-
DictyBase; DDB000133; Ddp2-rep.
InterPro; IPR007778; Dict_REP.
Pfam; PF05086; Dicty REP; 1.
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100.0%; Pred. No. 0.00078;
ative 0; Mismatches 0; Indels
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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Eukaryosta: Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Score 14; DB 2; Le
Pred. No. 0.00077;
0; Mismatches 0;
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
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Best Local Similarity 100.(
Matches 14; Conservative
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                                                                                                      Nature 418:79-85(2002).
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                                                                                                                                                                    Gaps
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01.JUN-2003 (TrEMBLrel. 24, Last sequence update)
01.JUN-2003 (TrEMBLrel. 26, Last amnotation update)
Similar to Arabidopsis thaliana (Mouse-ear cress). Hypothetical 79.2
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                                                                                                                     Score 14; DB 2; Length 889;
Pred. No. 0.00078;
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100.0%; Pred. No. 0.00079;
ive 0; Mismatches 0; Indels
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EMBL, AC116986; AAO51907.1; -.
DictyBase; DDB0168226; JC202 0 00892.
InterPro; IPR006768; CwfJ C I.
InterPro; IPR006769; CwfJ C I.
Fam; PF04677; CwfJ C I. I.
Pfam; PF04677; CwfJ C I. I.
                 11 protein.
895 AA; 104485 MW; 94895D6A284E3384 CRC64;
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
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Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
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  PIR; A35679; A35679
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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100.0%; Pred. No. 0.00082;
tive 0; Mismatches 0; Indels
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
05-007-2004 (TrEMBLrel. 28, Last annotation update)
CG3297-PB (REL6941p).
Name=BG:DS01523.2; ORFNames=CG32972;
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SMART; SM00382; AAA; 1.
ATP-binding; Hypothetical protein.
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Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
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EMBL; AE003642; AAN10874.1; -.
EMBL; BT010014; AAQ22483.1; -.
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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GO:0007155; P:cell adhesion; IEA.
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Nucleotide exchange
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                                                                                                                         Length 1166;
                                      SMART; SM00554; FAS1; 2.
PROSITE; PS50213; PAS1; 2.
SEQUENCE 1166 AA; 128893 MW; DD25F816E75F7CF9 CRC64;
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PROSITE; PS00659; GLYCOXYL HYDROL F5; UNKNOWN_1.
PROSITE; PS50018; RAS GTPAŽE ACTIV 2; 1.
SEQUENCE 1728 AA; 192334 MW; D8B4425042FF48EA CRC64;
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Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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100.0%; Pred. No. 0.00098;
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InterPro; IPR001547; Glyco hydro_5.
InterPro; IPR001936; RasGAP.
Pfam; PF04784; DUF547; 1.
Pfam; PF00616; RasGAP: 1.
InterPro; IPR000782; BIGH3 F.
Pfam; PF02469; Fasciclin; 2.
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                                                                                                                                                                                                        340 PTTTTTTTTT 353
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HSSP; P21359; 1NF1.
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Best Local Similarity 100.0
Matches 14; Conservative
                                                                                                                                          Local Similarity 100.
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Submitted (MAR-2003) to
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Q8SSU4;
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RADINE=20196006; Pubmed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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Burtis K.C., Bussam D.A., Burler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cavley B., Daynes M., Lugan R., Libarser K.,

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Randra S., McHalley R., McHolley R., Willeysen R., Sprier B., Syriskas R., Tector C., Turner R., Venter R., Wang S., Wang S., Wang S., Wa
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                                                                                                                           Barnes D.A., Bonnin A., Huang J.X., Gousset L., Wu J., Gut J., Doyle P., Dubremetz J.F., Ward H., Petersen C.; "A novel multi-domain mucin-like glycoprotein of Cryptosporidium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                 3.2%; Score 14; DB 2; Length 1832;
100.0%; Pred. No. 0.0014;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                     1832 AA; 192653 MW; 590E6ACB16BBE0D2 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1853 AA.
                                                                                                                                                                                                   parvum mediates invasion.";
MOL. Biochem. Parasitol. 96:93-110(1998).
EMBL; AFF06665; AAC98153.1; -.
PIR; T31113; T31113.
Cryptosporidiidae; Cryptosporidium
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Best Local Similarity
Matches 14; Conserv
                                                                        SEQUENCE FROM N.A.
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                              NCBI_TaxID=5807;
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                                                                                                                                                                                                                                                                                                        SEQUENCE
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Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                MEDLINE=22426065; PubMed=12537568;
MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe W., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Patel S., Peiffer B.D., Richards S., Sodergren E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., "Finiabing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E.; "The transposable elements of the Drosophila melanogaster euchromatin:
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Mistra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Mistra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P.,
Bettenourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.C., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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100.0%; Pred. No. 0.0015;
ive 0; Mismatches 0; Indels
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1853 AA; 201677 MW; 518684872828D53F CRC64;
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Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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GO; GO:0007155; P:cell adhesion; IEA.
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-MRA:2004 (TrEMBLrel. 26, Last ann
Hypothetical protein BG:DS01523.2.
Name=BG:DS01523.2; ORFNames=CG32972;
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Pfam; PF02469; Fasciclin; Z.
SMART; SM0554; FAS1; Z.
PROSTIE; PS50213; FAS1; Z.
SEQUENCE 1853 AA; 201677
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Matches 14; Conservative
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A Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,

A Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,

A Farfan D.B., Galle R., George R.A., Harris N.L., Hoskins R.A.,

RA Houston K.A., Hummasti S.R., Karra K., Kaarney L., Kim E., Lee B.,

RA Houston K.A., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

RA Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,

RA Sethi H., Snir B., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,

RA Zieran L.L., Rubin G.M.;

RA Zieran L.L., Rubin G.M.;

RA Sieran B.M., Asf44859 1;

B. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

BRBL; AE003409; AAF44859 1;

BR CG, GO:0007155; P:cell adhesion; IRA.

DR InterPro; IPR011009; Kinase_like.
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                                                                                                                                                                             ABDLINE-99403001; PubMed=10471707;
Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T.,
Boyle C., Galle R., George R., Harrisel G., Harvey D.,
Boyle C., Galle R., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K.
Celniker S., Rubin G.M.;
The exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Eukaryota; Mycetozoa; Dictyostelium, Dictyostelium.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Bypothetical protein.
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SMART, SM00554; FAS1; 2.
PROSITE; PS50213; FAS1; 2.
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nes 14; Conserv
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STRAIN=AX4;
Baumgart C.;
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                                                                                       NCBI_TaxID=7227;
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086HN4
1D Q86HN4
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCB_TaxID=10116;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.

-- SIMILIARITY: Belongs to the ubiquitin-conjugating enzyme family.

EMBL; AL116957; AA052538.1; -.

HSSP; PS1966; ICAZ.
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Culp D.J., Latchney L.R., Fallon M.A., Denny P.A., Denny P.C.,
Couwenhoven R.I., Chuang S.;
"The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
Relationship to SMGC.";
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                                                                                                 GO; GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR002083; MATH.
InterPro; IPR0008974; Traf like.
InterPro; IPR000689; UBQ_conjugat.
Pfam; PF00917; MATH; 4.
ProDom; PD000461; UBC conjugat; 1.
ProDom; PD000461; UBC conjugat; 1.
SMART; SM00012; UBCC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2208;
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PROSITE; PS50127; UBIQUITIN_CONJUGAT_2; 1.
Hypothetical protein.
SEQUENCE 2208 AA; 250169 MW; CF247BA9B0E2205C CRC64;
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
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100.0%; Pred. No. 0.0017;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 3295 AA.
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EMBL, BRO05556; DAA05596.1, -.
InterPro; IPR005207; Cys knot.
InterPro; IPR009041; PMP_SGCI.
InterPro; IPR001007; VWF_C.
SMART; SM00041; CT; 1.
SWART; SM00214; VWC; 2.
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Matches 14; Conservative
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les 14; Conserv
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Elchinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=V333;
Hoffmann B.H., Silveira L.A., Tonhosolo R., Pereira F.J.,
Ribeiro W.L., Tonon A.P., Marrelli M.T., Kawamoto F., Ferreira M.U.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AY008396; AAG30717.1; -.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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100.0%; Pred. No. 0.00074;
tive 0; Mismatches 0; Indels
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EMBL; AC116551; AA052164.1; -.
Hypothetical protein.
SEQUENCE 56 AA; 6096 MW; 5D1F0B92FE6D17C7 CRC64;
                                                                                                                                                                                                                                01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Dictyostellum discoideum (Slime mold).
Bukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 2 (Fragment).
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STRAINE-prototype form 1;
MEDLINE=95107908 form 1;
Linke M.J., Smullan A.G., Stringer J.R., Walzer P.D.;
Linke M.J., Smullan A.G., Stringer J.R., Walzer P.D.;
"Characterization of multiple unique cDNAs encoding the major surface glycoprotein of rat-derived Pneumocystis carinii.";
Parasitol. Res. 80:478-486 (1994).
                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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STRAIN-BN/SaNHsdMCW;

A Culp D.J. Latchney L.R., Fallon M.A., Denny P.C.,
Couwenhoven R.I., Chuang S.;

The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
I "The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
I Relationship to SWGC.";

Physiol. Genomics (Online) 0:0-0(2004).

EMBL, BXO0555; DAAO5595.1; -.

R InterPro; IPR006529; VWC out.

R InterPro; IPR006529; VWC out.

R InterPro; IPR001846; VWF_D.

R Pfam; PF00186; VWD; 3.

R SMART; SW00215; VWD; 3.

R SMART; SW00216; VWD; 3.
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3550 AA; 354982 MW; 108149CCSF35DBFC CRC64;
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                                                               Created)
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOT-2002 (TrEMBLrel. 22, Last annotation update)
Major surface glycoprotein (Fragment).
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PRT; 3550 AA
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                               Q66GT4;
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
25-OCT-2004 (TrEMBLrel. 28,
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PRELIMINARY;
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STRAIN=V57;
Hoffmann E.H., Silveira L.A., Tonhosolo R., Pereira F.J.,
Ribeiro W.L., Tonon A.P., Marrelli M.T., Kawamoto F., Ferreira M.U.;
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AY008394; AAG30715.1; -.
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SEQÜENCE 67 AA; 5706 MW; 6C5E89980203990C4 CRC64;
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O95UY6;
O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Merozoite surface protein 2 (Fragment).
Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NOB1_TAXID=5833;
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Search completed: June 28, 2005, 10:20:28 Job time : 119.949 secs

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GenCore version 5.1 Copyright (c) 1993 - 2005 Com	OM protein - protein search, using sw model	Run on: June 28, 2005, 09:54:53; Search time (without a 1429, 691 M	US-10-622-237-2	ct score: 442 nce: 1 MASVVLPSGSQCAAAAAAAA		Gapop 60.0 , Gapext 60.0	Searched: 2105692 seqs, 386760381 residues	Word size : 0	Total number of hits satisfying chosen parameter	Minimum DB seq length: 0	seq length:	Post-processing: Listing first 150 summaries	ام م	1: geneseqp1980s:* 2: geneseqp1990s:*	٠		6: geneseqp2003as:* 7: geneseqp2003bs:*	: geneseqp2004s	No. is t	score greater than or equal to the score o and is derived by analysis of the total sc	Sarawaiis	*	Result Query No. Score Match Length DB ID	100 0 442 3	442 100.0 442 3	442 100.0 442 3 442 100.0 442 5	442 100.0 442	442 100.0 442 6 442 100.0 442 7	442 100.0 442 8	417 94.3 440 2	417 94.3 440	417 94.3 440 6	417 94.3 440 6	417 94.3 440 6	417 94.3 440 6 417 94 3 440 6	417 94.3 440 6	417 94.3 440 6	417 94.3 440 6	417 94.3 440 6	23 417 94.3 440 6 ABU92576 24 417 94.3 440 6 ABO08653	417 94.3 440 6

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The present introduction retailers to 12 Secreted protein sequences given in page 18 and the protein sequences concludes the 12 secreted protein sequences given in AAA80666-A80623 encode the 12 secreted protein sequences given in the AAA816067-B25539. The human secreted proteins sequences given in dependent on the tissues in which they are expressed. Examples of the activities of the proteins include: immunosuppressant; anti-inflammatory; antiatreriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antiatreriosclerotic; anticancer; vulnerary; antiviral; antibacterial; antigonists may be used to treat prevent and/or diagnose various disease, antagonists may be used to treat prevent and/or diagnose various disease, disorders and conditions examples of which include: immune disorders e.g. Addison's disease and nephritis; dermatitis, dermatitis, and multiple sclerosis; inflammatory disorders e.g. inflammatory bowel disease, crohn's disease and nephritis; hyperproliferative disorders e.g. coronary arteriosclerosis and purpura; cardiovascular disorders e.g. coronary arteriosclerosis and myocarditis; cancer e.g. melanoma and lymphoma. The proteins and polymucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene #11 and protein sequences are represented in sequences AAA80616 and AAB2566 Sequences AAA80677-A80682 represent genes related to the
                                                                                                                                                                                    Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, ameliforation and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
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coronary arteriosclerosis; myocarditis; cancer;
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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cardiovascular disorder; coronary arteriomelanoma; lymphoma; wound healing; human
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                                                                                   99WO-US025031.
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241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
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                                                                                                                                                                                              Human; HCSRP; cytostatic; antiarthritic; antirheumatic; antiasthmatic; immunosuppressive; antiarteriosclerotic; antibacterial; antiparasitic; neuroprotective; nootropic; anticonvulsant; cancer; leukaemia; melanoma; rheumatoid arthritis; asthma; atherosclerosis; akathesia; Alzheimer's diseases; multiple sclerosis; epilepsy.
                       NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT
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/label= Signal_peptide
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antagonists, as a targeting or delivery mechanism for bringing pharmaceutical agents into contact with cells or tissues expressing HCSRP and for diagnosis of HCSRP-related disorders HCSRP and its catalytic or immunogenic fragments are useful for drug screening using libraries of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HCSRP) designated HCSRP-8. The nucleotide sequence was identified in Incyte Clone 312256 from the CDNA library LUNGNTO2, which was made from RNA isolated from lung tissue. A number of Incyte Clones were used to assemble the consensus sequence. BLAST analysis showed that the sequence is homologous to immuno-superfamily protein B12 g3779242. HCSRP and its antagonist are useful for preventing or treating disorders associated with decreased or increased expression or activity of HCSRP. Such disorders include cancers such as leukaemia and melanoma, immune disorders include cancers such as leukaemia and melanoma, immune disorders such as rheumatoid arthritis, asthma and atherosclerosis, bacterial and parasitic infections and neuronal disorders such as akathesia, Alzheimer's disease, multiple sclerosis and epilepsy. Polynucleotides encoding HSCRPs may be used as hybridisation probes to diagnose these conditions. Anti-HCSRP antibodies may be used as
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Bandman O, Azimzai Y,
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N-PSDB; AAA27051.
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                                                              SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
                                                                                                                                                                                                                                      B7-L1; T cell proliferation; natural killer cell; NK; tumour cell; biological activity; quality control reagent; treatment; inflammation; immune system disorder; autoimmune; infection; infectious disease; organ transplant rejection; hone marrow; modulator; immune response.
                                                                                                                                                                                                                               Jymphoid derived dendritic cell adhesion molecule; LDCAM; human; B7-1;
                                                                                   SRAGEEGSIRAVDHAVIGGVVAVVVRAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
                       YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
                                                    Human lymphoid derived dendritic cell adhesion molecule.
                                                                                                                                                                                                                                                                                                                                     /label= Mature_human_LDCAM_polypeptide
67. .69
                                                                                                                                                                                                                                                                                                                                                    "N-Glycosylation site"
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/note= "N-Glycosylation Bite"
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/note= "N-Glycosylation site"
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/label= Extracellular domain
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/label= Cytoplasmic_domain
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/note= "N-Glycosylation
304. 306
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/label= Leader_peptide
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The present amino acid sequence is the human lymphoid derived dendritic cell addesion molecule, LDCAM. It is found on lymphoid derived dendritic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-Li. Human LDCAM is expressed in breast, retina, foetal liver, spleen and heart, lung, muscle, placenta, thyroid and lung carcinoma. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used to treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant crejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7L-1
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                                                                                             Novel molecules designated LDCAM are capable of altering or modulating T
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                                                                                                                                                                                           Claim 7; Page 42-43; 44pp; English
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   2000-205712/18
WPI; 2000-205712,
N-PSDB; AAZ50882
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SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIIIGRYFARHKGTYFTHEAKGADDAADA 420
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(I) a useful for gene therapy of diseases and (II) can be used for therapeutic treatment. Diseases that may be treated include wound healing and tissue repair, burns, central nervous system disorders (e.g. Alzheimer's, Parkinson's, Huntington's and amylotrophic lateral aclerosis, immune déficiencies, cancer, autoimnume disorders, multiple sclerosis, diabetes and alleriges. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; vulnerary; dermatological; neuroprotective; nootropic; cancer; antiparkinsonian; immunostimulant; cytostatic; immunosuppressive; antidiabetic; antiallergic; gene therapy; wound healing; tissue repair; burn; central nervous system disorder; Alzheimer's disease; Parkinson's disease; Huntington's disease; immune disorder; autoimmune disorder; multiple sclerosis; diabetes; allergy.
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                                                                           SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA
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Wehrman T;
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100.0%; Pred. No. 0;
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iu C, Drmanac RT,
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Wang D, Liu C,
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                                                                 Human, hepatocellular carcinoma, tumour suppressor lung cancer 1, TSLC1,
liver; lung, pancreatic cancer, cell proliferative disorder; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detecting cell proliferative disorder associated with tumor suppressor lung cancer (TSLC) 1 in subject, comprises contacting proliferating cell of subject with reagent detecting TSLC1 and detecting modification in
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                    Human tumour suppressor lung cancer 1 (TSLC1) polypeptide.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Matches 442; Conserv
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     Gaps
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  0; Indels
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  0; Mismatches
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27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-019407P.
30-OCT-2000; 2000US-023732P.
18-APR-2001; 2001US-00836353.
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The invention relates to an isolated nucleic molecule that is at least CC 594 identical to 18 human cDNA sequences representing 12 novel genes encoding secreted proteins or a polymuclectide fragment of the CDNA.

CC defined in the specification, its species homologue, a variant or allelic variant of the polymuclecotide having a longuage capable of the CDNA.

CC defined in the specification, its species homologue, a variant or allelic variant of the polymuclecotide having a nucleic acid molecule conditions to a mucleic acid molecule desented by physidis under conditions to a mucleic acid molecule comprise under stringent conditions to a nucleic acid molecule desented polymuclecide feagment, domain, epitope, full-length secreted polypeptide fragment, domain, epitope, full-length protein, variant, allelic variant or species homologue), antibodies that protein, variant, allelic variant or species homologue), antibodies that protein, variant, allelic variant or species homologue), preventing or ameliorating a medical condition by administering the polymucleotide or ameliorating a medical condition by administering the polymucleotide or ameliorating an activity in a biological assay (by expressing the CDNA sequence in a cell, isolating the supernatant, and detecting an activity in a biological assay (by expressing the CC dentifying an activity). The polymptides, mucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are estruction mapping). The polymptides, mucleic acids are useful for thromosome identification), radiation hybrid mapping or long-range restriction mapping. The polymptides are also are also useful for thromosome immunological probes for differential identification of the restrictional mapping or proventing introduced as a content or other content or other contents or necentary assays. The polymptides are useful for pr
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                                                                                                                                                           New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
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100.0%; Pred. No. 0;
live 0; Mismatches
                                          Olsen HS,
                                                                                                                                                                                                                                                                           Disclosure; Page 72; 454pp; English.
                                                                    Crocker PR;
                                               Kenny JJ,
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Matches 442; Conservative
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                                            Young PE,
M, Liu D,
(CROC/) CROCKER P
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                                                                    Ruben SM,
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KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ

121

8 6 8 6 8

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241 YKPQVHIQMTYPLQGLTREGDALELTCRAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300

YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300

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98US-0105971P.
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2000US-0198407P.
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27-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the cutivity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating the polyment of the polyment o
                              pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating
                360
                                                                           SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
                                                                                            New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
               Human; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Costigan M;
                                                                                                                                                                                                                                                                                                                                                        Human Protein NP_055148, SEQ ID NO 41
                                                                                                                                           DTAIINAEGGONNSEEKKEYFI 442
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                                                                                                                                                                                                                                                        ADE54238 standard; protein; 442
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SDI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Pred. No. 0;
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                                                                                                                                                                                              allelic variant, a fragment of the CDNA sequence, or its fragment, domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Albiaimer's a disease. The present sequence represents the amino acid sequence of a novel human secreted protein associated
                                                                                                                                                                                                                                                                                                                                                                                                                                 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
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                                                                                                                            New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
                                                                               Greene JM;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                       The invention relates to an isolated nucleic acid sequence, or its
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                                                                                                                                                                                                                                                                                                  DB 8; Length 442;
                                                                              Wei Y,
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100.0%; Pred. No. 0;
tive 0; Mismatches
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                                                                              Olsen HS,
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                                                                              Young PE, Kenny JJ,
                                                                                                                                                                                                                                                                                                                     Conservative
         (KENN/) KENNY J J.
(OLSE/) OLSEN H S.
(MOOR/) MOORE P A.
(WEIY/) WEI Y.
(RREE/) GREENE J M.
(RUBE/) RUBEN S M.
                                                                                                          WPI; 2004-020335/02
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
                                                                                                                                                                                                                                                                                                          al Similarity
442; Conserv
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transmembrane proteins used therapeutically. The PRO proteins have evytostatic, anti-inflammatory, anti-proliferative and immunosuppressive activity. The proteins and polymuclectides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
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                                     Human; PRO protein; tumour necrosis factor family; TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder.
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Human PRO355 protein sequence.
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97US-0069334P.
97US-0069425P.
97US-0069694P.
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16-DEC-1997
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18-DEC-1997
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AAY17830 standard, protein; 440

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99WO-US028301
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                                                                                                                                             N-PSDB; AAA49563
                                                                                                                                                                                                                                                                                                  Sequence 440 AA;
                                            01-DEC-1998;
16-DEC-1998;
22-DEC-1998;
                           01-DEC-1999;
                                                                                                                  Hillan KJ,
           08-JUN-2000
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        TCEAIGKPOPUMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
                                  YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT338AGEEGSIRAVDHAVIGGVVAVVV 385
                                                                                                                                                                                                        PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243; PRO71; PRO341; PRO341; PRO343; PRO341; PRO345; Lransmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
                                                                       442
                                                                               FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
                                                                      FAMICLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
                                                                                                                                                                                                                                                                                                                                                 111. 115
/note= "N-glycosylation site"
163. .167
/note= "N-glycosylation site"
227. .233
/note= "N-myristoylation site"
223. .240
/note= "Tyrosine kinase phosphorylation site"
302. .306
/note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "N-myristoylation site"
319. 328
/note= "Tyrosine kinase phosphorylation site"
365. 371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102. .408
'note= "N-myristoylation site"
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/label= Transmembrane domain
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/note= "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                             306. .310
/note= "N-glycosylation
                                                                                                                                                                                                                                                                                                                            "N-glycosylation
                                                                                                                                                                                                                                                                                1. .36
/label= Signal peptide
                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                    AAB01321 standard; protein; 440 AA
                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                     .103
                                                                                                                                                                                        Human PRO355 polypeptide.
                                                                                                                                                                                                                                                                                                                  65. .69
/note= "1
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/note=
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptors/ligand interaction. Anti-PRO antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145
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designated as PRO polypeptides, useful as pharmaceutical and diagnostic
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                                                                                                                                                                                        Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
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98WO-USO25108.
98US-0112850P.
98US-0113296P.
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AAU29040
ID AAU29
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AC AAU29
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detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNP) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation of differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours, and also breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
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polypeptides and their associated nucleic acids can be used to
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dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;
antibody-dependent enzyme mediated prodrug therapy.
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                                                                                                                                                                                                                                                                                                                                                                                           94.3%; Score 417; DB 4; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
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Best Local Similarity 100.
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                       Sequence 440 AA;
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                                                                                                         PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and screen for modulators of the compounds.
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ng Z;
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nod WI, Zhang
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                                                                   Human PRO polypeptide sequence #17.
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Watanabe CK, W
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15 MAR. 2000; 2000US-0189320P.
11 MAR. 2000; 2000US-0189320P.
21 MAR. 2000; 2000US-0190828P.
21 MAR. 2000; 2000US-0191048P.
21 MAR. 2000; 2000US-0191048P.
22 MAR. 2000; 2000US-0191048P.
28 MAR. 2000; 2000US-0193032P.
29 MAR. 2000; 2000US-0193032P.
29 MAR. 2000; 2000US-0193032P.
30 MAR. 2000; 2000US-019303P.
11 APR. 2000; 2000US-0195975P.
11 APR. 2000; 2000US-019680P.
11 APR. 2000; 2000US-019680P.
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02-JUN-2000; 2
05-JUN-2000; 2
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20-DEC-2000;
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03-MAY-2000;
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                        18-DEC-2001
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention

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98US-0088738P. 98US-0088811P. 98US-0088824P. 98US-0088825P. 98US-0088825P. 98US-0088861P. 98US-0088861P. 98US-008861P. 98US-008861P.	98US-0089598P. 98US-0089998P. 98US-0089962P. 98US-0090246P. 98US-0090246P. 98US-0090254P. 98US-0090413P. 98US-0090413P. 98US-0090413P. 98US-0090618P. 98US-0090618P.	98US-00906595P. 98US-0105413. 98US-00105413. 98US-0090862P. 98US-00910815. 98US-0091135P. 98US-0091544P. 98US-0091548P. 98US-0091632P. 98US-0091632P. 98US-0091632P. 98US-0091632P. 98US-009598P. 98US-0095998P.	98US-0096867P. 98US-0096891P. 98US-0096891P. 98US-0096949P. 98US-0097022P. 98US-0097052P. 98US-0097952P. 98US-009791P. 98US-009791P. 98US-009791P. 98US-009791P. 98US-0099741P. 98US-0099741P. 98US-0099741P.
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24-0CT-1997;
28-0CT-1997;
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31-0CT-1997;
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01-APR-1998;
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06-MAY-1998
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     FRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches 0; Indels
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98US-0100388P.
98US-0100662P.
98US-0100663P.
98US-0101751P.
98US-0100681P.
98US-0100681P.
98US-0100684P.
98US-0100684P.
98US-010014P.
98US-0101472P.
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98US-0102571P.
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15-SEP-1998, 16-SEP-1998, 16-SEP-1998, 17-SEP-1998, 17-SEP-1998, 17-SEP-1998, 17-SEP-1998, 18-SEP-1998, 18-SEP-1998, 23-SEP-1998, 23-SEP-1998, 24-SEP-1998, 24-SEP-1998, 25-SEP-1998, 25-SE
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Movel human secreted and transmembrane protein PR0355.

Muman, secreted and transmembrane protein; PR0; gene therapy; tumour necrosis factor-alpha release; Mr -alpha telase; ```

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980S-0099812F.<br>980S-0100388P.<br>980S-0100662P.<br>980S-0100662P.<br>980S-0100684P.<br>980S-0100684P.<br>980S-0100849P.<br>980S-0100849P.<br>980S-0101472P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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2.3.58F-<br>24.58F-<br>24.58P-<br>24.58P-<br>24.58P-<br>25.58P-<br>25.58P-<br>29.58P-<br>29.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58P-<br>30.58 | 8       | 980S-0101475P. 980S-0101738P. 980S-0101738P. 980S-0101739P. 980S-0101784P. 980S-0101786P. 980S-0102207P. 980S-0102319P. 980S-0102570P. 980S-0102570P. 980S-0102570P. 980S-0102570P. 980S-0102684P. 980S-0102684P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                  |                   |
|   | Query<br>Best<br>Matcl<br>Qy<br>Db | Query Match<br>Best Local (<br>Matches 41)<br>26                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |         | 94.3%; Score 417; DB 6; Length 440 nrity 100.0%; Pred. No. 0; nservative 0; Mismatches 0; Indels LLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 0; Gaps OLLNPNROTIY           QLLNPNROTIY                        | 0;<br>85<br>83    |
|   | ප් සි ජ් <u>ල්</u>                 | 8 8 H                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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|   | 3 6 8 6                            | 206<br>204<br>206                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |         | NEATHIGNO FAVEGERIEVAN CHEMBANTEN TITAN FORMELLANGNOD VERNOOM IN VEGENALINGNED WEEKOOM IN VEGENALINGNED WEEKOOM IN VEGENALE WEEKOOM IN VEGENALE WEEKOOM IN VERNOOM IN VEGENALE WEEKOOM IN VERNOOM IN VERDOOM VEGENALE WEEKOOM IN VERNOOM IN VERNOOM IN VERNOOM VEGENALE WEEKOOM VEGENALE WEEK | REGDALEL<br>REGDALEL<br>REGDALEL<br>IVGKAHSD                     | 265<br>263<br>325 |

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9805-0083322P

9805-0083495P

9805-0083495P

9805-0084496P

9805-0084649P

9805-0084643P

9805-0084643P

9805-0084643P

9805-0084643P

9805-0084643P

9805-0084643P

9805-0084643P

9805-00865582P

9805-00865582P

9805-00865582P

9805-00865582P

9805-008632P

9805-008632P

9805-008632P

9805-008632P

9805-008632P

9805-008635B

9805-008632P

9805-008963P

9805-008963P

9805-009964P

 28-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
29-APR-1998;
05-MAY-1998;
 26-JUN-1998;
26-JUN-1998;
01-JUL-1998;
 07-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
15-MAY-1998;
 28-MAY-1998;
02-JUN-1998;
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 24-JUN-1998
 NUCY-0
 YMLXVYDPPTTIPPPTTTTTTTTTTTTLTITTISRAGEBGSIRAVDHAVIGGVVAVVV 385
FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 Human; secreted and transmembrane protein; PRO; TNF-alpha;
tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 Human secreted/transmembrane protein (PRO) #17.
 ABU84279 standard; protein; 440 AA
 970S-0059263P.
970S-0059266P.
970S-0063212P.
970S-0063121P.
970S-0063121P.
970S-0063541P.
970S-0063541P.
970S-0063541P.
970S-0063541P.
970S-0063541P.
970S-0063541P.
970S-0063541P.
970S-0063734P.
970S-0063734P.
970S-0063735P.
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980S-007964P.
980S-0080327P.
980S-0080337P.
980S-0081938P.
 2002US-00176756
 02-AUG-2003 (first entry)
 JS2003032112-A1
 tissue typing.
 Homo sapiens.
 18-SEP-1997;
18-SEP-1997;
21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
28-0CT-1997;
28-0CT-1997;
28-0CT-1997;
31-0CT-1997;
 15-APR-1998;
21-APR-1998;
21-APR-1998;
22-APR-1998;
 21-JUN-2002;
 10-MAR-1998
11-MAR-1998
20-MAR-1998
20-MAR-1998
27-MAR-1998
27-MAR-1998
31-MAR-1998
01-APR-1998
01-APR-1998
01-APR-1998
08-APR-1998
 12-DEC-1997;
17-DEC-1997;
18-DEC-1997;
 13-FEB-2003
 ABU84279;
 324
 264
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 384
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145
 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 85
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 Human; PRO; secreted protein, transmembrane protein, extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; carvix; liver; drug screening; transgenic anihal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSOL
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 ABR66153 standard; protein; 440 AA
 970S-0059263P.
970S-0059266P.
970S-0063280P.
970S-0063121P.
970S-0063541P.
970S-0063541P.
970S-0063544P.
970S-0063544P.
970S-0063541P.
970S-0063734P.
970S-0063734P.
970S-0064103P.
970S-0064103P.
970S-0064103P.
 2002US-00176987
 (first entry)
 US2003027278-A1
 Homo sapiens
 21-JUN-2002;
 21-0CT-1997;
24-0CT-1997;
24-0CT-1997;
28-0CT-1997;
28-0CT-1997;
29-0CT-1997;
31-0CT-1997;
31-0CT-1997;
31-0CT-1997;
 24-NOV-1997;
24-NOV-1997;
11-DEC-1997;
 05-AUG-2003
 06-FEB-2003
 18-SEP-1997
 21-NOV-1997
 24
 84
 146
 206
 204
 266
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 ABR66153;
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 RESULT 15
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 94.3%; Score 417; DB 6; Length 440; llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches 0; Indels
98US-009144BP

98US-009147BP

98US-0091626P

98US-0091622BP

98US-0091632P

98US-0091632P

98US-0091632P

98US-0091632P

98US-0091632P

98US-009174PP

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98US-0091733P

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98US-009173PP

98US-009173PP

98US-009173PP

98US-009173PP

98US-009173PP

98US-009173PP

98US-0100173PP

98US-010173PP

98US-010237PP

98US-010237PP

98US-010237PP

98US-010237PP
 Best Local Similarity
Matches 417; Conserv
01-JUL-1998, 02-JUL-1998, 02-JU
 29-SEP-1998
30-SEP-1998
30-SEP-1998
01-OCT-1998
02-OCT-1998
02-OCT-1998
06-OCT-1998
 Query Match
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| 98US-0090246P.<br>9US-0090252P.<br>9BUS-0090254P.<br>9BUS-0090439P.<br>9BUS-0090444P.<br>9BUS-0090444P.<br>9BUS-0090444P.<br>9BUS-0090444P.<br>9BUS-0090535P.<br>9BUS-0090540P. | 00000000000000000000000000000000000000                                                                                                                                                                                          | 98US-0096757P. 98US-0096867P. 98US-0096897P. 98US-0096897P. 98US-0096997P. 98US-0097022P. 98US-0097955P. 98US-0097955P. 98US-0097955P. 98US-0097955P. 98US-0097955P. 98US-0097955P. 98US-0097955P. 98US-0097955P. 98US-0097955P.                                                                                                                                                                                             | 98US-0099741P. 98US-0099764P. 98US-01009812P. 98US-0100664P. 98US-0100664P. 98US-0100664P. 98US-0100664P. 98US-0100684P. 98US-0100930P. 98US-0100930P. 98US-010094P. 98US-01014P. 98US-0101472P. 98US-0101472P. 98US-0101472P. 98US-0101472P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| 000000000000000000000000000000000000000                                                                                                                                         |                                                                                                                                                                                                                                 | 17-AUG-1998;<br>17-AUG-1998;<br>17-AUG-1998;<br>17-AUG-1998;<br>17-AUG-1998;<br>18-AUG-1998;<br>18-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>02-SEP-1998;<br>02-SEP-1998;<br>02-SEP-1998;<br>03-SEP-1998;<br>03-SEP-1998;<br>03-SEP-1998;<br>04-SEP-1998;<br>06-SEP-1998;<br>06-SEP-1998;<br>06-SEP-1998;<br>06-SEP-1998;<br>06-SEP-1998; | 10-SEP-1998;<br>10-SEP-1998;<br>10-SEP-1998;<br>16-SEP-1998;<br>16-SEP-1998;<br>16-SEP-1998;<br>17-SEP-1998;<br>17-SEP-1998;<br>17-SEP-1998;<br>17-SEP-1998;<br>18-SEP-1998;<br>18-SEP-1998;<br>18-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>23-SEP-1998;<br>24-SEP-1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
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| <del>.</del> , , , ,                                                                                                                                                            |                                                                                                                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 The invention relates to an isolated PRO polypeptide (a secreted or transmembrane protein) comprising: (a) at least 80% sequence identity or positives when compared to any of 15 sequences, fully defined in the specification, lacking or with its associated signal peptide, or least 80% sequence identity to a sequence encoded by the full-length coding sequence of a DNA deposited in the American Type Culture Collection (ATCC). Also included are: (1) an isolated nucleic acid comprising: (a) at least 80% sequence identity to a nucleotide sequence that encodes a PRO protein; (b) at least 80% sequence identity to a
 440
 442
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 A, Godowski PJ, Grimaldi JC, Gurney
Napier MA, Roy MA, Tumas D, Wood P
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 Human secreted/transmembrane protein PRO355.
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 Claim 12; Fig 24; 178pp; English.
 cardiac injury; organ failure
 98WO-US019330.
98WO-US025108.
99WO-US012252.
99WO-US021090.
99WO-US028313.
 99WO-US028301.
 2000WO-US004414
2000WO-US005841
2000WO-US008439
 2000WO-US020710.
2000WO-US032678.
2001WO-US006520.
 99WO-US028409
 31-AUG-2001; 2001US-00944654
 2000WO-US003565
 2000WO-US014042
 2001US-00866028
 26-MAR-2003 (first entry)
 Gerritsen ME, Goddard A
Hillan KJ, Kljavin IJ,
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 WPI; 2003-174141/17.
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 Human, secreted protein, transmembrane protein, PRO, tumour, proliferation, differentiation, chondrocyte cell, TNF-alpha, tumour necrosis factor-alpha, gene therapy.
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| S0866 - S0866                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | larity<br>Conserva                      | CLFS7                                                              |
|                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | Similarity<br>7; Conser                 | LRLLLLLF<br>       <br>LRLLLLF                                     |
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prostate tumour; rectal tumour; cervical tumour; liver tumour.
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 25-JUN-2002;
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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 FAMICLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
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 Human secreted polypeptide PRO355, SEQ ID NO:34.
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|                                                                      |                         |                      |       |       |       |                |                |                |                | •     |       |       |       |        |       |          |              |       |       |       |        |       |       |          |       |       |       |          |       |                                                                                  |            |              |       |       |       |                |       |       |
|                                                                      |                         |                      |       |       |       |                |                |                |                |       |       |       |       |        |       |          |              |       |       |       |        |       |       |          |       |       |       |          |       |                                                                                  |            |              |       |       |       |                |       |       |
|                                                                      |                         |                      |       |       |       |                |                |                |                |       |       |       |       |        |       |          |              |       |       |       |        |       |       |          |       |       |       |          |       |                                                                                  |            |              |       |       |       |                |       |       |
|                                                                      |                         |                      |       |       |       |                |                |                |                |       |       |       |       |        |       |          |              |       |       |       |        |       |       |          |       |       |       |          |       |                                                                                  |            |              |       |       |       |                |       |       |
|                                                                      |                         |                      |       |       |       |                |                |                |                |       |       |       |       |        |       |          |              |       |       |       |        |       |       |          |       |       |       |          |       |                                                                                  |            |              |       |       |       |                |       |       |
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|                                                                      |                         |                      |       |       |       |                |                |                |                |       |       |       |       |        |       |          |              |       |       |       |        |       |       |          |       |       |       |          |       |                                                                                  |            |              |       |       |       |                |       |       |
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 20-MAR-1998;
20-MAR-1998;
27-MAR-1998;
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31-MAR-1998;
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01-APR-1998;
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07-MAY-1998
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 28-APR-1998
 05-MAY-1998
 .5-MAY-1998
 28-MAY-1998
 05-JUN-1998
05-JUN-1998
 .0-JUN-1998
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 143
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 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3385
 82
 83
 440
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI OMTYPLQGLTREGDALEL
 LRILLILESAAALI PTGDGQNLFTKDVTVI EGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Gaps
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADAAIINAEGGONNSEEKKEYFI
 ö
 6; Length 440;
 Indels
 ;
0
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 DB
 94.3%; Score 417; DB
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
 ABR94621 standard; protein; 440 AA
98US-0102240P.
98US-0102330P.
98US-0102487P.
98US-0102570P.
98US-0102571P.
98US-0102584P.
 97US-0059263P.
97US-0059266P.
97US-0062250P.
97US-0063486P.
97US-0063120P.
 2002US-00183015
 (first entry)
 al Similarity
417; Conserv
 US2003044926-A1
 18-SEP-1997;
18-SEP-1997;
17-OCT-1997;
21-OCT-1997;
24-OCT-1997;
29-SEP-1998,
29-SEP-1998,
30-SEP-1998,
30-SEP-1998,
30-SEP-1998,
01-OCT-1998,
01-OCT-1998,
 26-JUN-2002;
 Homo sapiens
 13-SEP-2003
 06-MAR-2003
 ABR94621;
 Query Match
Best Local (
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The invention relates to a human secreted and transmembrane polypeptide (PRO) and the polynucleotide encoding it. The PRO polypeptide or polynucleotide is useful in pharmaceuticals, diagnostics, biosensors bioreactors. These are particularly useful for detecting or treating cancers, inflammatory diseases, atheroselerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs,
 New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
industry; cytostatic; antiinflammatory; cardiant; antiinfertility; anti-HIV; antiarteriosclerotic; antidiabetic.
 con DL, Ferrara N, Filvaroff E;
Godowski PJ, Grimaldi JC, Gurney AL;
ppier MA, Roy MA, Tumas D, Wood WI;
 Napier MA,
 Eaton DL,
 Claim 1; Fig 24; 173pp; English.
 97US-0067411P
97US-0069334P
97US-0069334P
97US-0069425P
97US-0069696P
97US-0069696P
97US-0069702P
97US-0069873P
97US-0069873P
97US-0069873P
98US-007440P
98US-00740P
98US-0074092P
98US-0074092P
98US-0074092P
 9805-00216021
9805-0021817.
9805-0113296P.
9805-013296P.
9900-00254311.
9900-00012252.
 99WO-US028313.
99WO-US028409.
99WO-US028301.
99WO-US030095.
 16-DEC-1999; 99WO-US030095.
11-FEB-2000; 2000WO-US003565.
22-FEB-2000; 2000WO-US005411.
02-WAR-2000; 2000WO-US005841.
 30-MAR-2000; 2000WO-US008439.
22-MAY-2000; 2000WO-US014042.
28-JUL-2000; 2000WO-US020710.
 01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
 99WO-US021090.
 2001US-00945015
 Botstein D, Ea
ME, Goddard A,
 Kljavin IJ,
 (GETH) GENENTECH INC
 2003-174088/17.
 WPI; 2003-174088/
N-PSDB; ABX89477.
 US2002132768-A1
 Gerritsen ME,
 12-DEC-1997;
16-DEC-1997;
16-DEC-1997;
16-DEC-1997;
17-DEC-1997;
 03-MAR-1999;
22-JUN-1999;
28-JUL-1999;
15-SEP-1999;
30-NOV-1999;
01-DEC-1999;
 31-AUG-2001;
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 22-DEC-1998;
22-DEC-1998;
 18-DEC-1997
05-JAN-1998
 25-FEB-1998
 16-DEC-1998
 16-DEC-1998
 16-SEP-1998
 DEC-1998
 19-SEP-2002
 11-DEC-1997
 Hillan KJ,
 Baker KP,
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 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various industrial applications. Sequences ABU60230-ABU60245 represent human PRO polypeptides of the invention
 85
 83
 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDBGRYFCQLYTDPPQESYTTITVLVPPR
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 TCEA1GKPQPVMVTWVRVDDEMPQHAVL,SGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 Gaps
 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
 Human, PRO, secreted polypeptide; transmembrane polypeptide;
tumour necrosis factor alpha; TNF-alpha; chondrocyte cell; tumour;
 ö
 94.3%; Score 417; DB 6; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
 ABU85594 standard; protein; 440 AA.
 98US-00105413.
98WO-US019330.
98US-00168978.
98WO-US021141.
98US-00187368.
 98WO-USO25108.
98US-0020264.
99US-00254311.
99WO-USO05028.
99US-00311832.
 2002US-00187588
 02-JUL-2003 (first entry)
 Human PRO polypeptide #17.
 Best Local Similarity 100.
Matches 417; Conservative
 Sequence 440 AA;
 US2003036140-A1
 Homo sapiens
 01-JUL-2002;
 03-MAR-1999;
08-MAR-1999;
14-MAY-1999;
14-MAY-1999;
 07-OCT-1998;
07-OCT-1998;
06-NOV-1998;
 26-JUN-1998
16-SEP-1998
 01-DEC-1998
07-DEC-1998
 20-FEB-2003
 cytostatic.
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 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 145
 | FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKKGNTELKGKSEVEEWSDMYTVTSQL 203
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 WELYVYDPPITIPPPITTTTTTTTTTTTTTTTTTTTTTT383
 proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide and a method for detecting the presence of a tumour in a mammal. The polypeptides and polynucleotides are useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. Sequences ABUS558-ABUS582 represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html
 Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy;
 82
 chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; Thy-alpha release; tumour necrosis factor alpha release; chondrocyte cell proliferation; chondrocyte cell differentiation; pharmaceutical; diagnostic; biosensor;
 83
 442
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
 FAMLCLL I LGRY FARHKGTY FTHEAKGADDAADADTAI INAEGGONNSEEKKEY FI
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 6; Length 440;
 0; Indels
 Novel human secreted and transmembrane protein PRO355.
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 ABU98754 standard; protein; 440
 97US-0059263P.
97US-0059266P.
97US-0062250P.
97US-0063486P.
 2002US-00175737
 (first entry)
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 Sequence 440 AA;
 US2003013153-A1
 18-SEP-1997;
17-OCT-1997;
21-OCT-1997;
 Homo sapiens
 19-JUN-2002;
 18-SEP-1997;
 01-AUG-2003
 16-JAN-2003
 bioreactor.
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 The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the PRO polynuclectides encoding them. The invention also relates to a method for stimulating the release of tumour necrosis factor alpha (TNR-alpha) from human blood by contacting the blood with a sequence of the invention, a method for stimulating the
 nucleic acids encoding PRO polypeptides, useful a medicament for diagnosing or treating tumor.
 Gurney AL;
 ₽3,
 Godowski F
ng Z;
 A, Go
Zhang
 Goddard /
 Wood
 five nucleic acids
 Claim 11; Fig 34; 707pp; English.
 ij
 Matanabe CK,
 99WG-US012252.
99US-00380137.
99US-00380138.
99US-00380142.
99WG-US020111.
99WG-US020111.
99US-00403297.
 2001WO-US006520.
2001US-00816744.
 2000WO-US020710
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 2000US-00747259
 2000WO-US034956
 2001WO-US017800
 2001US-00946374.
2002US-00052586.
 99WO-US031274
 2000WO-US013705
 2000WO-US014042
 2000WO-US032678
 2001WO-US021735
 2001US-00918585
 2001US-00924419
 2000WO-US005841
 2000WO-US014941
 2001US-00908827
 the manufacture of
 (GETH) GENENTECH INC
 WPI; 2003-332028/31.
N-PSDB; ACA72787.
 Chen J,
 hundred and
 Smith V,
 25-MAY-2001; 2
01-JUN-2001; 2
05-JUN-2001; 2
20-JUN-2001; 2
29-JUN-2001; 2
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02-JUN-2000;
28-JUL-2000;
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-SEP-1999;
-SEP-1999;
-OCT-1999;
 04-SEP-2001;
 30-DEC-1999;
05-JAN-2000;
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| ***************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | X                                                                                                                                                  |
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| 97US-0063120P<br>97US-0063121P<br>97US-0063121P<br>97US-0063544P<br>97US-0063544P<br>97US-0063544P<br>97US-0063544P<br>97US-0063544P<br>97US-006311P<br>97US-006311P<br>97US-006311P<br>97US-006311P<br>97US-006311P<br>97US-006311P<br>97US-006313P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-006931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P<br>97US-008931P                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086<br>0-S086           |
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| 24-OCT-1997; 28-OCT-1997; 28-OCT-1997; 28-OCT-1997; 28-OCT-1997; 28-OCT-1997; 21-000000000000000000000000000000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 11111111111111111111111111111111111111                                                                                                             |
| ######################################                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                    |
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98US-0088825P 98US-0088826P 98US-0088876P 98US-0089376P 98US-0089314P 98US-0089314P 98US-0089318P 98US-0089318P 98US-008932B 98US-008933B 
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06-MAY-1998
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 .5-MAY-1998
 5-MAY-1998
 2-MAY-1998
 2-MAY-1998
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 Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy; chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour;
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 82
 83
 PAMLCLLIILGRYFARHKGTYFTHBAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
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 24 LRLLLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNFNRQTIY
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
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 Gaps
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 Length 440;
 0; Indels
 Novel human secreted and transmembrane protein PRO355.
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9
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 Pred. No. 0;
Mismatches
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Pred. No.
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Conservative 0;
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 (first entry)
 y Match
Local Similarity
thes 417; Conserva
 17.58P-1998;
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 ABU97969;
 Query Mat
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 RESULT 31
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| 8US-0088029P<br>8US-0088023P<br>8US-008803P<br>8US-008812P<br>8US-008812P<br>8US-008812P<br>8US-008812P<br>8US-008813P<br>8US-008873P<br>8US-008873P<br>8US-008873P                                                                                      | 8015 - 0.088861 P 8015 - 0.088961 P 8015 - 0.08991 P 8015 - 0.089953 P 8015 - 0.089953 P 8015 - 0.089953 P 8015 - 0.099953 P 8015 - 0.099953 P 8015 - 0.099054 P 8015 - 0.099054 P 8015 - 0.099054 P 8015 - 0.099064 P 8015 - 0.099066 P 8015 - 0.09906 P P P P P P P P P P P P P P P P P P P | 9805-0090665P<br>9805-0090665P<br>9805-0090863P<br>9805-0091010P<br>9805-0091644P<br>9805-0091644P<br>9805-0091644P<br>9805-0091628P<br>9805-0091628P<br>9805-0091628P<br>9805-0091628P<br>9805-0091628P<br>9805-0091628P<br>9805-0091628P<br>9805-009168P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P<br>9805-0096691P |
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| 4 - JUN - 1998<br>4 - JUN - 1998<br>4 - JUN - 1998<br>5 - JUN - 1998<br>5 - JUN - 1998<br>6 - JUN - 1998<br>6 - JUN - 1998<br>7 - JUN - 1998<br>8 - JUN - 1998 | 11-00N-19998<br>12-00N-19998<br>12-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998<br>13-00N-19998                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | AUG AUG AAUG AAUG AAUG AAUG AAUG AAUG A                                                                                                                                                                                                                                                                                                                                                                                              |
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386 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442

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01-JUL-1998
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 22-JUN-1998
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 Human; gene therapy; chromosome identification; tissue typing.
 Novel human secreted and transmembrane protein PRO355.
 ABU91675 standard; protein; 440 AA
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970S-0063121P.
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970S-0063541P.
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970S-008194P.
970S-0081495P.
970S-0083495P.
970S-0083499P.
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98US-0084414P.
98US-0084639P.
98US-0084640P.
 2002US-00176985
 11-AUG-2003 (first entry)
 US2003027277-A1.
 Homo sapiens.
 21-JUN-2002;
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18-SEP-1997;
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30 - APR - 1998
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265
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 YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTITTDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 Human; PRO polypeptide; secreted protein; transmembrane protein; chromosome mapping; gene mapping; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical; liver; cancer; TNF-alpha; tumour necrosis factor-alpha; proliferation; differentiation; chondrocyte cell; bone disorder; cartilage disorder; sports injury; arthritis; cytostatic; antiarthritic; osteopathic.
 442
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADTAIINAEGGONNSEEKKEYFI
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97US-0053266P.
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 01-JUL-2002; 2002US-00187597
 09-JUL-2003 (first entry)
 Human PRO polypeptide #17.
 US2003036141-A1.
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24-0CT-1997;
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 10-MAR-1998
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDECRYFCQLYTDPPQESYTTITVLVPPR 145
 82
 83
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9805-0097952P

9805-0097974P

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9805-010284P

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| K K K 8                                                      |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
| <u>.</u>                                                     |             |                    |             |             |             |             |             | -           |             | _           |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             | _       |               |             |             |             | _           |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             | _           |              |             |             | _           | _           |             |             |             |              |             |             |             | _           | _           |                                         |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             | ٠           |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
|                                                              | •           |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |
| 07P.                                                         | 33P.        | 19P.               | 95P.        | Sar.        | 19P.        | )4P.        | 97P.        | 22P.        | 35P.        | 96P.        | 99P.        | 59P.        | 56P.        | (4P.        | 39P.        | OP.         | 13P.        | 79P.        | 30P.        | 32P.         | 00E          | . 02.       |             | 12P.        | 36Р.        | 18P.        | 780          |         |             | . Y.        | ?7P.        | 35P.         | :8P.        | .db.        | 35          | יעם         | 70      |               | )2P.        | .2P.        | .7P.        | 555.        | 12P.        | 18P.        | 10P.        | 11P.        | 34P.        | 55          | 96          | 0           | . 0         |                                         |             |             |             |             | . 4. 7.     |             | JRP.        | 53P.         | )8P.        | 52P.        |             |             |             | 54P.        | 39P.        | 35P.         | 14P.        |             | 51 P.       | ,           |             | ,                                       |
| 98US-0080107P.<br>98US-0080194P.<br>98US-0080327P.           | -00803      | -008104<br>-008107 | -008119     | -008783     | -008256     | -008270     | -008275     | -008332     | -008345     | -008345     | -008345     | -008355     | -008436     | -008441     | -008463     | -008464     | -008464     | -008557     | -008558     | -008558      | -008570      | 00000-      |             | -00863      | -008648     | -008709     | -008720      | 72.000- | 0000        | - 008/      | -008782     | -008800-     | -008802     | -008802     | -008803     | CF8800-     | -008816 | 10000         | -008820     | -008821     | -008821     | -008865     | -008872     | -008873     | -008874     | -008881     | -008882     | -008882     | -008882     | -008886     | 988800-     | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, | 00000       | 20000       | 710000      | 100000      | 100890-     | -00899-     | -008955     | -008965      | -008999     | -008999     | -0000-      | 100000      | -0000-      | -000002     | -009042     | -009043      | -009044     | 40000-      | -00904      | 10000       |             | ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,, |
| 8086<br>8086<br>8086                                         | 9808        | 8086<br>808        | 9808        | 9808        | 9808        | 9808        | 9808        | 9808        | 8086        | SDRG        | 9808        | 9808        | 9808        | 9808        | 9808        | 9808        | 980S        | 98US        | 98US        | 98US         | 98118        | 98178       |             | SORG        | 980S        | 98US        | 98118        | 21100   | 0000        | 9808        | 9808        | 98US         | 98US        | SUS         | 98118       | STIRE       | 98110   | 0000          | 5086        | 9808        | 9808        | 9805        | 80S         | 9808        | 9808        | 9808        | 9808        | SU86        | 98118       | 21186       | 01100       | 9000                                    | 0000        | 0000        |             | 2000        | 9808        | 2000        | 9808        | 980S         | 9808        | 9808        | 98118       | 0000        | 2086        | 8086        | 980S        | 980S         | 9808        | 9000        | 9805        | 0,100       |             | , x                                     |
| 1998;                                                        | -1998;      | -1998;             | -1998;      | 1998.       | -1998;      | -1998;      | -1998;      | - TAAR ;    | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;       | -1998:       | 1998.       | 0000        | 186T-       | -1998;      | -1998;      | -1998.       | 000     | 000         | 19881-      | -1998;      | -1998;       | -1998;      | -1998:      | -1998:      | -1998.      | -1000.  | 10001         | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998;      | -1998:      | -1998:      | -1998.      | 10001-      | . 8001-                                 | 000         | 10001       | 0000        | ,000,       | 0000        | -1998;      | -1998;      | -1998;       | -1998;      | -1998:      | -1998       | 1000        | -1998;      | -1998;      | -1998;      | -1998;       | -1998;      | 1000        | - TANR !    | 000         |             |                                         |
| 21-MAR-1998;<br>31-MAR-1998;<br>31-MAR-1998;<br>01-APR-1998; | 01-APR      | 08-APR<br>08-APR   | 09-APR      | 21 - APR    | 21-APR      | 22-APR      | 22-APR      | ZB-APR      | 29-APR      | ZY-APR      | 29-APR      | 29-APR      | 05-MAY      | 06-MAY      | 07-MAY      | 07-MAY      | 07-MAY      | 15-MAY      | 15-MAY      | 15-MAY       | 15-MAY       | 18-MAV      |             | 22-MAX      | 22-MAY      | 28-MAY      | 28-MAY       | NTTT-CO |             | 02-20       | 03-50N      | 04 - JUN     | 04 - JUN    | 04 - JUN    | 04 - JUN    | 04 - TIN    | NTT20   | 200-00        | NDC-50      | 05-3UN      | 05-5UN      | NDD-60      | 10-JUN      | 11-11       | 11TIN       | 11 - TIN                                | 100         | 121         | 100-24      | 10-01       | 10-01       | NOD-/1      | 10-11       | 17-5UN       | 18-JUN      | 19-4T       | NITI-CC     | 22 - CC     | ADD-22      | 22-JUN      | 24 - JUN    | 24 - JUN     | 24 - JUN    | 24 - TTN    | 24-00N      | ATT. 10     |             | 201                                     |
|                                                              |             |                    |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |              |         |             |             |             |              |             |             |             |             |         |               |             |             |             |             |             |             |             |             |             |             |             |             |             |                                         |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |              |             |             |             |             |             |                                         |

98US-0090678P 98US-009068P 98US-009068P 98US-0090659P 98US-0090655F 98US-0090655F 98US-0090652P 98US-0090652P 98US-0090652P 98US-0090652P 98US-0090652P 98US-0090652P 98US-009063P 98US-009162P 98US-009163P 98US-009163P 98US-009163P 98US-009163P 98US-009163P 98US-0100144P 98US-0101147P 98US-0101240P 98US-0101240P

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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEBEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVKVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT3385
 82
 83
 Human, immunogen, secreted protein, transmembrane protein, PRO; tumour, proliferation; differentiation; chondrocyte cells; tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 440
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Gaps
 ;;
0
 DB 6; Length 440;
 0; Indels
 Human secreted/transmembrane protein (PRO) #17.
 94.3%; Score 41., 100.0%; Pred. No. 0;
 Ź
 ABU86209 standard; protein; 440
98US-0102571P.
98US-0102684P.
98US-0102687P.
98US-0102965P.
 98WO-US019330.
98US-00168978.
98WO-US021141.
98US-00187368.
 98WO-US025108.
98US-00202054.
99US-00254311.
 99WO-US005028.
99US-00311832.
99WO-US010733.
 99WO-US012252
99US-00380137
 2002US-00187603
 (first entry)
 al Similarity 100.
417; Conservative
 JS2003036146-A1
 01-OCT-1998;
01-OCT-1998;
02-OCT-1998;
 02-JUL-2002;
 16-SEP-1998;
07-OCT-1998;
07-OCT-1998;
06-NOV-1998;
01-DEC-1998;
03-MAR-1999;
08-MAR-1999;
 14-MAY-1999;
14-MAY-1999;
02-JUN-1999;
25-AUG-1999;
 Homo sapiens
 01-JUL-2003
 30-SEP-1998;
 20-FEB-2003
 56
 84
 204
 266
 326
 386
 Query Match
Best Local S
 98
 146
 206
 264
 324
 384
 ABU86209
 Matches
 RESULT 34
ABU86209
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Godowski PJ,
 P, Chen J, Desnoyers L, Goddard A, Godo
Smith V, Watanabe CK, Wood WI, Zhang Z;
 2000WO-US020710.
2000US-00644848.
2000WO-US023328.
2000US-00664610.
2000US-00665350.
 2001WO-US006520.
2001US-0081674.
2001US-00854208.
2001US-0086628.
2001WO-US01780.
2001WS-00874503.
2001WO-US0120962.
2001WO-US0120962.
 99US-00380139.
99US-00380142.
99WO-US020111.
99US-00403297.
99US-00403297.
 2001US-00918585.
2001US-00924419.
2001US-00929404.
2001US-00931836.
2001US-00941992.
 2000WO-US030952
2000WO-US032678
 2000US-00747259
2000WO-US034956
 2001US-00946374
2002US-00052586
 99WO-US028551
 99WO-US031274
 2000WO-US004341
 2000WO-US004342
 2000WO-US005601
 2000WO-US008439
 2000WO-US014941
 2000WO-US015264
 2001US-00908827
 (GETH) GENENTECH INC.
 WPI; 2003-332034/31.
 N-PSDB; ACA73401
 18-SEP-2000;
18-SEP-2000;
08-NOV-2000;
 05-JAN-2000;
18-FEB-2000;
18-FEB-2000;
22-FEB-2000;
 28-JUL-2000;
22-AUG-2000;
24-AUG-2000;
 25-AUG-1999;
15-AUG-1999;
115-SEP-1999;
118-OCT-1999;
12-NOV-1999;
01-DEC-1999;
30-DEC-1999;
 24-FEB-2000;
01-MAR-2000;
 15-MAR-2000;
 20-DEC-2000;
 28-FEB-2001;
 22-MAR-2001;
 25-MAY-2001;
 01-JUN-2001;
05-JUN-2001;
 29-JUN-2001;
 06-AUG-2001;
 16-AUG-2001;
28-AUG-2001;
 15-JAN-2002;
 02-JUN-2000;
 08-NOV-2000;
 DEC-2000;
 10-MAY-2001;
 20-JUN-2001;
 04-SEP-200
 Baker KP,
 Pan J,
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Gurney AL;

Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal. Claim 11; Fig 34; 707pp; English The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a PRO polypeptide lacking its associated signal peptide or an extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO expression vectors; host cells transformed with the vector (used to

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necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 2001US-00931836
2001US-00941992
 US2003036162-A1
 tumour necrosi
tissue typing.
 Homo sapiens.
 16-AUG-2001;
28-AUG-2001;
 06-NOV-1998
 produce PRO proteins), a chimaeric molecule comprising the PRO
polypeptide fused to a heterologous amino acid sequence, an anti-PRO
antibody, a method for stimulating the release of tumor necrosis factor
alpha (TNR-alpha) from human blood (by contacting the blood with PRO1079,
PRO827, PRO791, PRO1131, PRO1316, PRO1183, PRO1343, PRO1760, PRO1567 or
PRO4331), a method for stimulating the proliferation or differentiation
of chondrocyte cells by contacting the cells with a PRO6029 polypeptide,
a method for detecting the presence of tumour in a mammal and an
oligomuclectide probe derived from any of the nuclectide sequences cited
above. The PRO polypeptide or anti-PRO antibody is useful for preparing a
condition that is responsive to the PRO
polypeptide or anti-PRO antibody. The PRO nuclectide sequences are useful
complement for treating a condition that is responsive to the PRO
polypeptide or anti-PRO antibody. The PRO nuclectide sequences are useful
complements and DNA. PRO nucleic acids are also useful in preparing propoptides, in assays to identify other proteins or molecules involved
antisense RNA and DNA. PRO nucleic acids are also useful in transpentically useful reagence for canneals or knockout
animals, which in turn are useful in the development and screening of
therapeutically useful reagence of a tumour in a mammal, simulating
proliferation or differentiation of chondrocyte cells, stimulating
curlease of tumour necrosis factor-alpha from human blood, in gene
chergy, or as molecular weight markers for protein electrophoresis
culture or natural sources. The present sequence represents a PRO protein
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKKSEVEEWSDMYTVTSQL 203
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT338AGEEGSIRAVDHAVIGGVVAVVV 385
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 442
 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADAAIINAEGGQNNSBEKKEYFI 440
 0; Gaps
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
 94.3%; Score 417; DB 6; Length 440; 100.0%; Pred. No. 0; Nismatches 0; Indels
 Human; secreted and transmembrane protein; PRO; TNF-alpha;
 Human secreted/transmembrane protein (PRO) #17.
 ABU67422 standard; protein; 440 AA
 (first entry)
 Matches 417; Conservative
 Local Similarity
 Sequence 440 AA;
 29-MAY-2003
 324
 326
 386
 ABU67422;
 146
 204
 Query Match
 266
 RESULT 35
 ABU67422
ID ABU6
XX
XX ABU6
XX DT 29-P
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XX XX
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12-JUL-2002; 2002US-00194423
 98US-00202054
99US-00254311
 99WO-US012252
 99US-00380139
 99US-00403297
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25-MAY-2001;
01-JUN-2001;
 ABU80450;
 25-AUG-1
25-AUG-1
 14-MAY-
 liver;
 RESULT 36
 ABU80450
 New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification.
 in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 205
 265
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the release of TNR-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes and detecting the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ABU67406-ABU67710 are the PRO polypeptides of the invention
 82
 83
 transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for detecting the tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes,
 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADADIAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 Gurney AL;
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 0; Gaps
 invention discloses human nucleic acids encoding secreted and
 94.3%; Score 417; DB 6; Length 440;
100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
 Godowski PJ,
 KP, Chen J, Desnoyers L, Goddard A, Godon,
Smith V, Watanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 706pp; English
29-AUG-2001; 2001WO-US027099.
04-SEP-2001; 2001US-00946374.
15-JAN-2002; 2002US-00052586.
 Best Local Similarity 100.
Matches 417; Conservative
 (GETH) GENENTECH INC.
 WPI; 2003-332039/31.
N-PSDB; ACA05716.
 Sequence 440 AA;
 86
 146
 84
 206
 266
 264
 324
 386
 326
 Query Match
 Baker KP
Pan J,
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8

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tumour; adrenal; lung; colon; breast; prostate; rectal; cervical; PRO; gene therapy.
Ä.
ABU80450 standard; protein; 440
 98WO-US019330.
98US-00168978.
98WO-US021141.
 99US-00380137.
99US-00380138.
99US-00380139.
99US-00380142.
99WO-US020111.
 99WO-US021090.
99US-00403297.
99US-00423844.
 2001US-00816744.
2001US-00854208.
2001US-00854280.
2001US-00866028.
2001WO-US017800.
 2000WO-US004414
 2000WO-US023328
2000US-00664610
 27-JUN-2002; 2002US-00184640
 98US-00187368
98WO-US025108
 98US-00202054
 99US-00254311
 99WO-US005028
 99US-00311832
 99WO-US010733
 99WO-US012252
 99WO-US031274
 2000WO-US004341
 2000WO-US004342
 2000WO-US005004
 2000WO-US005601
 2000WO-US013705
 2000WO-US015264
 2000WO-US020710
 2000WO-US030952
 99WO-US028551
 99WO-US028301
 (first entry)
 Human PRO protein #17.
 US2003036137-A1.
 Homo sapiens.
 18-FEB-2000;
 22-FEB-2000;
 02-MAR-2000;
 22-MAY-2000;
 18-SEP-2000;
 18-FEB-2000;
 L7-MAY-2000;
 02-JUN-2000;
 22-AUG-2000;
 28-JUL-2000;
 23-JUN-2003
 01-DEC-1999;
02-DEC-1999;
 10-MAY-2000
 01-DEC-2000
 16-SEP-1998
07-OCT-1998
 06-NOV-1998
 03-MAR-1999
 08-MAR-1999
 02-JUN-1999
 25-AUG-1999
 25-AUG-1999
 18-OCT-1999
 12-NOV-1999
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Homo sapiens.
 28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
28-OCT-1997;
31-OCT-1997;
31-OCT-1997;
 24-NOV-1997;
11-DEC-1997;
12-DEC-1997;
 20-MAR-1998;
20-MAR-1998;
27-MAR-1998;
 10-MAR-1998;
11-MAR-1998;
 18-SEP-2003
 24-OCT-1997
24-OCT-1997
 13-NOV-1997
21-NOV-1997
 29-APR-1998
29-APR-1998
 27-FEB-2003
 24-NOV-1997
 17-DEC-1997
 11-MAR-1998
 08-APR-1998
 09-APR-1998
 15-APR-1998
 ABR99368;
 RESULT 37
 ABR99368
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPDQESYTTITVLVPPR 145
 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 MENOVEDPITIPPPITITITITITITITITITESRAGEEGSIRAVDHAVIGGVVAVVV 383
 Three hundred and five nucleic acids encoding secreted and transmembrane RNO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumors.
 The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as adenal, lung, colon, breast, prostate, rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human CDNA, genomic DNA or mRNA. The PRO genes amy also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a human PRO polypeptide of the invention
 83
 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 Gurney AL;
 FAMICILIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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29-AUG-2001; 2001US-0091836.
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| 24-JUL-199<br>04-AUG-199<br>10-AUG-199<br>10-AUG-199<br>17-AUG-199                     | 17-AUG-199<br>17-AUG-199<br>17-AUG-199             | 18-AUG-199<br>18-AUG-199         | 26-AUG-199<br>26-AUG-199<br>26-AUG-199 | 26-AUG-199<br>26-AUG-199         | 26-AUG-199<br>26-AUG-199         | 01-SEP-199<br>01-SEP-199         | 02-SEP-199<br>02-SEP-199         | 02-SEP-199<br>09-SEP-199         | 10-SEP-199<br>10-SEP-199         | 10-SEP-199                       | 15-SEP-199     | 16-SEP-199     | 16-SEP-199     | 17-SEP-199     | 17-SEP-199     | 18-SEP-199     | 23-SEP-199     | 23-SEP-199<br>23-SEP-199         | 24-SEP-199<br>24-SEP-199         | 24-SEP-199<br>24-SEP-199         | 24-SEP-199<br>25-SEP-199         | 29-SEP-199     | 29-SEP-199     | 29-SEP-199<br>30-SEP-199 | 30-SEP-199<br>30-SEP-199         | 01-0CT-199     | 01-10CT-199                      | Query Match<br>Best Local Si     | accnes 41/;    | P              | 24 Ľ                             | 86 F           | 84 F           | 146 N                            |
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|                                                                                        |                                                    |                                  |                                        |                                  |                                  |                                  |                                  |                                  |                                  |                                  |                |                |                |                |                |                |                |                                  |                                  |                                  |                                  |                |                |                          |                                  |                |                                  |                                  |                |                |                                  |                |                |                                  |
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|                                                                                        |                                                    |                                  |                                        |                                  |                                  |                                  |                                  |                                  |                                  |                                  |                |                |                |                |                |                |                |                                  |                                  |                                  |                                  |                |                |                          |                                  |                | •                                |                                  |                |                |                                  |                |                |                                  |
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| 98<br>98<br>98<br>98                                                                   |                                                    |                                  |                                        |                                  |                                  |                                  |                                  |                                  |                                  |                                  |                |                |                |                |                |                |                |                                  |                                  |                                  |                                  |                |                |                          |                                  |                |                                  |                                  |                |                |                                  |                |                |                                  |

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0
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9
 Human secreted/transmembrane protein (PRO) #17.
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| 24-NOV-1997;<br>24-NOV-1997;<br>11-DEC-1997;<br>17-DEC-1997;<br>17-DEC-1997;<br>10-MAR-1998;             |                                                                      |                                                                              | 08-APR-1998;<br>08-APR-1998;<br>09-APR-1998;<br>15-APR-1998;<br>21-APR-1998;<br>21-APR-1998;             | . യ യ യ യ യ യ യ <u>യ</u>                                                                                 |                                                                                              |                                                                                                              | 02-UM-1998;<br>03-UM-1998;<br>04-UM-1998;<br>04-UM-1998;<br>04-UM-1998;<br>04-UM-1998;<br>05-UM-1998;<br>05-UM-1998;<br>05-UM-1998;          |                                                                                                                                              | 10 - JUN - 1998;<br>11 - JUN - 1998;<br>11 - JUN - 1998;<br>12 - JUN - 1998;<br>12 - JUN - 1998;<br>16 - JUN - 1998;<br>16 - JUN - 1998;<br>17 - JUN - 1998; |
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 82
 83
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung, colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; colon; breast; prostate; kidney; rectum; cervix; antiarthritic; vulnerary; gene therapy.
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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 Human secreted polypeptide PRO355, SEQ ID NO:34.
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| 805-<br>805-<br>805-<br>805-<br>805-<br>805-<br>805-<br>805-                                                         | 8008-<br>8008-<br>8008-<br>8008-<br>8008-<br>8008-<br>8008-<br>8008-<br>8008-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 000 - S086<br>000 - S086 | - S. C.                                                                                                        |
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 Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
 Human secreted/transmembrane protein (PRO) #17.
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9705-0053264P

9705-0063121P

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9705-0063121P

9705-0063131P

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9705-0063131P

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9705-0064103P

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9805-0080137P

9805-0080137P

9805-0080194P

9805-008195P

9805-008185P

9805-00835P

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 2002US-00180560
 (first entry)
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18-SEP-1997;
18-SEP-1997;
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28-OCT-1997;
31-OCT-1997;
31-OCT-1998;
31-OCT-1997;
31-OC
 25-JUN-2002;
 Homo Bapiens
 30-AUG-2003
 06-MAR-2003
 AB018822;
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New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, or for preparing a medicament for treating a condition
 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTLTILTITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 The invention relates to human PRO secreted/transmembrane polypeptides (ABR78227-ABR78531) and nucleic acids encoding them (ACF00100-00404). The invention also relates to sequences at least 80% identical to the PRO nucleic acid back cells comprising a PRO nucleic acid, a method for the recombinant production of a PRO polypeptide, and fusion proteins comprising a PRO nucleic acid, a method for the recombinant production of a PRO polypeptide, antibodies against a PRO polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic acids encoding PRO polypeptides of the invention were initially identified via homology screening using consensus sequences based on the extracellular domain sequences from known secreted proteins. Human cDNA libraries containing sequences of interest were identified using oligonuclectides based on the consensus sequences, and cDNA clones were isolated and characterised. The PRO polypeptides are useful for
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 442
 extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 440
 Gurney AL;
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
 in gene therapy, or for preparing a medicament for treating a c
that is responsive to the PRO polypeptide or anti-PRO antibody.
 Godowski PJ,
 PRO; secreted protein; transmembrane protein;
 Goddard A, Godov
Wood WI, Zhang Z;
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 Claim 11; Fig 34; 700pp; English.
 Desnoyers L,
 ABR78243 standard; protein; 440
 Watanabe CK,
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02-JUN-1999; 99WO-US01255.
25-AUG-1999; 99US-00380137.
28-FEB-2001; 20UNO-US06520.
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 (first entry)
 (GETH) GENENTECH INC
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 Smith V,
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 US2003054474-A1.
 Homo sapiens.
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FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTT3385 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442 24 LRILLIFSAAALIPTGDGQNLFTKDVTVIBGEVATISCQVNKSDDSVIQLLNPNRQTIY FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL LRLLLLLFSAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIOLLNPNRQTIY 0; Gaps DB 6; Length 440; 0; Indels 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches 417; Conservative Similarity Sequence 440 AA; Query Match Best Local S 56 324 86 84 146 144 206 204 566 264 326 386 Matches 셤 qq g g 원 ò ð ઠ QQ ઠ ò ò ò

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Human; PRO; secreted protein; transmembrane protein;
Cornelia de Lange syndrome; gene therapy; immune disorder;
 Human secreted/transmembrane protein PRO355.
 ABU64926 standard; protein; 440 AA
 (first entry)
 15-MAY-2003
 ABU64926
ABU64926
ID ABU
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AC ABU
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DT 15-1
XX
DE Hum
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XW
XW
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Hum
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FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGQNNSEEKKEYFI 440

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inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; cardiac injury; AIDS; cancer; diabetic complication. 97US-0069278P 97US-0069334P 97US-0069425P 97US-0069664P 97US-0069667P 97US-0069870P 97US-0069870P 97US-0069870P 97US-0074086P 98US-0074086P 98US-0074086P 98US-0112850P. 98US-0113296P. 99WO-US028313. 99WO-US028301. 2000WO-US004414. 2000WO-US008439. 2000WO-US014042. 98WO-US025108 99WO-US012252. 99US-0146222P. 99WO-US021090 99WO-US030095 2000WO-US005841. 2001US-00944944 99WO-US028409 2000WO-US003565 2000WO-US020710 2000WO-US032678 2001US-00866028 2001WO-US (GETH ) GENENTECH INC. US2002173463-A1. 31-AUG-2001; 11-FEB-2000; 22-FEB-2000; 02-MAR-2000; 01-DEC-2000; 05-JAN-1998; 09-FEB-1998; 09-FEB-1998; 25-FEB-1998; 30-MAR-2000; 22-MAY-2000; 28-JUL-2000; 25-MAY-2001; 1997; 1997: 1998; 01-DEC-1998; 16-DEC-1998; 1997 1997 1997 22-DEC-1998 30-NOV-1999 21-NOV-2002 18-DEC-1997 02-JUN-1999 28-JUL-1999 15-SEP-1999 30-NOV-1999 01-DEC-1999 16-DEC-1999 11-DEC-1997 12-DEC-1997 16-SEP-

transmembrane polypeptides and polynucleotides useful for chromosome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers. con DL, Ferrara N, Filvaroff E; Godowski PJ, Grimaldi JC, Gurney AL ppier MA, Roy MA, Tumas D, Wood WI; Napier MA, Kljavin IJ, WPI: 2003-311003/30. N-PSDB; ABX96814. Gerritsen ME, Hillan KJ,

Eaton DL,

Goddard

Baker KP, Botstein D,

Claim 12; Fig 24; 172pp; English.

The invention relates to an isolated nucleic acid encoding a secreted/ transmembrane polypeptide (designated as PRO proteins). 15 PRO polypeptides and their encoding polymucleotides are disclosed. Also included are a vector comprising the PRO nucleic acid, a host cell comprising the vector, a process for producing a PRO polypeptide (by culturing the host cell under conditions for the expression of the PRO polypeptide, and recovering the PRO polypeptide from the cell culture, an isolated polypeptide having at least 80% amino acid sequence identity to the PRO polypeptides, a chimaeric molecule comprising PRO fused to a heterologous amino acid sequence and an antibody which specifically binds

us-10-622-237-2.oligo.rag

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970S-0063486P
970S-0063120P
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 TCEAIGKPOPVWVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
to PRO. The PRO nucleotide sequences are useful as hybridisation probes, in chromosome and gene mapping, in generating sense and antisense RNA or DNA, in generating transgenic or knock-out animals which can be used in the development and screening of therapeutically useful reagents, and in gene therapy. The polypeptides may be used as molecular weight markers for protein electrophoresis purposes. The PRO polypeptides and nucleic acids may also be used for chromosome identification, and tissue typing. PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange syndrome. Other PRO proteins are variously implicated in immune disorders, inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, cardiac injury, AIDS, cancer and diabetic complications. The present sequence represents
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTBBRAGEEGSIRAVDHAVIGGVVAVVV 385
 Human; secreted and transmembrane protein; PRO; cytostatic; gene therapy; chondrocyte stimulator; chromosome mapping; gene mapping; transgenic animal; knock-out animal; tumour.
 85
 83
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 442
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATISCQVNKSDDSVIQLLNPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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 Novel human secreted and transmembrane protein PRO355.
 94.3%; Scor.
100.0%; Pred. No. v,
0; Mismatches
 ABU84979 standard; protein; 440
 20-JUN-2002; 2002US-00176919.
 97US-0059263P
 (first entry)
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Best Local Similarity 100.0
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18-SEP-1997;
 30-JUN-2003
 Homo sapiens
 13-FEB-2003
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 21 - APR - 1998

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28 - APR - 1998

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Human; secreted and transmembrane protein; PRO; TNP-alpha; tumour secrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
 442
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 Human secreted/transmembrane protein (PRO) #17.
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 ABO11450 standard; protein; 440
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 Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; brostate tumour; rectal tumour; cervical tumour; liver tumour.
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 Human, antiinflammatory, antiarteriosclerotic, cardiant, gynecological, anti-HIV, cytostatic, antidiabetic; BMP-agonist; BMP-Antagonist, cytokine-agonist; cytokine-agonist; cytokine-agonist cytokine-antagonist, gene-Therapy, inflammatory disease, organ failure; atherosclerosis; cardiac injury, inflammatory birth defect; premature aging; AIDS; cancer;
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144 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEBWSDMYTVTSQL 203
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 Human, gene therapy; chondrocyte stimulation; TNF-alpha release; chondrocyte proliferation; chondrocyte differentiation; tumour detection;
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9705-006351319-
9705-00641209-
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 US2003036133-A1.
 tissue typing.
 Homo sapiens.
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 24-NOV-1997
 11-DEC-1997
 20-MAR-1998
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 85
 83
 New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic
 The invention describes a novel isolated PRO polypeptide. The methods a compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. This is the amino acid sequence of a novel human secreted PRO protein
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Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
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100.0%; Pred. No. 0;
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 Claim 12; Fig 24; 171pp; English
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2000WO-US032678.
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2000WO-US005841.
 99WO-US028313
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|                |                |               |                |                |                |                |                |                |                |                |                 |                |                |                |               |                |                |                |               |                |                |                |                |                |                |                |                |                |                |                                  |                |                |                |                |                |                |                              |                |                |                |                |                              |                |                              |                |                |                |                |                                  |                |                                  | • |
|                |                |               |                |                |                |                |                |                |                |                |                 |                |                |                |               |                |                |                |               |                |                |                |                |                |                |                |                |                |                |                                  |                |                |                |                |                |                |                              |                |                |                |                |                              |                |                              |                |                |                |                |                                  |                |                                  |   |
|                |                |               |                |                |                |                |                |                |                |                |                 |                |                |                |               |                |                |                |               |                |                |                |                |                |                |                |                |                |                |                                  |                |                |                |                |                |                |                              |                |                |                |                |                              | ٠              |                              |                |                |                |                |                                  |                |                                  |   |
|                |                | • • •         |                |                |                |                | .•.            |                |                | _• _           |                 |                | _•_            |                |               |                |                |                | •             |                |                |                |                |                |                | _•             |                |                |                | • .                              | •              |                |                |                |                | _              |                              |                | .• .           |                |                |                              |                |                              |                | •              |                |                |                                  |                |                                  |   |
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 Human; secreted and transmembrane protein; PRO; chromosome mapping; gene mapping; gene therapy; tumour necrosis factor alpha; TNF-alpha; chondrocyte; tumour.
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 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADAAIINAEGGONNSEEKKEYFI
 chondrocyte proliferation; chondrocyte differentiation;
tumour necrosis factor-alpha stimulation; TNF-alpha stimulation
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 Human; secreted and transmembrane protein; PRO; gene therapy; chondrocyte stimulator; chromosome mapping; gene mapping; transgenic animal; knockout animal; tissue typing;
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 Indels
 Novel human secreted and transmembrane protein PRO355
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 DB 6;
94.3%; Score 417; DE llarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
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 (first entry)
 Similarity
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| ***************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 7                                                                                      |
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| X                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | # # # # # # #<br># # # # # # # #                                                       |

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extracellular domain; tumour necrosis factor-alpha; TNP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 Human; PRO; secreted protein; transmembrane protein;
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| 8US-0084643F<br>8US-0085579F<br>8US-0085582P<br>8US-0085582P<br>8US-0086023F<br>8US-0086023F             | 8US00870989 8US-00872098 8US-00872098 8US-00872098 8US-00880239 8US-00880239 8US-0088039 8US-00881389 8US-00881389 8US-00881389 8US-00881319                                     | 805-00887388<br>805-00887388<br>805-00887388<br>805-0088219<br>805-0088259<br>805-0088259<br>805-0088269<br>805-0088269<br>805-0088269<br>805-0089269<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289<br>805-0089289                                                          | 98US-0090443P<br>98US-0090444P<br>98US-0090545P<br>98US-0090535P<br>98US-0090676P<br>98US-0090678P<br>98US-009069B<br>98US-009069B<br>98US-009069B<br>98US-009069B<br>98US-009069B<br>98US-009069B<br>98US-0090663P<br>98US-0090663P<br>98US-0091010P<br>98US-0091010P<br>98US-0091139P<br>98US-0091139P<br>98US-0091622P<br>98US-0091622P<br>98US-0091628P<br>98US-0091628P<br>98US-0091628P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P<br>98US-0091632P                                                                                                                                          |
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Query Match 94.3%; Score 417; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps

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 06-FEB-2003
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 Novel human secreted and transmembrane protein PRO355
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99US-00254311.
99WO-US05028.
99WO-US011832.
99WO-US010733.
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Length 440;

9 B

94.3%; Score 417;

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v secreted and transmembrane PRO polypeptides and nucleic acids, useful
gene therapy, chromosome identification, tissue typing, for detecting
presence of tumor in a mammal, or as hybridization probes in gene
Wood WI,
Watanabe CK,
 WPI; 2003-402071/38.
 Smith V,
 N-PSDB; ACD25374
 mapping
 Pan J,
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# Claim 11; Fig 34; 707pp; English

The invention describes a novel isolated PRO polypeptide. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nuclectide sequences are useful as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA and DNA. PRO nucleic acids are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically

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useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of tumour in a mammal, stimulating proliferation or differentiation of chondrocyte cells, stimulating the release of tumour necrosis factor-alpha from human blood, in gene therapy, or as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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 265
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100.0%; Pred. No. 0;
ive 0; Mismatches
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| 970S-0063120P<br>970S-0063121P<br>970S-0063544P<br>970S-0063544P<br>970S-006311P<br>970S-006311P<br>970S-006311P<br>970S-006311P<br>970S-006313P<br>970S-006933SP<br>970S-006933SP<br>970S-006933SP<br>970S-006933SP<br>970S-006933SP<br>970S-006933SP<br>970S-006933SP<br>970S-006933SP<br>970S-00693SP<br>970S-00693SP<br>970S-00693SP<br>970S-00693SP<br>970S-00693SP<br>970S-00693SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-00893SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-0089SP<br>970S-008SP<br>970S-008SP<br>970S-008S                                                                                                                                                                        | S-0088029P. S-008813P. S-0088126P. S-008812P. S-0088212P. S-0088212P. S-0088212P. S-0088112P. S-008812P. S-008812P. S-008812P. S-008812P.                                                    |
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| 24-0CT-1997/<br>28-0CT-1997/<br>28-0CT-1997/<br>28-0CT-1997/<br>28-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1997/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0CT-1998/<br>31-0C |                                                                                                                                                                                              |
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Human; PRO; secreted protein; transmembrane protein; TNP-alpha; extracellular domain; tumour necrosis factor-alpha; rnP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 970S-0059263P.
970S-0059266P.
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 28-0CT-1997;
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31-0CT-1997;
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31-MAR-1998;
01-APR-1998;
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24-OCT-1997;
24-OCT-1997;
 17-DEC-1997;
18-DEC-1997;
 08-APR-1998
09-APR-1998
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22-APR-1998
 28-APR-1998
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 22-MAY-1998
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 20-FEB-2003
 18-SEP-1997
17-OCT-1997
 21-NOV-1997
24-NOV-1997
 11-DEC-1997
 08-APR-1998
 145
 143
 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3385
 82
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGONNSEEKKEYFI 442
 FRDFRPLKDSRFQLLAFSSSELKVSLTAVSISDEGRYFCQLYIDPQGSYITITVLVPPR
 LRLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 LRLLLLLFSAAALIPTGDGQNLFTXDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ö
 DB 6; Length 440;
 0; Indels
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 100.0%; Pred. No. 0; ive 0; Mismatches
 Score 417;
 ABR66763 standard; protein; 440
98WO-US019330.
98US-0100683P.
98US-0100919P.
98US-0100849P.
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98US-0103258P.
98US-0103449P.
 94.3%;
 05-AUG-2003 (first entry)
 Local Similarity 100.
Les 417; Conservative
 16 - SEP - 1998;
17 - SEP - 1998;
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17 - SEP - 1998;
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 24
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| 26-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>26-AUG-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>02-SEP-1998;<br>02-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;<br>01-SEP-1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | PR 15-SEP-1998; 980S-0100562P. PR 16-SEP-1998; 980S-0100564P. PR 16-SEP-1998; 980S-0100564P. PR 16-SEP-1998; 980S-0100564P. PR 17-SEP-1998; 980S-010063P. PR 17-SEP-1998; 980S-010063P. PR 17-SEP-1998; 980S-0100930P. PR 18-SEP-1998; 980S-0100930P. PR 18-SEP-1998; 980S-010014P. PR 23-SEP-1998; 980S-010147P. PR 23-SEP-1998; 980S-010147P. PR 23-SEP-1998; 980S-0101473P. PR 24-SEP-1998; 980S-010143P. PR 24-SEP-1998; 980S-0101738P. PR 25-SEP-1998; 980S-0101738P. PR 25-SEP-1998; 980S-010123P. PR 29-SEP-1998; 980S-010237P. PR 29-SEP-1998; 980S-0102330P. PR 29-SEP-1998; 980S-0102330P. PR 29-SEP-1998; 980S-0102331P. PR 29-SEP-1998; 980S-0102331P. PR 29-SEP-1998; 980S-0102331P. PR 29-SEP-1998; 980S-0102331P. PR 30-SEP-1998; 980S-0102231P. PR 30-SEP-1998; 980S-0102231P. PR 30-SEP-1998; 980S-0102231P. PR 30-SEP-1998; 980S-0102231P. PR 30-SEP-1998; 980S-0102207P. PR 30-SEP-1998; 980S-0102207P. PR 30-SEP-1998; 980S-0102207P. PR 30-SE | 30-SEP-1998; 310-CT-1998; 01-CCT-1998; 01-CCT-1998; 01-CCT-1998; 01-CCT-1998; 02-CT-1998; 03-CT-1998; 01-CCT-1998; 03-CT-1998; 01-CT-1998; 03-CT-1998; 01-CT-1998; |
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| 28 - MAY - 1998; 98UG 28 - MAY - 1998; 98UG 02 - JUN - 1998; 98UG 03 - JUN - 1998; 98UG 04 - JUN - 1998; 98UG 04 - JUN - 1998; 98UG 05 - JUN - 1998; 98UG | 10 - JUN-1998; 9800; 10 - JUN-1998; 9800; 10 - JUN-1998; 9800; 10 - JUN-1998; 9800; 11 - JUN-1998; 9800; 11 - JUN-1998; 9800; 12 - JUN-1998; 9800; 12 - JUN-1998; 9800; 17 - JUN-1998; 9800; 17 - JUN-1998; 9800; 12 - JUN-1998; 9800; 22 - JUN-1998; 9800; 22 - JUN-1998; 9800; 24 - JUN- | PR 25-JUN-1998; 98US-0090676P. PR 25-JUN-1998; 98US-0090676P. PR 25-JUN-1998; 98US-0090676P. PR 25-JUN-1998; 98US-0090634P. PR 25-JUN-1998; 98US-0090634P. PR 25-JUN-1998; 98US-0090634P. PR 25-JUN-1998; 98US-0090635P. PR 26-JUN-1998; 98US-0090635P. PR 26-JUN-1998; 98US-0090635P. PR 26-JUN-1998; 98US-0090635P. PR 26-JUN-1998; 98US-009154P. PR 01-JUL-1998; 98US-009154P. PR 02-JUL-1998; 98US-009154P. PR 02-JUL-1998; 98US-009154P. PR 02-JUL-1998; 98US-0091628P. PR 02-JUL-1998; 98US-0091628P. PR 02-JUL-1998; 98US-009162P. PR 03-JUL-1998; 98US-009598P. PR 17-AUG-1998; 98US-0096757P. PR 17-AUG-1998; 98US-009698P. PR 17-AUG-1998; 98US-009691P. PR 17-AUG-1998; 98US-009698P. PR 11-AUG-1998; 98US-00969B. PR 11-AUG-1998; 98US-009 |

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| 98US-0097952P. 98US-0097954P. 98US-0097954P. 98US-0097971P. 98US-0099014P. 98US-0098014P. 98US-0098813P. 98US-0098843P. 98US-0098843P. 98US-0099843P. 98US-0099762P. 98US-0099762P. 98US-0099763P. 98US-0099763P. 98US-0099763P. 98US-0100662P. 98US-0100684P. 98US-0100684P. 98US-0100684P. 98US-0100684P. 98US-0101731P. 98US-0101731P. 98US-0101731P. 98US-0101733P.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 94.3%; S<br>100.0%;<br>vative 0;                                            | LLESAAALI PTGDGONLE<br>                                       | FRDFRPLKOSRFQLLNFSSSELKVSLTNVSI.  |
| 26-AUG-1998, 30-AUG-1998, 30-AU | Query Match<br>Best Local Similarity<br>Matches 417; Conser                 | 26 LRLLLLLE<br>       <br>24 LRLLLLE                          | 86 FRDF<br>    <br>84 FRDF        |
| K K K K K K K K K K K K K K K K K K K                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | δmž                                                                         | ò a                                                           | Qy<br>Db                          |

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9805-0084519-9805-0084519-9805-0084519-9805-0084519-9805-0084536-9-9805-0084513-68-9805-0084513-9805-0084513-9805-0084513-9805-0085582-9805-0085582-9805-0086559-9805-0089512-9805-0089512-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-0089513-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-009952-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9805-00995-9905-9905
 15-MAY-1998;
18-MAY-1998;
 03-JUN-1998
 04-JUN-1998
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 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
 Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
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 2002US-00179525
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 24-0CT-1997
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 22-APR-1998
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 AB015976
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 203
 263
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour aecrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
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 324 YMLXVYDPPTTIPPPTTTTTTTTTTTTITTITDSRAGEEGSIRAVDHAVIGGVVAVVV
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 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
 Human secreted/transmembrane protein (PRO) #17.
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97US-0063266P.
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 18-SEP-1997
 17-OCT-1997
21-OCT-1997
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02-JUL-1998

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10-AUG-1998

110-AUG-1998

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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145

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18-DEC-1997 .0-MAR-1998

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| 98US-0090540F<br>98US-0090676F<br>98US-0090678F<br>98US-0090688F             | 98US-00906941<br>98US-00906951<br>98US-00906961    | 98US-00105413<br>98US-0090862E<br>98US-0090863E    | 98US-0091010F                    | 98US-0091544E<br>98US-0091478E   | 98US-0091626E                                     | 98US-0091632E  | 98US-00940061<br>98US-00952821                    | 98US-0096012E  | 98US-0096766                     | 98US-0096867E                    | 98US-0096897E                    | 16569600-SD86  | 98US-0097952E  | 98US-0097954E<br>98US-0097955E   | 98US-0097971E  | 98US-0098014E  | 98US-0098723E  | 98US-0098803E                    | 98US-0098843E<br>98US-0099602E   | 98US-0099741E  | 98US-0099763E  | 98US-00398178  | 98US-0100662E<br>98US-0100664E   | 98US-0101751E  | 98US-0100683E  | 98US-0100684E<br>98US-0100919E   | 98US-0100930E  | 98US-0101014E  | 98US-0101068E<br>98US-0101471E   | 98US-0101472E  | 98US-0101477F  | 98US-0101739E                    | 98US-0101743E  | 98US-0101786E  | 98US-0102240F  | 98US-0102330F<br>98US-0102331F<br>98US-0102487F    |
|------------------------------------------------------------------------------|----------------------------------------------------|----------------------------------------------------|----------------------------------|----------------------------------|---------------------------------------------------|----------------|---------------------------------------------------|----------------|----------------------------------|----------------------------------|----------------------------------|----------------|----------------|----------------------------------|----------------|----------------|----------------|----------------------------------|----------------------------------|----------------|----------------|----------------|----------------------------------|----------------|----------------|----------------------------------|----------------|----------------|----------------------------------|----------------|----------------|----------------------------------|----------------|----------------|----------------|----------------------------------------------------|
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| 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8                                        | 88 88 88 88 88 88 88 88 88 88 88 88 88             | # # #<br># # #                                     | PR PR                            | PR R                             | 4 4 G                                             | £ & &          |                                                   | £ & £          | <b></b>                          | P P                              | P. R. G.                         | . E. E.        |                | R R                              | PR             | £ & 6          | 자<br>보고<br>보고  | # #<br># #                       | # #<br># #                       | PR             | . E. E         | <br>X &        |                                  | <b>8</b> 8     | PR             |                                  | P.R. 94        | PR             | PR PR                            | PR             |                | <br>¥                            | P. P. R.       | PR C           | 유              | PR<br>PR<br>PR                                     |
|                                                                              |                                                    |                                                    |                                  |                                  |                                                   |                |                                                   |                |                                  |                                  |                                  |                |                |                                  |                |                |                |                                  |                                  |                |                |                |                                  |                | ,              |                                  |                |                |                                  |                |                |                                  |                |                |                |                                                    |
|                                                                              |                                                    |                                                    |                                  |                                  |                                                   |                |                                                   |                |                                  |                                  |                                  |                |                |                                  |                |                |                |                                  |                                  |                |                |                |                                  |                |                |                                  |                |                |                                  |                |                |                                  |                |                |                |                                                    |
|                                                                              |                                                    |                                                    |                                  |                                  |                                                   |                |                                                   |                |                                  |                                  |                                  |                |                |                                  |                |                |                |                                  |                                  |                |                |                |                                  |                |                |                                  |                | •              |                                  |                |                |                                  |                |                |                |                                                    |
|                                                                              |                                                    |                                                    |                                  |                                  |                                                   |                |                                                   |                |                                  | ٠                                |                                  |                |                |                                  |                |                |                |                                  |                                  |                |                |                |                                  |                |                |                                  |                |                |                                  |                |                |                                  |                |                |                |                                                    |
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| <b>ጸ ፕ ፕ ፕ ፕ</b>                                                             |                                                    |                                                    |                                  |                                  |                                                   |                |                                                   |                |                                  |                                  |                                  |                |                |                                  |                |                |                |                                  |                                  |                |                |                |                                  |                |                |                                  |                |                |                                  |                |                |                                  |                |                |                |                                                    |

us-10-622-237-2.oligo.rag

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 2003-174140/17.
 WPI; 2003-174140/
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 TCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 85
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 83
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 0; Indels
 premature aging; AIDS; cancer; diabetic complication
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 94.3%; Scor.
100.0%; Pred. No. v,
'.. 0; Mismatches
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98US-0102571P.
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98US-0102687P.
98US-0103256P.
98US-01033268P.
 98WO-US019330.
98WO-US025108.
99WO-US012252.
99WO-US028313.
99WO-US028419.
99WO-US028409.
 2001US-00943762
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 JS2002142958-A1.
30-SEP-1998;
30-SEP-1998;
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02-OCT-1998;
06-OCT-1998;
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15-SEP-1999;
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01-DEC-1999;
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 Homo sapiens
 03-OCT-2002
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This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HIV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3383
 biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a protein encoded by the nucleic acids of the
 442
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 24 LRILLILESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Baker KP, Botstein D, Eaton DL, F
Gerritsen ME, Goddard A, Godowski
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 Claim 1; Fig 24; 173pp; English.
 2000WO-US008439.
2000WO-US014042.
2000WO-US020710.
2000WO-US032678.
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 28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
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Matches 417; Conservative
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 86-JUN-1998
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 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 Human secreted/transmembrane protein, SEQ ID 34.
 ABU65585 standard; protein; 440
 9705-0059261P

9705-0059266P

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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides, with or without their associated signal peptide. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNR-alpha) from human blood by contacting the blood with a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide, a method for detecting the presence of a tumour in a mammal and an oligonucleotide sequences are useful as probes, in chromosome and gene mapping, in generating antisense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as molecular weight markers for protein electrophoresis purposes, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the presence of TNF-alpha from human blood, for stimulating the presence, prevention and/or treatment of a tumour, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour. The PRO polypeptides and nucleic acids may also be used disapnostically for the sequence data for this patent can also be betained to invention. Note: The sequence data for this patent can also be betained to in electronic format directly from USPTO at
 Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour accrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour;
 26 LRILLILLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 Three hundred and five nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor or for measuring or detecting expression of an associated gene.
 Gurney AL;
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 Human secreted/transmembrane protein (PRO) #17.
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 05-JUN-2000; 2000US-0209832P.
28-FEB-2001; 2001WO-US006520.
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 26-JUL-2002; 2002US-00205907
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 27-AUG-2003
 20-MAR-2003
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 Human; secreted protein; transmembrane protein; PRO; antiarthritic; vulnerary; tumour necrosis factor-alpha; chondrocyte cell proliferation; chondrocyte cell differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; broast tumour; b
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 arthritis; sports injury
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 18-SEP-1997
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ive 0; Mismatches
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 94.3%; Sco...
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 24-JUL-2003
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Query Match

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|                                                                                         |                                                                                         |                                                                                                                                                                                  |                                                                                  |                                              |                                                  |                                              |                                     |                                                  |                                        |                                     |                                     |
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325
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rectum; cervix; liver.
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24-OCT-1997;
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11-MAR-1998;
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27-MAR-1998;
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31-MAR-1998;
 13-FEB-2003
 18-SEP-1997
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 LRELLELERSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLIANPRQTIY
 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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0
 DB 6; Length 440;
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 94.3%; Score 417; DE 100.0%; Pred. No. 0; ive 0; Mismatches
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168 417; Conservative
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26-AUG-1998

26-AUG-1998

10-SEP-1998

10-SEP-1998

10-SEP-1998

10-SEP-1998

10-SEP-1998

10-SEP-1998

10-SEP-1998

11-SEP-1998

11-SE
 26
 24
 86
 Query Match
 Matches
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| 25-JUN-1998;<br>25-JUN-1998;<br>25-JUN-1998;<br>25-JUN-1998;         | BAAT-NOO-9  | 6-UUN-1998; | . 1998 - NITIN-1998 : | 1-TTT-1998:  | 1-,TTT,-1998; | 2TTT1998.    | 2-UUD-1998,  | 2-UUD-1996;  | 2-00E-1996; | 2-JUL-1998; | 1000T-TOO-7 | 4-00E-1996; | 4 - AUG-1996; | 0-AUG-1998; | 7-AUG-1998,  | 7-ATG-1998;  | 7-AUG-1998; | 7-AUG-1998; | 7-AUG-1998; | 8-AUG-1998; | 8-AUG-1998; | 8-AUG-1998; | 6-AUG-1998; | 6-AUG-1998; | 6-AUG-1998; | 6-AUG-1998; | 6-AUG-1998; | 6-AUG-1998; | 1-SEP-1998; | 1-SEP-1998; | 2-SEP-1998; | 2-SEP-1998; | 2-SEP-1998; | 9-SEP-1998; | 0-SEP-1999; | 0-SEP-1998:  | 0-SEP-1998:  | 5-SEP-1998; | 6-SEP-1998; | 6-SEP-1998; | 6-SEP-1998; | 6-SEP-1998; | 7-SEP-1998; | 7-SEP-1998; | 7-SEP-1998; | 8-SEP-1998:  | 8-SEP-1998: | 8-SEP-1998; | 3-SEP-1998; | 3-SEP-1998; | 3-SEP-1998; | 3-SEP-1998; | 4-SEP-1998; | 4-SEP-1998; | 4-SEP-1998;<br>4-SED-1998. | 5-SEP-1998:  | 9-SEP-1998; | 9-SEP-1998; | 9-SEP-1998; | 9-SEP-1998; | 0-SEP-1998; | 0-SEP-1998; | 0-SEP-1998; | 1-0CT-1998; |            |
|----------------------------------------------------------------------|-------------|-------------|-----------------------|--------------|---------------|--------------|--------------|--------------|-------------|-------------|-------------|-------------|---------------|-------------|--------------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--------------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|----------------------------|--------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|-------------|------------|
| ######################################                               |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             |             |             |             |             |             |             | PR 0        | PR 0       |
| <u> </u>                                                             |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             | •           | •           |             |             |             |             |             | -          |
|                                                                      |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             | ·           |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             |             |             |             |             |             |             |             |            |
|                                                                      |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             | •           |             |             |             |             |                            |              |             |             |             |             |             |             |             |             |            |
|                                                                      |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             |             |             |             |             |             |             |             |            |
|                                                                      |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             |             |             |             |             |             |             |             |            |
| 7P.<br>3P.<br>0P.                                                    |             | α<br>υν.    | . d6                  | 4 D          | 7P.           | 20           | . 0          |              |             |             |             |             |               |             | . 05.        |              | 0P.         | 2P.         | 0P.         | ЗР.         | 2P.         | 6P.         | 8P.         | 8P.         | 9P.         | 9P.         | 7P.         | SP.         | 8P.         | 9P.         | 3P.         | 6P.         | 7P.         | ZP.         | 75.         | , r.         | 25.          | 8P.         | 0P.         | 1P.         | 4P.         | 5P.         | 6P.         | 1P.         | 3P.         |              | , L         | 2P.         | 4P.         | 8P.         | 8P.         | ЗР.         | С. с.       | ZP.         | 50.                        | 4 P          | . d.6       | 5P.         | 4P.         | 1P.         | 5P.         | 0P.         | 6P.         | 8P.         | 8P.        |
| 98US-0080327P.<br>98US-0080333P.<br>98US-0081049P.<br>98US-0081070P. | 98US-008119 | 98US-008183 | 98US-008256           | 98IIS-008270 | 98113-008279  | 98TIS-008332 | 98TIC-008349 | 99116-008349 | 2000-0100   | 98US-008349 | 2000-0100   | 96US-006436 | 2003-000441   | 98US-008463 | 98115-008464 | 981IS-008557 | 98US-008558 | 98US-008558 | 98US-008570 | 98US-008602 | 98US-008639 | 98US-008648 | 98US-008709 | 98US-008720 | 98US-008760 | 98US-008775 | 98US-008782 | 98US-008802 | 98US-008802 | 98US-008802 | 98US-008803 | 98US-008832 | 98US-008816 | 98US-008820 | 9805-008821 | 9811S-008865 | 9811S-008872 | 98US-008873 | 98US-008874 | 98US-008881 | 98US-008882 | 98US-008882 | 98US-008882 | 980S-008886 | 980S-008886 | 98115-008909 | 98US-008910 | 98US-008951 | 98US-008951 | 98US-008953 | 98US-008959 | 98US-008965 | 980S-008990 | 2802-2086   | 98US-009UZ4                | 98IIS-009025 | 98US-009042 | 98US-009043 | 98US-009044 | 98US-009046 | 98US-009053 | 98US-009054 | 98US-009067 | 98US-009067 | 980S-00906 |
| 01-APR-1998;<br>01-APR-1998;<br>08-APR-1998;<br>08-APR-1998;         |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             |             |             |             |             |             |             |             |            |
| PR 01-A<br>PR 01-A<br>PR 08-A                                        |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              |              |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |             |              |              |             |             |             |             |             |             |             |             |              |             |             |             |             |             |             |             |             |                            |              |             |             |             |             |             |             |             |             |            |
|                                                                      |             |             |                       |              |               |              |              |              |             |             |             |             |               |             |              | _            | _           |             | _           |             |             | _           | _           |             |             |             |             |             |             | _           |             |             |             |             |             |              |              |             |             |             |             |             | _           | _           |             |              |             |             | _           | _           |             | '           |             |             |                            |              |             |             |             |             |             |             |             |             |            |

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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthrits; sports injury; cancer; tumour; dagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis;
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 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ;
0
 Length 440;
 0; Indels
 DB 6;
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 94.3%; Scor.
100.0%; Pred. No. v.
... 0; Mismatches
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 ABR69979 standard; protein; 440 AA
98US-0102965P.
98US-0103258P.
98US-0103449P.
98US-00168978.
 99WO-US005108.
99WO-US005028.
99WO-US010733.
 99WO-US012252.
99US-0145698P.
99US-00380137.
 98US-0090540P
 2002US-00187885
 98WO-US021141
 (first entry)
 417; Conservative
 Similarity
 US2003032138-A1
02-OCT-1998;
06-OCT-1998;
06-OCT-1998;
07-OCT-1998;
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 02-JUL-2002;
 07-OCT-1998;
01-DEC-1998;
08-MAR-1999;
14-MAY-1999;
26-JUL-1999;
25-AUG-1999;
 19-AUG-2003
 13-FEB-2003
 24-JUN-1998
 SEP-1998
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, Desnoyers L, Goddard A, Godo
Watanabe CK, Wood WI, Zhang Z;
 99WO-US028313
 99WO-US028409
 99WO-US028551
 99WO-US028565
 99WO-US031274
 2000WO-US000219
 2000WO-US003565
 2000WO-US004341
 2000WO-US004342
 2000WO-US004914
 2000WO-US006319
 2000WO-US006884
 2000WO-US008439
 2000WO-US015264
 2000WO-US023328
 2000WO-US030952
 2000WO-US032678
 2001WO-US027099
 2002US-00052586
 GETH) GENENTECH INC.
 P, Chen J,
Smith V, W
 22-FEB-2000;
24-FEB-2000;
24-FEB-2000;
01-MAR-2000;
02-MAR-2000;
 17-MAY-2000;
22-MAY-2000;
30-MAY-2000;
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02-DEC-1999;
16-DEC-1999;
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15-MAR-2000;
 30-MAR-2000;
 28-JUL-2000;
 24-AUG-2000;
08-NOV-2000;
 01-DEC-2000;
20-DEC-2000;
 01-JUN-2001;
 20-JUN-2001;
 29-AUG-2001;
 11-FEB-2000;
 02-JUN-2000;
 Baker KP,
 Pan J,
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Gurney AL; Godowski PJ,

#### 2003-341977/32. N-PSDB; ACC91010.

ø New secreted and transmembrane PRO polypeptide useful in preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody.

## Claim 11; Fig 34; 707pp; English.

The invention relates to human PRO secreted/transmembrane polypeptides (ABR6963-ABR70267) and nucleic acids encoding them (ACC90994-ACC91298).

The invention also relates to sequences at least 80% identical to the PRO nucleic acid and polypeptide sequences of the invention, recombinant production of a RNO polypeptide, and though for the recombinant production of a RNO polypeptide, and though for the invention were initially polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic acids encoding PRO polypeptides of the invention were initially incleived and host centain using consensus sequences based on the extracellular domain sequences from known secreted proteins. Human cDNA libraries containing sequences of interest were identified using consensus sequences, and cDNA clones were isolated and characterised. The PRO polypeptides are useful for stimulating release of tumour necrosis factor—alpha (TNF-alpha) from chanced TNR-alpha release would be beneficial. They are also useful for chanced TNR-alpha release would be beneficial. They are also useful for stimulating the proliferation or differentiation of chondrocytes and as

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antiarthritic; vulnerary; gene therapy.
 US2003036132-A1.
 Homo sapiens.
 1997
 31-MAR-1998
01-APR-1998
 15-MAY-1998
15-MAY-1998
 03-JUN-1998
04-JUN-1998
 20-FEB-2003
 18-SEP-1997
 21-OCT-1997
 24-OCT-1997
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 28-OCT-1997
 29-OCT-1997
 31-OCT-1997
 24-NOV-1997
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 09-APR-1998
 29-APR-1998
 02-JUN-1998
 02-JUN-1998
 17-0CT-1997
 .3-NOV-1997
 24-NOV-1997
 28-OCT-1
 -APR-1
 cuch may be used in the treatment of various bone and/or cartilage
disorders such as arthritis and sports injuries. The PRO polypeptides may
be used in a method for detecting the presence of a tumour (e.g., an
adrenal tumour, lung tumour, colon tumour, breast tumour, prostate
tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This
cumethod involves comparing the level of expression of the PRO polypeptide
in test and control samples, where a higher level of expression of PRO
conditionally useful for in drug screening to identify agonists and
antagonists of PRO polypeptides. PRO nucleic acids are useful as
contagonists of PRO polypeptides. PRO nucleic acids are useful as
contagonists of PRO polypeptides of attisense RNA and DNA and in gene
therapy. The nucleic acids can also be used for mapping genes encoding
contagonists, for genetic analysis of individuals with genetic
disorders, and for generating either transgenic animals or knock-out
animals which are useful in the development and screening of
therapy the nucleic acids can also be used for mapping genes encoding
contagonists and for generating either transgenic animals or knock-out
animals which are useful in the development and screening of
the respectionally useful compounds. Sequences ABR6963-ABR70267 represent
the human PRO secreted/transmembrane polypeptides of the invention. Note:
The sequence data for this patent is also available in electronic format
contagonists.
 205
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 24 LRLILLIFEPSAAALIPTGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 PAMLCLIIILGRYFARHKGTYFTHEAKGADDAADAATAIINAEGGONNSEEKKEYFI 440
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthrits; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis;
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 0; Gaps
 Query Match
94.3%; Score 417; DB 6; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 ABR69312 standard; protein; 440 AA
 11-AUG-2003 (first entry)
 Sequence 440 AA;
 ABR69312;
 56
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 RESULT 71
ABR69312
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| PR 01-SEP-1996; 990S-0098716P. PR 02-SEP-1996; 990S-0098712P. PR 02-SEP-1996; 990S-0098712P. PR 02-SEP-1996; 990S-0098871P. PR 03-SEP-1996; 990S-0098871P. PR 10-SEP-1996; 990S-0099744P. PR 10-SEP-1996; 990S-0099742P. PR 10-SEP-1996; 990S-0099762P. PR 110-SEP-1996; 990S-0099762P. PR 15-SEP-1996; 990S-010036P. PR 15-SEP-1996; 990S-010036P. PR 15-SEP-1996; 990S-010036P. PR 15-SEP-1996; 990S-010034P. PR 17-SEP-1996; 990S-010064P. PR 17-SEP-1996; 990S-010064P. PR 17-SEP-1996; 990S-010064P. PR 18-SEP-1996; 990S-010173P. PR 23-SEP-1996; 990S-010147P. PR 23-SEP-1996; 990S-010147P. PR 23-SEP-1996; 990S-010147P. PR 23-SEP-1996; 990S-0101474P. PR 23-SEP-1996; 990S-0101472P. PR 23-SEP-1996; 990S-0101474P. PR 23-SEP-1996; 990S-0101230P. PR 23-SEP-1996; 990S-0101230P. PR 23-SEP-1996; 990S-010230P. PR 23-SEP-19 | #atch   Similarity   1   417; Conservatis   26 LRLLLLESAAAI   24 LRLLLLESAAAI   1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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transmembrane protein; tumour necrosis factor alpha; TNF-alpha; adrenal; chondrocyte cell; colon; breast; prostate; rectum; cervix; liver.
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98WO-US025108.
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 29-AUG-2001
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### (GETH ) GENENTECH INC.

Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL; Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;

#### WPI; 2003-341328/32. N-PSDB; ACD06949.

Three hundred and five nucleic acids encoding secreted and transmembrane by/peptides, designated as PRO, useful for detecting the presence of, or treating tumor, e.g. adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumor.

## Claim 11; Fig 34; 707pp; English.

The invention relates to human PRO polypeptides (secreted and transmembrane polypeptides) and the polymuclectides encoding them. The invention also relates to an antibody that specifically binds to a PRO polypeptide, a method for stimulating the release of tumour necrosis actor alpha (TWF-alpha) from human blood by contacting the blood with a PRO polypeptide and a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the blood with a PRO polypeptide. The polypeptides and polymucleotides are useful for detecting the presence of a tumour, such as an adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour, and for treating such tumours. The polymucleotides are useful as hybridisation probes, in chromosome and gene mapping and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, blosensors or bioreactors. Both are useful in tissue typing. Sequences AB001437-AB001741 represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at sequence.html

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Query Match 94.3%; Score 417; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 0;

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rectum; cervix; liver; cytostatic.
 82
 83
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144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; TNF-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; civix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
Human secreted polypeptide PRO355, SEQ ID NO:34.
 9710S-0059266P

9710S-0063280P

9710S-00633121P

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9710S-00633134P

9710S-0063311P

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Query Match 94.3%; Score 417; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels

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 Sequence 2, Application US/09778187B
PETENT NO. US20020168712A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Baum, Peter R.
TILLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILLE OF INVENTION: MOLECULES DESIGNATED LDCAM
CURRENT APPLICATION NUMBER: US/09/778,187B
CURRENT FILING DATE: 2001-02-06
PRIOR FILING DATE: 1999-08-05
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR APPLICATION NUMBER: US 60/095,672
PRIOR APLICATION NUMBER: US 60/095,672
NUMBER OF SEQ ID NOS: 10
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 TITLE OF INVENTION:
FILE REPERENCE:
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CURRENT APPLICATION NUMBER: US/09/778,510
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PRIOR PILING DATE: 1990-08-05
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NUMBER: OF SEQ ID NOS: 22
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1999-08-05
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 Patent No. US20020164686A1
GENERAL INFORMATION:
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 APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF48991
CURRENT APPLICATION NUMBER: US/09/836,353A
CURRENT FILING DATE: 2001-04-18
FRIOR REPLICATION NUMBER: 60/198,407
PRIOR PILING DATE: 2000-04-19
FRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR FILING DATE: 1999-10-27
PRIOR FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 147
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0; Mismatches
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US-09-836-353A-136
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 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300
 TISCQVNKSDDSVIQLLAPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 KGNTELKCKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTILTIITD 360
 301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT 360
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 4.4
 1 MASVVLPSGSQCAAAAAAAAPGIRLRLILIFSAAALIPTGGGQNLFTKDVTVIEGEVA 60
 1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 100.0%; Score 442; DB 10; Length 442;
 Length 442;
 Indels
 ;
 DB 9;
 AFLICANT N at C at 1.

TITLE OF INVENTION: 12 Human Secreted Proteins FILE REFERENCE: PP489P2
CURRENT APPLICATION NUMBER: US/09/984,130
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,792
PRIOR PILING DATE: 2000-10-30
PRIOR PILING DATE: 2000-10-30
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR PILING DATE: 2000-04-19
PRIOR PILING DATE: 1909-10-27
PRIOR PILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR PILING DATE: 1998-10-28
NUMBER OF SEQ ID NOS: 149
SOFTWARE: PatentIN Ver: 2.0
SEQ ID NO 136
 100.0%; Score 442; D
100.0%; Pred. No. 0;
tive 0; Mismatches
 DTAIINAEGGONNSEEKKEYFI 442
 DTAIINAEGGONNSEEKKEYFI 442
 ; Sequence 136, Application US/09984130; Publication No. US20030055231A1; GENERAL INFORMATION:
SOFTWARE: Patentin version 3.1 SEQ ID NO 2
 Query Match 100.
Best Local Similarity 100.
Matches 442; Conservative
 ; TYPE: PRT
; ORGANISM: homo sapiens
US-09-778-187B-2
 Homo sapiens
 APPLICANT: Ni et al.
 US-09-984-130-136
 US-09-984-130-136
 61
 241
 61
 121
 121
 181
 181
 301
 361
 361
 421
 421
 Query Match
 ORGANISM
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DISORDERS

|  | 421 DTAIINAEGGONNSEEKKEYFI 442<br> | RESULT 6 US-10-403-107-1 ; Sequence 1, Application US/10403107 ; Publication No. US20030165974A1 ; GENERAL INFORMATION: ; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE | 70                                    | CURRENT FILING DATE: 2003-28 ; PRIOR APPLICATION NUMBER: US/09/930,803 ; PRIOR FILING DATE: 2001-08-15 ; PRIOR FILING DATE: 2001-08-15 ; NUMBER OF SEQ ID NOS: 32 ; SOFTWARE: Patentin version 3.0 ; SEQ ID NO 1 ; LENGTH: 442 ; TYPE: RRT CORANISM: Homo sapiens US-10-403-107-1 | Query Match 100.0%; Score 442; DB 14; Length 442; Best Local Similarity 100.0%; Pred. No. 0; Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0;       | Qy         1 MASVVLPSGSQCAAAAAAPGIRLRILILFSAAALIPTGDGQNLFTKDVTVIEGEVA 60                                                                                                    | 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 1<br>                                      | Qy                                                                                                                                                                            | 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLLEVQ 241 YKPOVHIOMTYPLOGLTREGDALELICEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFI | 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVVYDPPTTIPPFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | Db 301 NNINKTDNGTYRCEASNIVGKAHSDYMLYVYDPFTTIPPFTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | Db 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420  Qy 421 DTAIINAEGGQNNSEEKKEYFI 442 | 421                                                          | RESULT 7<br>US-10-015-115-111 |
|--|------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------|-------------------------------|
|  |                                    | QY         301 NNLNKTDNGTYRCEASNIVGRAHSDYMLYVYDPPTTTPTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT                                                                                                  | Oy 421 DTAIINAEGCONNSEEKKEYFI 442<br> | RESULT 5 US-10-302-041-20 ; Sequence 20, Application US/10302041 ; Publication No. US20030144478A1 ; GENERAL INFORMATION: ; APPLICANT: Baum, Peter ; TILE OF INVENTION: Molecules Designated B7L1 ; FILE REFERENCE: 2844-US ; CURRENT APPLICATION NUMBER: US/10/302,041           | ; CURRENT FILING DATE: 2002-11-21<br>; PRIOR APPLICATION NUMBER: US/09/778,510<br>; PRIOR FILING DATE: 2001-02-07<br>; PRIOR APPLICATION NUMBER: PCT/US99/17906 | FRIOR FILING DATE: 1999-08-05 FRIOR APPLICATION NUMBER: 60/095,663 FRIOR FILING DATE: 1998-08-07 FORDER: DATE: 1998-08-07 FORDER: DATE: 1998-08-07 FORDER: DATE: 1998-08-07 | ; SOFIWARE: FACERCIN VET. 2.0<br>; SED TD NO 20<br>; IENCTH: 442<br>; TYPE: PRT<br>; ORGANISM: Homo sapien | US-10-302-041-20  Query Match 100.0%; Score 442; DB 14; Length 442;  Best Local Similarity 100.0%; Pred. No. 0;  Matches 442; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 1 MASYVLPSGSOCAAAAAAAAAPEGLRLELLLLESAAALIPTGDGONLFTKOVTVIEGEVA 60                                                                  | ISDEG<br>     <br>ISDEG                                                                                                                       | Qy 121 RYFCQLYIDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180        | Qy 181 KGNTELKGKSEVEEWSDMYTUTSQLMLKVHKEDDGVPVICQVEHPAVTGNLGYQRYLEVQ 240                                    | YKPQVHIQMTYPLOGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI | 301                           |

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SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 61 TISCQVNKSDDSVIQLLMPNRQTIVFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 181 - KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLF1 300
 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 61 TISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPFTTTTTTTTTTTTTILTIITD 360
 301 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT 360
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 1 MASVVI.PSGSQCAAAAAAAAPPGLRLRILILLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
 1 MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 ö
 Length 442;
 Indels
 APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-113 (793)
CURRENT APPLICATION NUMBER: US/10/363,616
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 09/654,935
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 490
 DB 15;
 ö
 Sequence 2, Application US/10622237
, Publication No. US20040204568A1
, GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
, TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
PILE REPERENCE: 2873-US
 100.0%; Score 442; I
 0; Mismatches
 442
 442
 DTAIINAEGGONNSEEKKEYFI 442
 ; Sequence 262, Application US/10363616; Publication No. US20040044181A1; GENERAL INFORMATION:
 421 DTAIINAEGGONNSEEKKEYFI
 421 DTAIINAEGGONNSEEKKEYFI
 Query Match
Best Local Similarity 100.0
Matches 442; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
US-10-363-616-262
 US-10-363-616-262
 US-10-622-237-2
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 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 NNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTT
 301 NNINKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT 360
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 1 MASVVLPSGSQCAAAAAAAAPGIRLRLILILFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
 1 MASVVLPSGSQCAAAAAAAAAPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA 60
 Gaps
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 DB 15; Length 442;
 Indels
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0
 0; Mismatches
 100.0%; Score 442; 100.0%; Pred. No. 0;
Application US/10015115
 Li, Li
Padigaru, Muralidhara
 APPLICANT: Malyankar, Uriel M
APPLICANT: Shenoy, Suresh G
APPLICANT: Spytek, Kimberly A
APPLICANT: Zerhusen, Bryan D
APPLICANT: Petturajan, Meera
APPLICANT: Kekuda, Kaojia
APPLICANT: Kekuda, Ramesha
 Gangolli, Esha A
Shimkets, Richard A
 Taupier, Raymond J
 US20030207800A
 SOFTWARE: Patentin Ver. 2.1
 Matches 442; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 Query Match
Best Local Similarity
 Sequence 111, Applic
Publication No. US20
GENERAL INFORMATION:
 US-10-015-115-111
 SEQ ID NO 111
 181
 241
 301
 121
 121
 181
 361
 APPLICANT:
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Kljavin, Ivar
 Wood, William
 Tumas, Daniel
 Napier, Mary
Roy, Margaret
 ORGANISM: Homo Sapien
 Eaton, Dan
 RESULT 11
US-09-866-028-61
 US-09-866-028-61
 APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 301
 421
 APPLICANT:
 APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT:
 TYPE: PRT
 Query Match
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 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLILLGRYFARHKGTYFTHEAKGADDAADA 420
 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF 180
 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI 300
 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 9
 APPLICANT: GALIBERT, Laurent J.
APPLICANT: YAN, Wei
TILE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-A
FILE REFERENCE: 3467-A
CURRENT APPLICATION NUMBER: US/10/898,408
CURRENT FILING DATE: 2004-07-23
FILE REPLICATION NUMBER: 60/490,027
PRIOR APPLICATION NUMBER: 60/490,027
PRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
 1 MASVVLPSGSQCAAAAAAAAPGGLRLRLLLLFSAAALIPTGGGNLFTKDVTVIBGEVA
 1 MASVVLPSGSQCAAAAAAAAPPGLRLRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 Gaps
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 DB 16; Length 442;
 Indels
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0
 100.0%; Score 442; D
100.0%; Pred. No. 0;
Live 0; Mismatches
 CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US/09/778,187B
PRIOR FILING DATE: 2001-02-06
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
CURRENT APPLICATION NUMBER: US/10/622,237 CURRENT FILING DATE: 2003-07-17
 DTAIINAEGGONNSEEKKEYFI 442
 ; Sequence 2, Application US/10898408
; Publication No. US20050058642A1
; GENERAL INFORMATION:
 Conservative
 TYPE: PRT
ORGANISM: homo sapiens
US-10-622-237-2
 ; TYPE: PRT
; ORGANISM: homo sapiens
US-10-898-408-2
 Query Match
Best Local Similarity
Matches 442; Conserv
 LENGTH: 442
 LENGTH: 442
 US-10-898-408-2
 181
 121
 181
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 421
 SEQ ID NO 2
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 361 SRAGEEGSIRAVDHAVIGGVVAVVVPAMLCLLIILGRYPARHKGTYFTHEAKGADDAADA 420
 61 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 361 SRAGEEGSIRAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADA 420
 9
 1 MASVVLPSGSQCAAAAAAAAAPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
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 1 MASVVLPSGSQCAAAAAAAAAPPGLRLRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVA
 121 RYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWF
 241 YKPQVHIQMTYPLQGLTREGDALELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFI
 NUCLEIC
 ó
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PICI.
CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
 Length 442;
 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 120 SEQ ID NO 61 LENGTH: 440
 94.3%; Score 417; DB 9; Length 440;
 Indels
 ö
 DB 17;
Score 442; DF
 Query Match
100.0%; Score 442; Dest Local Similarity 100.0%; Pred. No. 0; Matches 442; Conservative 0; Mismatches
 442
 ; Sequence 61, Application US/09866028; Patent No. US20020058309A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin; APPLICANT: Botstein, David
 421 DTAIINAEGGONNSEEKKEYFI
 DTAIINAEGGONNSEEKKEYFI
 Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary
Goddard, Audrey
 Godowski, Paul
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US-09-944-449-61
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 APPLICANT: Najati, Ivar
APPLICANT: Najati, Ivar
APPLICANT: Najati, Ivar
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION NUMBER: US/09/44,449
PRIOR PILING DATE: 2001-09-26
PRIOR PAPLICATION NUMBER: 60/067,411
PRIOR PLILING DATE: December 11, 1997
PRIOR PLILING DATE: December 12, 1997
PRIOR PLILING DATE: December 16, 1997
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADADIAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
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 0; Indels
100.0%; Pred. No. 0;
tive 0; Mismatches
 Sequence 61, Application US/09944449
Patent No. US20020102647A1
GENERAL INFORMATION:
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Kljavin, Ivar
 Eaton, Dan
 US-09-944-449-61
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86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 26 LRILLLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 IRELELLESAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 94.3%; Score 417; DB 9; Length 440
 OR FILING DATE: December 1, 1998
CR APPLICATION NUMBER: 09/216,021
CR FILING DATE: December 16, 1998
CR FILING DATE: December 16, 1998
CR FILING DATE: December 22, 1999
CR APPLICATION NUMBER: 09/254,311
CR FILING DATE: SEPTEMBER: PCT/US99/21090
CR FILING DATE: September 15, 1999
CR FILING DATE: September 15, 1999
CR FILING DATE: September 15, 1999
CR FILING DATE: OW UNMBER: PCT/US99/28409
CR FILING DATE: OW UNMBER: PCT/US99/28313
 FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION UNDRER: PCT/US99/28301
FILING DATE: December1, 1999
APPLICATION NUMBER: PCT/US99/30095
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 Query Match 94.3%; Score 417; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 PRIOR APPLICATION NUMBER: PCT/USO/0414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO/05841
PRIOR FILING DATE: MARCH 2, 2000
PRIOR APPLICATION NUMBER: PCT/USO/06439
PRIOR PLING DATE: MARCH 30, 2000
PRIOR PELING DATE: MACH 30, 2000
PRIOR PELING DATE: MAY 22, 2000
PRIOR PILING DATE: MAY 22, 2000
PRIOR PLING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USO/20710
PRIOR PLING DATE: July 28, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO/06520
PRIOR PLING DATE: PEDTUARY 28, 2001
NUMBER: OF SEQ ID NOS: 120
 RELIGION DATE: PEDLUARY 25, 1998
REPLICATION NUMBER: 60/112,850
RELING DATE: December 16, 1998
REPLICATION NUMBER: 60/113,296
RETLING DATE: December 22, 1998
RETLING DATE: DECEMBER: 60/146,222
REPLING DATE: July 28, 1999
REAPPLICATION NUMBER: PCT/US98/19330
 FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
 APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
 FILING DATE: December 18, 1997 APPLICATION NUMBER: 60/070,440
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 FILING DATE: December 16, 1999
 FILING DATE: December 17, 1997 APPLICATION NUMBER: 60/068,017
 APPLICATION NUMBER: 60/074,092
 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
 FILING DATE: December 17,
 FILING DATE: February
 ORGANISM: Homo Sapien
 SEQ ID NO 61
LENGTH: 440
TYPE: PRT
 US-09-944-457-61
 PRIOR
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 APPLICANT: Kliavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Napier, Mary
APPLICANT: Noy, Margaret
APPLICANT: Town Subjer, Mary
APPLICANT: Town Subjer, Mary
APPLICANT: Town Subjer, Mary
APPLICANT: Town Subjer, Mary
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P25448P1C1
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: Docember 13, 1997
PRIOR PELICATION NUMBER: 60/669, 334
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 12, 1997
PRIOR PELICATION NUMBER: 60/669, 425
PRIOR FILING DATE: December 12, 1997
PRIOR PELICATION NUMBER: 60/669, 696
PRIOR FILING DATE: December 16, 1997
PRIOR PELICATION NUMBER: 60/669, 696
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PRIOR PELICATION NUMBER: 60/669, 696
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 Sequence 61, Application US/09944457
Patent No. US20020110859A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Botstein, David
 Hillan, Kenneth
 Gurney, Austin
 APPLICANT: Baker, Kevin
 US-09-944-457-61
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146 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 84 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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 DB 9; Length 440;
 0; Indels
 PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020115145Alember 30, 1999
PRIOR APPLICATION: UNDER: PCT/US99/28313
PRIOR FILING DATE: No. US20020115145Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PECAMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
 OR APPLICATION NUMBER: 09/216,021
OR FILING DATE: December 16, 1998
OR APPLICATION NUMBER: 09/218,517
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR FILING DATE: June 22, 1999
OR FILING DATE: June 22, 1999
OR PILING DATE: June 22, 1999
 APPLICATION NUMBER: 60/146,222
FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
 FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
 PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR PELING DATE: DECEMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04114
PRIOR FILING DATE: February 22, 2000
 APPLICATION NUMBER: PCT/US00/05841
FILING DATE: March 2, 2000
 FILING DATE: January 5, 1998
APPLICATION WUMBER: 60/074,086
ELING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
 LING DATE: December 18, 1997
PLICATION NUMBER: 60/070,440
 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
APPLICATION UNMBER: 60/112,850
 FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
 LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-862-61
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 AFPLICANT:
MOGO, WALIDIAM

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2248P1C1
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT PILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: December 3, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR PLING DATE: December 16, 1997
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 PAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 442
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APPLICATION NUMBER: 60/069,873
FILING DATE: December 17, 1997
 APPLICATION NUMBER: 60/068,017
 RESULT 14
US-09-944-862-61
; Sequence 61, Application US/09944862
; Patent No. US20020115145A1
; GENERAL INFORMATION
 YMLYVYDPPTTIPPPTTTTTT
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Goddard, Audrey
Godowski, Paul
 Hillan, Kenneth
 Gerritsen, Mary
 Gurney, Austin
 Tumas, Daniel
Wood, William
 Kljavin, Ivar
 Roy, Margaret
 Napier, Mary
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 APPLICANT:
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206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 84 FRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
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 146 NIMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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 Query Match 94.3%; Score 417; DB 9; Length 440; Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches 0; Indels
 PRIOR APPLICATION NUMBER: 60/074,092
PRIOR PILING DATE: February 25, 1998
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PRIOR PILING DATE: February 25, 1998
PRIOR PILING DATE: December 16, 1998
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PRIOR APPLICATION NUMBER: 60/113,296
PRIOR PELING DATE: December 16, 1998
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PRIOR PELING DATE: PECT/USO9/03565
PRIOR PELING DATE: PECT/USO9/03565
PRIOR PELING DATE: PECT-USO9/03565

PRIOR PELING DATE: PECT-USO9/035678
PRIOR PELING DATE: PECT-USO9/03678
PRIOR PELING DATE:
 February 9, 1998
 ORGANISM: Homo Sapien
 US-09-945-587-61
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 TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR PLING DATE: 2001-05-26
PRIOR PLING DATE: 2001-05-32
PRIOR PLING DATE: December 3, 1997
PRIOR PLING DATE: December 11, 1997
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PRIOR PRIOR DATE: DECEMBER: 60/069,010
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Sequence 61, Application US/09945587
Patent No. US20020127643A1
GENERAL INFORMATION:
 Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Baton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Fartara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritaen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christop
APPLICANT: Grimaldi, Christop
APPLICANT: Gurney, Austin
APPLICANT: Gurney, Austin
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Wood, William
 Napier, Mary
 RESULT 15
US-09-945-587-61
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND TITLE OF INVENTION: SECRETED SENCODING THE SAME CURRENT PELIGR DATE: 2010-09-26

PRIOR PILLOR DATE: 2001-05-25

PRIOR PILLOR DATE: December 13, 1997

PRIOR PILLOR DATE: December 11, 1997

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PRIOR PILLOR DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR PILLOR DATE: December 16, 1997

PRIOR PILLOR DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,694

PRIOR PILLOR DATE: December 16, 1997

PRIOR PILLOR DATE: December 16, 1997

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR PILLOR DATE: December 17, 1997

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PRIOR PILLOR DATE: December 16, 1997

PRIOR PILLOR DATE: December 16, 1997

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PRIOR PILLOR DATE: December 16, 1997

PRIOR PILLOR DATE: December 16, 1997

PRIOR PILLOR DATE: PEDELUARY 9, 1998

PRIOR APPLICATION NUMBER: 60/069,873

PRIOR APPLICATION NUMBER: 60/070,406

PRIOR PILLOR DATE: PEDELUARY 9, 1998

PRIOR PILLOR DATE: PEDELUARY 9, 1998

PRIOR PRILOR PILLOR DATE: PEDELUARY 9, 1998

PRIOR PILLOR DATE: PEDELUARY 9, 1998

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PRIOR PRILOR DATE: PEDELUARY 9, 1998
TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTT383
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 ; Sequence 61, Application US/09945015; Patent No. US20020132768A1; GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 Gurney, Austin
 Tumas, Daniel
Wood, William
 Kljavin, Ivar
 Roy, Margaret
 Napier, Mary
 09-945-015-61
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 APPLICANT:
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 0; Indels
 FRIOR FILING DATE: December 1, 1998
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FRIOR APPLICATION NUMBER: 09/218,021
FRIOR APPLICATION NUMBER: 09/218,1998
FRIOR APPLICATION NUMBER: 09/218,517
FRIOR APPLICATION NUMBER: 09/218,517
FRIOR FILING DATE: December 22, 1999
FRIOR FILING DATE: March 3, 1999
FRIOR FILING DATE: March 3, 1999
FRIOR PELLOR FILING BATE: June 22, 1999
FRIOR APPLICATION NUMBER: PCT/US99/21090
FRIOR APPLICATION NUMBER: PCT/US99/2813
FRIOR APPLICATION NUMBER: PCT/US99/2813
FRIOR FILING DATE: NO. US2002013768Alember 30, 1999
FRIOR FILING DATE: NO. US2002013768Alember 30, 1999
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FRIOR APPLICATION NUMBER: PCT/US99/28101
FRIOR APPLICATION NUMBER: PCT/US99/2810
FRIOR APPLICATION NUMBER: PCT/US00/0414
FRIOR APPLICATION NUMBER: PCT/US00/0414
FRIOR APPLICATION NUMBER: PCT/US00/0414
FRIOR FILING DATE: March 30, 2000
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 94.3%; Score 417; DB 9;
100.0%; Pred. No. 0;
iive 0; Mismatches 0
 R FILING DATE: December 16, 1998
RR APPLICATION NUMBER: 60/13,296
RR FILING DATE: December 22, 1998
RR FILING DATE: JULY 28, 1999
RR FILING DATE: JULY 28, 1999
RR FILING DATE: September 16, 1998
RR APPLICATION NUMBER: PCT/US98/19310
RR APPLICATION NUMBER: PCT/US98/19310
 60/112,850
February
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-945-015-61
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC CURRENT APPLICATION NUMBER: US/09/944,396

CURRENT PELLICATION NUMBER: US/09/944,396

PRIOR PELLICATION NUMBER: 00/066,088

PRIOR PELLICATION NUMBER: 00/066,128

PRIOR PELLING DATE: December 11, 1997

PRIOR PELLING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR PELLING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

PRIOR PELLING DATE: December 11, 1997

PRIOR PELLING DATE: December 11, 1997

PRIOR APPLICATION NUMBER: 60/069,278

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PRIOR PELLING DATE: Pebruary 9, 1998

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US-09-944-396-61
; Sequence 61, Application US/09944396
; Patent No. US20020132981A1
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
Napier, Mary
 Ferrara, Napoleone
Filvaroff, Ellen
 Baker, Kevin
Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Tumas, Daniel
Wood, William
 Roy, Margaret
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 94.3%; Score 417; DB 9; Length 440;
100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
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PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 22, 1998
PRIOR FILING DATE: March 3, 1999
PRIOR FILING DATE: March 3, 1999
PRIOR PILING DATE: March 3, 1999
PRIOR PILING DATE: Warch 3, 1999
PRIOR PILING DATE: Warch 3, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR PILING DATE: September 15, 1999
PRIOR FILING DATE: NO. US20020132981Alember 30, 1999
PRIOR PILING DATE: NO. US20020132981Alember 30, 1999
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FRICK FILING DATE: December1, 1999
FRICK FILING DATE: December 16, 1999
FRICK FILING DATE: December 16, 1999
FRICK PRILING DATE: Pebruary 11, 2000
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FRICK APPLICATION NUMBER: PC7/US00/04414
FRICK FILING DATE: February 22, 2000
FRICK FILING DATE: March 2, 2000
FRICK FILING DATE: March 30, 2000
FRICK FILING DATE: March 30, 2000
FRICK FILING DATE: March 30, 2000
FRICK FILING DATE: JULY 28, 2000
FRICK FILING DATE: JULY 28, 2000
FRICK FILING DATE: December 1, 2000
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PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
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442
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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PRIOR PILING DATE: December 11, 1997
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PRIOR APPLICATION NUMBER: 60/069,334
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PRIOR PILING DATE: December 11, 1997
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PRIOR PILING DATE: December 17, 1997
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PRIOR PILING DATE: PEDPURATY 9, 1998
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 APPLICATION NUMBER: PCT/US98/19330
 APPLICATION NUMBER: 60/146,222
 Sequence 61, Application US/09944432
Patent No. US20020142419A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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 Baker, Kevin
Botstein,David
 Hillan, Kenneth
 Gurney, Austin
 Kljavin, Ivar
 Wood, William
 Roy, Margaret
 Tumas, Daniel
 Napier, Mary
 Eaton, Dan
 US-09-944-432-61
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 DB 9; Length 440;
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 PRIOR FILING DATE: June 22, 1999
PRIOR PLING DATE: June 22, 1999
PRIOR PLING DATE: September: 15, 1999
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PRIOR PILING DATE: No. US20020142419Alember 30, 1999
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PRIOR APPLICATION NUMBER: PCT/US99/30095
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PRIOR PILING DATE: February 11, 2000
PRIOR PILING DATE: February 22, 2000
PRIOR PILING DATE: February 22, 2000
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PRIOR FILING DATE: March 2, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
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PRIOR PILING DATE: July 28, 2000
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PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDRUARY 28, 2001
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 FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
 FILING DATE: December 16, 1999
APPLICATION NUMBER: PCT/US00/03565
FILING DATE: December 1, 1998
APPLICATION WINDBER: 09/216,021
FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
 FILING DATE: December 22, 1998 APPLICATION NUMBER: 09/254,311
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Best Local Similarity 100.
Matches 417; Conservative
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
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Sequence 61, Application US/09943762
Patent No. US200220142558A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Baker, Kevin
Botstein, David
 Hillan, Kenneth
 Goddard, Audrey
 Gurney, Austin
 Kljavin, Ivar
Napier, Mary
 Tumas, Daniel
Wood, William
 Roy, Margaret
 RESULT 19
US-09-943-762-61
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 APPLICANT:
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FRIOR FILLING DATE: December 15, 1299
FRIOR FILLING DATE: March 3, 1999
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FRIOR APPLICATION NUMBER: PCT/US00/04414
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FRIOR FILLING DATE: March 30, 2000
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 APPLICATION NUMBER: 09/218,517
FILING DATE: December 22, 1998
 FILING DATE: December 22, 1998 APPLICATION NUMBER: 09/254,311
 December 16, 1998
 ; ORGANISM: Homo Sapien
US-09-943-762-61
FILING DATE:
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 OR FILING DATE: June 22, 1999

OR APPLICATION NUMBER: PCT/US99/21090

OR FILING DATE: September 15, 1999

OR FILING DATE: September 15, 1999

OR FILING DATE: No. US/020142959Alember 30, 1999

OR FILING DATE: No. US/020142959Alember 30, 1999

OR RILING DATE: No. US/020142959Alember 30, 1999

OR APPLICATION NUMBER: PCT/US99/28301

OR APPLICATION NUMBER: PCT/US99/30095

OR APPLICATION NUMBER: PCT/US99/30095

OR APPLICATION NUMBER: PCT/US99/30095

OR APPLICATION NUMBER: PCT/US99/30095

OR PRILING DATE: December 16, 1999

OR PRILING DATE: PCENDER 11, 2000

OR PILING DATE: PCENDER 11, 2000

OR PILING DATE: PCENDER 11, 2000

OR PILING DATE: PCENDER PCT/US90/04144
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 DB 9;
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 PRIOR AFFLICATION WINGER: PEDITARY 22, 2000
PRIOR FILING DATE: FEBRUARY 22, 2000
PRIOR PILING DATE: March 2, 2000
PRIOR PILING DATE: March 3, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR FILING DATE: May 22, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: December 1, 2000
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PRIOR PILING DATE: PEDTARY 28, 2001
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120

LENGTH: 440
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 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 ; ORGANISM: Homo Sapien
US-09-944-654-61
 US-09-943-851A-61
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 RESULT 21
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 PAPLICANT: Wood, MILLIAM
TITLE OF INVENTION: EXCEPTED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: EXCEPTED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: EXCEPTED AND TRANSHEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE REPERENCE: P254ePt.
CURRENT APPLICATION NUMBER: 05/06/028
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REIOR PLILING DATE: DECEMBER 11, 1997
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 Sequence 61, Application US/09944654
Patent No. US20020142959A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 Baker, Kevin
Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Hillan, Kenneth
 Gurney, Austin
 Kljavin, Ivar
 Roy, Margaret
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 94.3%; Score 417; DB 9; Length 440;
100.0%; Pred. No. 0;
ive 0; Mismatches 0; Indels
 PRIOR FILING DATE: Supcerior 12, 1399
PRIOR FILING DATE: No. US2002015095Alember 30, 1999
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PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR APPLICATION NUMBER: PCT/US00/0414
PRIOR PELING DATE: Pebruary 22, 2000
PRIOR PELING DATE: Pebruary 22, 2000
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR PELING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR APPLICATION NUMBER: PCT/US00/2678
PRIOR APPLICATION NUMBER: PCT/US00/2678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PELING DATE: December 1, 2000
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PRIOR FILING DATE: December 1, 2000
PRIOR PELING DATE: PERIOR RESULT 22
US-09-944-413-61
; Sequence 61, Application US/09944413
; Patent No. US20020156004A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
 September 15, 1999
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 US-09-943-851A-61
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 ##PLICANT: THINGS AND NUCLEIC
TITLE OF INVESTION: ACIDS ENCODING THE SAME
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CURRENT FALLOCATION NOTICE: DO 10.00-50
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Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Baker, Kevin
Botstein, David
 Hillan, Kenneth
 Gurney, Austin
 Kljavin, Ivar
 Roy, Margaret
 Tumas, Daniel
 Napier, Mary
 Eaton, Dan
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 APPLICANT
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No. US20020156004Alember 30, 1999
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PRIOR FILING DATE: December1, 1999
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PRIOR FILING DATE: December 16, 1999
PRIOR PLING DATE: PEDTUARY 11, 2000
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PRIOR PLING DATE: PEDTUARY 22, 2000
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PRIOR PLING DATE: March 30, 2000
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PRIOR PLING DATE: March 30, 2000
PRIOR PLING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PLING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: December 1, 2000
PRIOR PLING DATE: PEDTUARY 26, 2001
NUMBER OF SEQ ID NOS: 120

LENGTH: HOMO 61

LENGTH: HOMO SADIEN
 PLICATION NUMBER: PCT/US99/28301
 Sequence 61, Application US/09944403
Patent No. US20020165143A1
GENERAL INPORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Bater, Land
APPLICANT: Ferrara, Napoleone
APPLICANT: Fivaroff, Ellen
APPLICANT: Fivaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
FILING DATE:
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 US-09-944-413-61
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 APPLICANT: AUMBAL SICRERED AND TRANSHERBANE POLYPEFTIDES AND NUCLEIC TITLE REPRESENTATIONS ASCRETCHED AND TRANSHERBANE POLYPEFTIDES AND NUCLEIC TITLE REPRESENTATIONS ASCRETCHED AND TRANSHERANE POLYPEFTIDES AND NUCLEIC CURRENT APPLICATION NUMBER: 105/966.028

RECOR PELLING DATE: 2001-09-25 0966.028

RECOR PELLING DATE: 2001-09-25 0966.028

RECOR PELLING DATE: 2001-09-25 0966.028

RECOR PELLING DATE: 1001-09-25 0966.038

RECOR PELLING DATE: December 3, 1997

RECOR PELLING DATE: December 11, 1997

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RECOR PELLING DATE: DECEMBER 109/216, 1998

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RECOR RELLING DATE: RECORDER TOTAL SEPTIME 1999

RECOR RELLIN
 Grimaldi, Christopher
Ferrara, Napoleone
 Gerritsen, Mary
Goddard, Audrey
 Napier, Mary
Roy, Margaret
Tumas, Daniel
 Godowski, Paul
 Kljavin, Ivar
 APPLICANT:
APPLICANT:
APPLICANT:
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Gaps ; 0

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 Length 440;
 0; Indels
 DB 9;
 94.3%; Score 41,, ___ 100.0%; Pred. No. 0; +ive 0; Mismatches
 FRIOR RIFILING DATE: February 11, 2000
PRIOR FILING DATE: February 11, 2000
PRIOR PLING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: March 30, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR PILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/20710
PRIOR PILING DATE: December 1, 2000
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PRIOR PILING DATE: PEDVING
 APPLICATION NUMBER: PCT/US00/03565
 Sequence 61, Application US/09944896 Patent No. US20020168715A1
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Hillan, Kenneth
 TYPE: PRT
ORGANISM: Homo Sapien
 Eaton, Dan
 GENERAL INFORMATION:
FILING DATE:
 JS-09-944-896-61
 US-09-944-403-61
 APPLICANT:
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 Grimaldi, Christopher
 Gurney, Austin
Hillan, Kenneth
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Gaps

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 APPLICANT: Tumas,Daniel
APPLICANT: Wood,William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Length 440;
 0; Indels
 94.3%; Score 417; DB 9;
100.0%; Pred. No. 0;
iive 0; Mismatches 0
 PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR FILING DATE: MArch 30, 2000
PRIOR PELLING DATE: MArch 30, 2000
PRIOR APPLICATION NUMBER: PCT/USO0/14042
PRIOR APPLICATION NUMBER: PCT/USO0/20710
PRIOR PILING DATE: MJY 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: PEDIVARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 Sequence 61, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Query Match
Best Local Similarity 100.0
Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Goddard, Audrey
 Kljavin, Ivar
 Roy, Margaret
 Napier, Mary
 ; ORGANISM: Homo Sapien
US-09-944-896-61
 APPLICANT:
APPLICANT:
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APPLICANT:
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 APPLICANT:
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 APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: December 22, 1998
OR APPLICATION NUMBER: 09/254,311
OR FILING DATE: March 3, 1999
OR APPLICATION NUMBER: PCT/US99/12252
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: September 15, 1999
OR FILING DATE: September 15, 1999
OR FILING DATE: No. US20020168715A1ember 30, 1999
OR APPLICATION NUMBER: PCT/US99/28313
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 THILD OF ANY ANY ANY ANY STATES ENCODING THE SAME FILLS REFERENCE: P25.48PICL
CUCKRENT FILLING DATE: 2001-08-11
PRIOR APPLICATION NUMBER: 05/066,028
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PRIOR PILLING DATE: December 11, 1997
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Kljavin, Ivar
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P25.49PIC.
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILING DATE: 2001-08-31
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 Query Match 94.3%; Score 417; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: DECEMBER: PCT/US00/32678
PRIOR PILING DATE: DECEMBER: PCT/US00/32678
PRIOR PILING DATE: PEDRUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 Sequence 61, Application US/09944929
Publication No. US20020197612A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Goddard, Audrey
 Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
 Kljavin, Ivar
 US-09-944-944-61
 US-09-944-929-61
 APPLICANT:
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TYPE: PRT
ORGANISM: Homo Sapien
 US-09-944-907-61
 US-09-944-884-61
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 APPLICANT:
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 386
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 145
 84 FRDFRPLKDSRFQLINFSSSELKVSLINVSISDEGRYFCQLYIDPPQESYTIITVLVPPR 143
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 265
 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT3385
 82
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCOVNKSDDSVIOLLNPNROTIY 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1 CURRENT APPLICATION NUMBER: US/09/944,907 CURRENT FILING DATE: 2001-08-31 PRIOR APPLICATION NUMBER: 09/866,028 PRIOR APPLICATION NUMBER: 09/866,028
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Gaps
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 DB 9; Length 440;
0;
 0; Indels
 94.3%; Scor.
100.0%; Pred. No. v,
... 0; Mismatches
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
 ; Sequence 61, Application US/09944907
; Publication No. US20020198147A1
; GENERAL INFORMATION:
 Grimaldi, Christopher
Gurney, Austin
 Filvaroff, Ellen
 Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
Kljavin, Ivar
 Goddard, Audrey
 Gerritsen, Mary
 NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
 Godowski, Paul
 Tumas, Daniel
Wood, William
 Napier, Mary
Roy, Margaret
 TYPE: PRT
ORGANISM: Homo Sapien
 Eaton, Dan
 Query Match
Best Local Similarity
 RESULT 27
US-09-944-907-61
 US-09-944-929-61
 LENGTH: 440
 LENGTH: 440
 264
 326
 324
 386
 146
 206
 204
 266
 384
 APPLICANT:
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143
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 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 384 FAMLCLLILIGRYFARHKGTYFTHEAKGADDAADDAINNAEGGONNSEEKKEYFI 440
 FAMICLIIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 144 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVBEWSDMYTVTSQL
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTREGDALEL
 24 IRILILIFSAAALIPTGGGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLINPNRQTIY
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTDS ENCODING THE SAME FILE REFERENCE: P25.49PICT CURRENT APPLICATION NUMBER: US/09/944,884
CURRENT FILING DATE: 2001-08-31
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ;
0
 94.3%; Score 417; DB 10; Length 440;
 Length 440;
 Indels
 ;
0
94.3%; Score 417; DB 9;
100.0%; Pred. No. 0;
ive 0; Mismatches 0
 PRIOR APPLICATION NUMBER: 09/866,028 PRIOR FILING DATE: 2001-05-25 NUMBER OF SEQ ID NOS: 120 SEQ ID NO 61
 Sequence 61, Application US/09944884 Publication No. US20030077698A1 GENERAL INFORMATION:
 Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
 Ferrara, Napoleone
 Filvaroff, Ellen
 Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
 Hillan, Kenneth
 Kljavin, Ivar
Napier, Mary
Roy, Margaret
 Wood, William
 Tumas, Daniel
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 Eaton, Dan
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144 NIMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 204 MLKVHKEDDGVPVICQVEHPAVTGNLÇTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVWYTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 442
 440
 84 FRDFRPLKDSRFOLLNFSSSELKVSLINVSISDEGRYFCOLYTDFPOESYTTITVLVPPR
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
 FILE KEFEKENCE: PASABLICA:
CURRENT PILLING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILLING DATE: 2001-05-25
PRIOR FILLING DATE: 2001-05-25
PRIOR FILLING DATE: 2001-05-25
PRIOR PLICATION NUMBER: 60/067,411
PRIOR PLILING DATE: December 1, 1997
PRIOR FILLING DATE: December 11, 1997
PRIOR FILLING DATE: December 11, 1997
PRIOR FILLING DATE: December 11, 1997
PRIOR FILLING DATE: December 11, 1997
PRIOR PILLING DATE: December 11, 1997
PRIOR PELLING DATE: December 12, 1997
PRIOR PELLING DATE: December 16, 1997
PRIOR PELLING DATE: December 16, 1997
PRIOR PELLING DATE: December 16, 1997
PRIOR PELLING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
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PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR APPLICATION NUMBER: 60/069,696
 PILLING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
FILLING DATE: December 17, 1997
 ; Sequence 61, Application US/09943780; Publication No. US20030096742A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin; APPLICANT: Botstein, David
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 Godowski, Paul
 Napier, Mary
Roy, Margaret
Tumas, Daniel
 Wood, William
 Kljavin, Ivar
 Eaton, Dan
 98
 APPLICANT:
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCBAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3385
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
 83
 442
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 M.KVHKEDDGVPVI.CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTIY
 Gaps
 FAMLCLL I ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGONNSEEKKEYFI
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 Length 440;
 Indels
 0; Indels
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 DB 10;
 94.3%; Score 417; DB ilarity 100.0%; Pred. No. 0; Conservative 0; Mismatches
 Pred. No. 0;
0; Mismatches
 FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,852
CURRENT FILING DATE: 2001-08-31
 PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
 ; Sequence 61, Application US/09944852; Publication No. US20030083479A1; GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
100.08;
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Matches 417; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 Kljavin, Ivar
 Tumas, Daniel
Wood, William
 Roy, Margaret
 Napler, Mary
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
Matches 417; Conserva
 Eaton, Dan
 Best Local Similarity
 US-09-944-852-61
 APPLICANT:
APPLICANT:
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APPLICANT:
 SEQ ID NO 61
 324
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206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 84 FRDFRPLKDSRFQLLNFSSSBLKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERDERCE: P2548PH1C1
CURRENT APPLICATION NUMBER: US/09/945,584
CURRENT FILING DATE: 2001-09-26
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
 PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR PELING DATE: December 11, 1997
 FILING DATE: December 12, 1997
APPLICATION WUMBER: 60/069,697
FILING DATE: December 16, 197
APPLICATION NUMBER: 60/069,694
 Sequence 61, Application US/09945584 Publication No. US20030211570A1 GENERAL INFORMATION:
 APPLICATION NUMBER: 60/06933
FILING DATE: December 11, 19
APPLICATION NUMBER: 60/069,2
 Grimaldi,Christopher
 APPLICATION NUMBER: 60/
 FILING DATE: December 1 APPLICATION NUMBER: 60/
 APPLICATION NUMBER: 60
FILING DATE: December
 FILING DATE: December
 FILING DATE: December
 FILING DATE: December
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
 Goddard, Audrey
 Gurney, Austin
 Godowski, Paul
 Kljavin, Ivar
 doy, Margare
 Tumas, Danie]
 Napier, Mary
 Eaton, Dan
 FILING DATE:
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 APPLICANT:
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 24 IRLILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Length 440;
 Indels
 FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20030096742Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28313
APLILNG DATE: No. US20030096742Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
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 DB 10;
 94.3%; Score 417; DE 100.0%; Pred. No. 0; tive 0; Mismatches
 R FILING DATE: December 16, 1998
R APPLICATION UNDRER: 09/218,517
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 09/254,311
R FILING DATE: MATCH 3, 1999
R APPLICATION NUMBER: PCT/US99/12552
R FILING DATE: June 22, 1999
 FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
FILING DATE: December 1, 1998
 APPLICATION NUMBER: PCT/US99/30095
FILING DATE: December 16 100
 APPLICATION NUMBER: PCT/US09/30095
APPLICATION NUMBER: PCT/US00/03565
FILLING DATE: February 11
 APPLICATION NUMBER. 22, 2000
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/US00/20710
APPLICATION NUMBER: PCT/US00/20710
 FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
 APPLICATION NUMBER: PCT/US99/21090
 APPLICATION NUMBER: PCT/US00/08439
FILING DATE: March 30, 2000
 February 22, 2000
UMBER: PCT/US00/05841
 R FILING DATE: January 5, 1998
R APPLICATION NUMBER: 60/074,086
R FILING DATE: February 9, 1998
R APPLICATION NUMBER: 60/074,092
R FILING DATE: February 9, 1998
R APPLICATION NUMBER: 60/075,945
 R FILING DATE: February 25, 1998
R APPLICATION NUMBER: 60/112,850
R FILING DATE: December 16, 1998
R PILICATION NUMBER: 60/113,296
R FILING DATE: December 22, 1998
R APPLICATION NUMBER: 60/146,222
 FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
 APPLICATION NUMBER: 09/216,021
 PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 FILING DATE: February
APPLICATION NUMBER: PC
FILING DATE: March 2,
 Conservative
 TYPE: PRT
CORGANISM: Homo Sapien
US-09-943-780-61
 Query Match
Best Local Similarity
Matches 417; Conserv
 98
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264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 TCEA1GKPQPVMVTWVRVDDEMPQHAVL,SGPNLF1NNLNKTDNGTYRCEASN1VGKAHSD
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACLDS ENCODING THE SAME FILE REPERENCE: P2548PIC1
 FILE KEFEKENES: 123 PETCL.
CURRENT APPLICATION NUMBER: US/09/943,664
CURRENT FILING DATE: 2001-09-26
PRIOR PRICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: DOCEMBER: 60/067,411
PRIOR FILING DATE: DECEMBER: 60/069,334
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR PELICATION NUMBER: 60/069,335
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR FILING DATE: DECEMBER: 11,1997
PRIOR PRILING DATE: DECEMBER: 11,1997
PRIOR APPLICATION NUMBER: 60/069,25
 FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 APPLICATION NUMBER: 60/069,702
 APPLICATION NUMBER: 60/069,87
 Sequence 61, Application US/09943664 Publication No. US20040091972A1 GENERAL INFORMATION:
 FILING DATE: December 16, 199' APPLICATION NUMBER: 60/069,69
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
 FILING DATE: February 9, 1998
 APPLICATION NUMBER: 60/068,
 Godowski, Paul
Grimaldi, Christopher
 FILING DATE: December 16,
 FILING DATE: December 17
 December 17
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 Wood, William
 Roy,Margaret
Tumas,Daniel
 Napier, Mary
 FILING DATE:
 206
 266
 326
 APPLICANT:
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYIDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y
 Gaps
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 Length 440;
 0; Indels
 OR APPLICATION NUMBER: PCT/US99/28409
OR APPLICATION NUMBER: PCT/US99/28409
OR FILING DATE: No. US20030211570Alember 30, 1999
OR FILING DATE: No. US20030211570Alember 30, 1999
OR APPLICATION NUMBER: PCT/US99/2831
OR FILING DATE: December1, 1999
OR APPLICATION NUMBER: PCT/US99/30095
OR APPLICATION NUMBER: PCT/US99/30095
OR APPLICATION NUMBER: PCT/US09/30095
OR APPLICATION NUMBER: PCT/US09/03565
) DB 10;
 94.3%; Sco...
100.0%; Pred. No. v,
... 0; Mismatches
 THE APPLICATION NUMBER: PLAY, 2000

THE APPLICATION NUMBER: PCT/USOO/04414

THING DATE: February 11, 2000

THING DATE: February 22, 2000

THING DATE: MARCH 2, 2000

THING DATE: MARCH 2, 2000

THING DATE: MARCH 2, 2000

THING DATE: MAY 22, 2000

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THING DATE: MAY 22, 2000

THING DATE: MAY 22, 2000

THING DATE: MAY 28, 2000

THING DATE: MAY 28, 2000

THING DATE: JULY 28, 2000

THING DATE: JULY 28, 2000

THING DATE: JULY 28, 2000

THING DATE: MAY 28, 2000

THING DATE: MAY 28, 2000

THING DATE: MAY 28, 2000

THING DATE: MAY 28, 2000

THING DATE: MAY 28, 2000
 PR FILING DATE: January 5, 1998

RAPPLICATION NUMBER: 60/074,086

RELING DATE: FEBRUARY 9, 1998

RELING DATE: FEBRUARY 9, 1998

RELING DATE: FEBRUARY 9, 1998

RELING DATE: FEBRUARY 9, 1998

RELING DATE: December 25, 1998

RAPPLICATION NUMBER: 60/113,296

RELING DATE: December 16, 1998

RELING DATE: December 22, 1998

RELING DATE: December 22, 1998

RELING DATE: December 22, 1998

RELING DATE: SEGURARY 28, 1999

RELING DATE: SEGURARY 28, 1999

RELING DATE: SEGURARY 28, 1999

RELING DATE: SEGURARY 28, 1999

RELING DATE: SEGURARY 1998

RELING DATE: December 16, 1998

RELING DATE: December 16, 1998

RELING DATE: December 16, 1998

RELING DATE: December 16, 1998

RELING DATE: December 16, 1998

RELING DATE: December 16, 1998
 APPLICATION NUMBER: 09/216,021
BR FILING DATE: December 16, 1998
DR APPLICATION NUMBER: 09/218,517
DR APLICATION NUMBER: 09/254,311
DR FILING DATE: December 22, 1998
RILING DATE: MATCH 3, 1999
DR APPLICATION NUMBER: PCT/US99/12252
DR FILING DATE: June 22, 1999
DR APPLICATION NUMBER: PCT/US99/12109
 FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
FILING DATE: February 28, 2001
 PRIOR FILING DATE: January S, PRIOR PLICATION NUMBER: 60/ PRIOR APPLICATION NUMBER: 60/ PRIOR PILING DATE: February S, PRIOR FILING DATE: February S, PRIOR FILING DATE: February S, PRIOR FILING DATE: Pebruary S, PRIOR PLING DATE: December PRIOR PRIOR PLING DATE: December PRIOR PLING DATE: December PRIOR FILING DATE: December PRIOR PLING DATE: December PRIOR FILING DATE: December PRIOR FILING DATE: December PRIOR PRIOR FILING DATE: December PRIOR FILING DATE: December PRIOR FILING DATE: December PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: December PRIOR PRIOR PLING DATE: December PRIOR PRIOR PLING DATE: December PRIOR PRIOR DATE: December PRIOR PRIOR DATE: December PRIOR PRIOR DATE: December PRIOR APPLICATION NUMBER: PRIOR PRIOR PRIOR DATE: No. US200 PRIOR PRIOR DATE: No. US200 PRIOR PRIOR DATE: No. US200 PRIOR PLING DATE: Pebruary PRIOR PLING DATE: Pebruary PRIOR PLING DATE: Pebruary PRIOR PLING DATE: Pebruary PRIOR PLING DATE: Pebruary PRIOR PLING DATE: Pebruary PRIOR PLING DATE: Pebruary PRIOR PLING DATE: PEBRUARY PRIOR PLING DATE: MAY 22, PRIOR PLING DATE: MAY 22, PRIOR PPLING DATE: MAY 22, PRIOR PLING DATE: December PRIOR PLING DATE: December PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING DATE: PEDRUARY PRIOR PLING D
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Best Local Similarity 100.
Matches 417; Conservative
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ORGANISM: Homo Sapien
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CURRENT PILING DATE: 2002-01-15

PRIOR PELING DATE: 1997-09-18

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PRIOR PILING DATE: 1997-11-24
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 APPLICATION NUMBER: 60/069335
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069425
 Sequence 34, Application US/10052586 Publication No. US20020127584A1 GENERAL INFORMATION:
 PRIOR FILLING DATE: 1997-10-28
PRIOR APPLICATION NUMBER: 60/063541
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PRIOR APPLICATION NUMBER: 60/063544
 FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063564
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PRIOR APPLICATION NUMBER: 60/063734
 FILING DATE: 1997-10-29
APPLICATION NUMBER: 60/063870
 FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/064103
 APPLICATION NUMBER: 60/065311
 Watanabe, Colin K. Wood, William I.
 1997-11-13
 FILING DATE: 1997-10-3
 Gurney, Austin L.
 Goddard, Audrey
 Godowski, Paul
 Zhang, Zemin
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
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 OR PILING DATE: Pebruary 9, 1998
OR APPLICATION NUMBER: 60/012,956
OR PILING DATE: Pebruary 25, 1998
OR PILING DATE: Pebruary 25, 1998
OR PILING DATE: Pebruary 25, 1998
OR PILING DATE: December 16, 1998
OR PILING DATE: December 22, 1998
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OR FILING DATE: September 15, 1999
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RELING DATE: Pebruary 11, 2000
RAPLICATION NUMBER: PCT/USO0/04414
RELING DATE: Pebruary 22, 2000
RAPLICATION NUMBER: PCT/USO0/05641
RELING DATE: March 2, 2000
RAPLICATION NUMBER: PCT/USO0/06439
RELING DATE: March 3, 2000
 APPLICATION NUMBER: PCT/USO0/14042
FILING DATE: May 22, 2000
APPLICATION NUMBER: PCT/USO0/2010
FILING DATE: Ully 28, 2000
APPLICATION NUMBER: PCT/USO0/32678
 FILING DATE: December 1, 2000
APPLICATION NUMBER: PCT/US01/06520
APPLICATION NUMBER: 60/074,092
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ORGANISM: Homo Sapien
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| 1997-12-12<br>NUMBER: 60/69870<br>1997-12-17<br>NUMBER: 60/068017<br>1997-12-18<br>NUMBER: 60/077450<br>1998-03-11<br>NUMBER: 60/077649<br>1998-03-11<br>NUMBER: 60/077649                                         | 2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1998-05-07<br>1998-05-15<br>1998-05-15<br>NUMBER: 60/085579<br>1998-05-15<br>NUMBER: 60/08580<br>1998-05-15<br>NUMBER: 60/08582<br>1998-05-15<br>NUMBER: 60/085700 |
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94.3%; Score 417; DB 13; Length 440;

Query Match

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204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 146 NIMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTILTITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT 1383
 146 NLMIDIQKDTAVEGERIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 386 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Shang, Zemin I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176, 758
CURRENT APPLICATION NUMBER: US/10/176, 758
FILO APPLICATION TEMOVED - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTREGDALEL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 Length 440;
 Indels
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 14;
 94.3%; Scor.
100.0%; Pred. No. v,
... 0; Mismatches
 В
 ; Sequence 34, Application US/10176758; Publication No. US20030008353A1; GENERAL INFORMATION:
 APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 94.34
Best Local Similarity 100.0
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
CRGANISM: Homo Sapien
US-10-176-758-34
 US-10-176-758-34
 LENGTH: 440
 206
 266
 264
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 324
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 APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Coddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Pan, James
APPLICANT: San, James
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: Shang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PANJORICAL
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT PILING DATE: 2002-06-18
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NIMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 FRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPOPVMVTWVKVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTLTITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 LRLILLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 24 LRILLELPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYFI 442
 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 Gaps
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0
 DB 14; Length 440;
 0; Indels
 0; Indels
 Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 tch
al Similarity 100.0%; Pred. No. 0;
417; Conservative 0; Mismatches
 Pred. No. 0; Mismatches
 Sequence 34, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:
100.0%; Pre-
 417; Conservative
 APPLICANT: Baker, Kevin P.
 TYPE: PRT
ORGANISM: Homo Sapien
 Best Local Similarity
 US-10-174-590-34
 LENGTH: 440
 Query Match
Best Local S
Matches 417
 98
 84
 146
 204
 326
 386
 SEQ ID NO 34
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APPLICANT:
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APPLICANT:
 Sequence 34, Application US/10175737
Publication No. US20030013153A1
GENERAL INFORMATION:
APPLICANT: Desnoyers, Luc
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godweki, Paul J.
APPLICANT: Gutney, Austin L.
APPLICANT: Matanbe, Colin K.
APPLICANT: Matanbe, Colin K.
APPLICANT: Smith, Victoria
APPLICANT: Matanbe, Colin K.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Attang, Zemin
APPLICANT: Attang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF SPELICATION NUMBER: US/10/175,737
CURRENT PILING DATE: 2002-06-19
PULOT AND ACIDS ENCODING THE SAME
CURRENT PILICATION NUMBER: US/10/175,737
CURRENT PILICATION NUMBER: 2002-06-19
NUMBER OF SEQ ID NOS: 612
MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 265
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGQNNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 24 LRILILIESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 94.3%; Score 417; DB 14; Length 440; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 36
US-10-175-737-34
 US-10-175-737-34
 SEQ ID NO 34
 204
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 206
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P943-0811-C41
CURRENT APPLICATION NUMBER: US/10/174,581
CURRENT FILING DATE: 2002-06-18
 CURRENT FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: 10/052586
PRIOR APPLICATION NUMBER: 10/05268
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-09-18
PRIOR PILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063120
PRIOR PILING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-24
PRIOR PELING DATE: 1997-10-28
PRIOR PELING DATE: 1997-10-28
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PRIOR PELING DATE: 1997-10-31
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PRIOR PELING DATE: 1997-11-3
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PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1997-11-21
Sequence 34, Application US/10174581 Publication No. US20030017540A1 GENERAL INFORMATION:
 FILING DATE: 1997-12-17
APPLICATION NUMBER: 60/068017
 FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/077450
 PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION UNDBER: 60/078886
PRIOR FLING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078939
 APPLICATION NUMBER: 60/077632
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 1998-03-10
 FILING DATE: 1998-03-11
 Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
 Chen, Jian
 FILING DATE: 1
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FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-09
 APPLICATION NUMBER: 60/084639
TITING DATE: 1998-05-07
 APPLICATION NUMBER: 60/081049
FILING DATE: 1998-04-08
 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/084366
 FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
 FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
 APPLICATION NUMBER: 60/08582
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085700
FILING DATE: 1998-05-15
 FILING DATE: 1998-05-18
APPLICATION UNMBER: 60/086392
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/086486
 FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087098
FILING DATE: 1998-05-28
 FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
 APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
 APPLICATION NUMBER: 60/079786
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/080107
 FILING DATE: 1998-03-31
APPLICATION WIMBER: 60/080194
FILING DATE: 1998-03-31
APPLICATION NUMBER: 60/080327
 FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
FILING DATE: 1998-04-01
 APPLICATION NUMBER: 60/081070
 FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
 APPLICATION NUMBER: 60/082569
 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082797
 FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/083322
 APPLICATION NUMBER: 60/083495
 APPLICATION NUMBER: 60/083496
 APPLICATION NUMBER: 60/084414
 FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084643
 APPLICATION NUMBER: 60/085573
 APPLICATION NUMBER: 60/085580
 APPLICATION NUMBER: 60/086023
 APPLICATION NUMBER: 60/081838
 FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
 APPLICATION NUMBER: 60/083559
 FILING DATE: 1998-04-28
 FILING DATE: 1998-04-29
 FILING DATE: 1998-05-15
 FILING DATE: 1998-04-29
 FILING DATE: 1998-05-05
 FILING DATE: 1998-05-07
 1998-03-27
 FILING DATE:
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84 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143 144 NLMIDIQKDTAVEGEBIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL LRILLLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY LRILLILEPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY NLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL ö Length 440; Indels 94.3%; Score 417; DB 14; 100.0%; Pred. No. 0; iive 0; Mismatches 0; FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/08855
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088722 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088740 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088811 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088825 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088826 FILING DATE: 1998-06-10 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/089090 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 APPLICATION NUMBER: 60/088212 APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088326 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088861 APPLICATION NUMBER: 60/088863 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 Query Match 94.3%; Best Local Similarity 100.0%; Matches 417; Conservative 0 FILING DATE: 1998-06-05 1998-06-03 FILING DATE: 1998-06-04 FILING DATE: 1998-06-05 FILING DATE: 1998-06-11 FILING DATE: 1998-06-12 FILING DATE: 1998-06-17 56 98 146 윱 ò ò ò

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206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 384 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAINAEGGQNNSEEKKEYFI 440
 APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACTIOS ENCODING THE SAME
FILE REPERENCE: P343,0R.1076
CURRENT APPLICATION NUMBER: US/10/176,749
CURRENT PILING DATE: 2002-06-20
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLILLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI
 386 FAMLCLIILGRYFARHKGTVFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
 386 FAMLCLLILLGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
 .;
0
 14; Length 440;
 Indels
 Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 .
0
 DB
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 RESULT 40
US-10-176-914-34
Sequence 34, Application US/10176914
Publication No. US20030017543A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
 Sequence 34, Application US/10176749
Publication No. US20030017542A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match
Best Local Similarity 100. Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-749-34
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 APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: APPLICANT: APPLICANT: Stang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE REFERENCE: P3430RIC68
CURRENT APPLICATION NUMBER: US/10/176,483
CURRENT FILING DATE: 2002-06-20
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFOLLNFSSSELKVSLTNVSISDEGRYFCOLYTDPPOESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT3385
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
 325
 264 TCEAIGKPQPVMVTWTVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 YMLYVYDPPITIPPPTITITTTTTTTTTTTTTTTTTTT383
83
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 PAMLCLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 440
 24 IRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 DB 14; Length 440;
 0; Indels
 Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 94.3%; Scor.
100.0%; Pred. No. v,
... 0; Mismatches
 Sequence 34, Application US/10176483
Publication No. US20030017541A1
GENERAL INFORMATION:
APPLICANT: BAKET Kevin P.
 Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
Matches 417; Conserv
 US-10-176-483-34
 324
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86 FRDFRPLKDSRFQLLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT3388
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAAIINAEGGONNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 144 NLMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTREGDALEL
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 APPLICANT: Wood, William I.

PEDLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENE APPLICATION NUMBER: US/10/173,706
CURRENT APPLICATION DATE: 2002-06-17
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Query Match
94.3%; Score 417; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels (
 PILE REFERENCE: P3430R1C110
CURRENT APPLICATION NUMBER: US/10/176,915
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper NUMBER OF SEQ ID NOS: 612
LENGTH: 440
 Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 TITLE OF INVENTION: ACIDS ENCODING
 Sequence 34, Application US/10173706
Publication No. US20030022293A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-706-34
 TYPE: PRT
ORGANISM: Homo Sapien
 Pan,James
 US-10-176-915-34
 APPLICANT:
APPLICANT:
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 APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Bar, James a
APPLICANT: Watcanabe, Colin K.
APPLICANT: Watcanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: BECREED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPRENCE: P342081C83
CURRENT APPLICATION NUMBER: US/10/176,914
CURRENT FILING DATE: 2002-06-20
PTIOR APPLICATION NUMBER: US/2002-06-20
FILE REPRENCE: SEQ ID NOS: 612
SEQ ID NO 34
FERRAL AAA
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 263
 96 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 Gaps
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 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10176915
Publication No. US20030017544A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Watanabe, Colin K.
Wood, William I.
 Matches 417; Conservative
 Pan, James
Smith, Victoria
 TYPE: PRT
ORGANISM: Homo Sapien
 Chen, Jian
 Similarity
 RESULT 41
US-10-176-915-34
 US-10-176-914-34
 APPLICANT:
APPLICANT:
APPLICANT:
 326
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APPLICANT:
 Query Match
Best Local 9
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266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 384 FAMLCLLILIGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGQNNSEEKKEYFI 440
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 144 NLMIDIOKOTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C60
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
 24 LRILLILFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 84 FRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITULVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 0; Gaps
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 .
0
 Query Match
94.3%; Score 417; DB 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0;
 ; Sequence 34, Application US/10175752; Publication No. US20030022295A1; GENERAL INFORMATION:
 Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 RESULT 44
US-10-175-752-34
 LENGTH: 440
 US-10-175-752-34
 APPLICANT:
APPLICANT:
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 APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Alang Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDE ENCODING THE SAME
FILE REPERENCE: P3430R1c45
CURRENT PILING DATE: 2002-06-19
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 265
 145
 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTT3388
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 143
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 24 LRILLLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY 83
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 LRILLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 DB 14; Length 440;
 Length 440;
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al Similarity 100.0%; Pred. No. 0;
417; Conservative 0; Mismatches
 Query Match 94.3%; Score 417; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 // Sequence 34, Application US/10175738
// Publication No. US20030022294A1
// GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc APPLICANT: Goddard, Audre)
 TYPE: PRT
ORGANISM: Homo Sapien
 JS-10-175-738-34
 SEQ ID NO 34
 204
 326
 86
 84
 206
 266
 264
 324
 386
 384
 98
 146
 Query Match
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 APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Apari, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C70
CURRENT APPLICATION NUMBER: US/10/176,482
CURRENT APPLICATION THOUGHER: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
264 TCEAIGKPQPVMVTWTVBVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT338AGEEGSIRAVDHAVIGGVVAVVV 385
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 83
 PAMLCLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 442
 PAMLCLIILGRYFARHKGTYFTHEAKGADDAADADAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 442
 24 LRLLLLLFSAAALIPTGGGNLFTKDVTVIBGEVATISCQVNKSDDSVIQLLNPRRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
tive 0; Mismatches
 Sequence 34, Application US/10176482; Publication No. US20030022296A1; GENERAL INFORMATION: APPLICANT: Baker Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
 417; Conservative
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-482-34
 Query Match
Best Local Similarity
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265
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 83
 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 84 FRDFRPLKDSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430RTON: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 ö
 94.3%; Score 417; DB 14; Length 440; 100.0%; Pred. No. 0; Live 0; Mismatches 0; Indels (
 Sequence 34, Application US/10176913; Publication No. US20030022298A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P.; APPLICANT: Chen, Jian; APPLICANT: Goddard, Audrey; APPLICANT: Goddowski, Paul J.
Sequence 34, Application US/10176757; Publication No. US20030022297A1; GENERAL INFORMATION:
 APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Garney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Wacsnabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-757-34
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- See File Wrapper or Palm
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J.
 Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
 Prior Application removed
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 APPLICANT: Baker, Kevin P.
 ; ORGANISM: Homo Sapien
US-10-180-552-34
 ORGANISM: Homo Sapien
 Chen, Jian
 US-10-180-557-34
 US-10-180-557-34
 LENGTH: 440
TYPE: PRT
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 146
 TYPE: PRT
 Query Match
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 Sequence 34, Application US/10180552

Sequence 34, Application US/10180552

Publication No. US20030022300A1

GENERAL INFORMATION:
APPLICANT: Baker,Kevin P.
APPLICANT: Chen,Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Pan,James
APPLICANT: Garney,Austin L.
APPLICANT: Graney,Austin L.
APPLICANT: Matanabe,Colin K.
APPLICANT: Watanabe,Colin K.
APPLICANT: Watanabe,Colin K.
APPLICANT: APPLICANT: Appliliam I.
APPLICANT: Appliliam I.
APPLICANT: Appliliam I.
APPLICANT: Appliliam I.
APPLICANT: Alang,Zemin
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R153
CURRENT APPLICATION NUMBER: US/10/180,552
 ö
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C66
CURRENT APPLICATION NUMBER: US/10/176, 913
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See file Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
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 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MLKVHKEDDGVPVICQVEHPAVTGNIQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTJBSRAGEEGSIRAVDHAVIGGVVAVVV 385
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTT383
 82
 83
 FAMLCLLILLGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCOLYTDPPOESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ö
 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
:ive 0; Mismatches
 Best Local Similarity 100.
Matches 417; Conservative
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-913-34
 RESULT 48
US-10-180-552-34
 56
 146
 206
 204
 266
 326
 324
 386
 384
 Query Match
Best Local
 264
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 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 85
 83
 442
 384 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: 19430RICL47
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
 .;
0
 ö
 94.3%; Score 417; DB 14; Length 440; 100.0%; Pred. No. 0;
 Length 440;
 Indels
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Query Match 94.3%; Score 417; DB 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0;
 ö
 Prior Application removed - See File Wrapper or
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 0; Mismatches
 Sequence 34, Application US/10180557 Publication No. US20030022301A1 GENERAL INFORMATION:
 Best Local Similarity 100.
Matches 417; Conservative
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325

323

440

265 263

203

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YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT338AGEEGSIRAVDHAVIGGVVAVVV 385
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTILIIIDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCBAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCBASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 386 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADDAINAEGGONNSEEKKEYFI 442
 APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zeniam I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C40
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT APPLICATION THE SAME FILING DATE: 2002-06-18
PILOT Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLLLLESAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIX
 NLMIDIQKDTAVEGEEI EVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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0
 94.3%; Score 417; DB 14; Length 440;
 0; Indels
 0; Mismatches
 US-10-174-572-34
Sequence 34, Application US/10174572
Publication No. US20030027263A1
GENERAL INFORMATION:
 100.08;
 Godowski, Paul J.
Gurney, Austin L.
 Best Local Similarity 100.
Matches 417; Conservative
 Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-174-572-34
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 206
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NIMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTLTIITDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 83
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 85
 83
 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: GUNDEY, AUSTIL D.
APPLICANT: GUNDEY, AUSTIL D.
APPLICANT: SHILLY, VICTORIA
APPLICANT: SHILLY, VICTORIA
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: ADARGA Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
FURRENT APPLICANTON NUMBER: US/10/173,700
CURRENT APPLICANTON NUMBER: US/10/173,700
FILE APPLICANTON NUMBER: US/202-06-17
Prior Application removed - See File Wrapper or Palm
 LRLILLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTI Y
 Gaps
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 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DE 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10173700; Publication No. US20030027262A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
US-10-173-700-34
 APPLICANT:
APPLICANT:
APPLICANT:
 98
 SEQ ID NO 34
 24
 84
 56
 146
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 324
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145

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Publication No. US20030027265A1
 RESULT 54
US-10-174-588-34
 SEQ ID NO 34
LENGTH: 440
 386
 146
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 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
APPLICANT: Zhang, Zemin I.
APPLICANT: APPLICATION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND CURRENT APPLICATION NUMBER: US/10/174,579
CURRENT APPLICATION NUMBER: US/10/174,579
 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MIKVHKEDDGVPVICQVEHPAVTGNLOTORYLEVOYKPOVHIQMTYPLOGLTREGDALEL 263
MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 83
 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 26 LRLLLLFSAAALIPTGDGQNLFTKDVTVIBGBVATISCQVNKSDDSVIQLLNDNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
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 ö
 DB 14; Length 440;
 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
tive 0; Mismatches
 ; Sequence 34, Application US/10174579; Publication No. US20030027264A1; GENERAL INFORMATION:
 RESULT 53
US-10-174-582-34
; Sequence 34, Application US/10174582
 Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 Similarity
 RESULT 52
US-10-174-579-34
 417;
 JS-10-174-579-34
 Query Match
Best Local S:
Matches 417,
 384
 204
 324
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 98
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 266
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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zemin
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
ITILE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1036
CURRENT APPLICATION NUMBER: US/10/174,582
CURRENT PILING DATE: 2002-06-18
FILE APPLICATION FROWER: 2002-06-18
FILE REPERENCE: SECOLO FROWER: SecOLO FROME FROM
 145
 205
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 82
 83
 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 Gaps
 ö
 Query Match

94.3%; Score 417; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
 Sequence 34, Application US/10174588; Publication No. US20030027266A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Pan, James
Smith, Victoria
Watanabe, Colin K.
 Godowski, Paul J. Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc APPLICANT: Goddard, Audre
), ORGANISM: Homo Sapien
US-10-174-582-34
 APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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 TCEAIGKPOPUMVTWVVDDEMPQHAVLSGPNLFINNLNKTDNGTVRCEASNIVGKAHSD 325
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT338AGEEGSIRAVDHAVIGGVVAVVV 385
 83
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDTAIINAECGONNSEEKKEYFI 440
APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: AZIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC38
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
 APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Saith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Sang, Zemin J.
APPLICANT: Zang, Zemin J.
APPLICANT: Zang, Zemin J.
APPLICANT: Zang, Zemin J.
APPLICANT: APPLICANT: AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: D43,07176, 739
CURRENT APPLICATION NUMBER: 108,10/175, 739
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 FAMLCLLI1LGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI
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 DB 14; Length 440;
 0; Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10175739; Publication No. US20030027267A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-174-588-34
 RESULT 55
US-10-175-739-34
 98
 204
 264
 84
 146
 206
 266
 326
 386
 Query Match
 APPLICANT:
APPLICANT:
APPLICANT:
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MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 204 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 85
 83
 83
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430FILC41
CURRENT APPLICATION NUMBER: US/10/175,740
CURRENT FILING DATE: 2002-06-18
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 ö
 94.3%; Score 417; DB 14; Length 440; 100.0%; Pred. No. 0; Indels (ive 0; Mismatches 0; Indels (
 14; Length 440;
 Indels
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 Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 Sequence 34, Application US/10175740 Publication No. US20030027268A1 GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J.
Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 Zhang, Zemin
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-739-34
 , ORGANISM: Homo Sapien
US-10-175-740-34
 Pan. James
 JS-10-175-740-34
 SEQ ID NO 34
LENGTH: 440
 APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
 84
 146
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 386
 384
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APPLICANT:
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R FILING DATE: 1997-11-24

R APPLICATION NUMBER: 60/069335

R FILING DATE: 1997-12-11

R FILING DATE: 1997-12-12

R APPLICATION NUMBER: 60/069425

R APPLICATION NUMBER: 60/069870

R FILING DATE: 1997-12-17

R FILING DATE: 1997-12-17

R FILING DATE: 1997-12-18

R APPLICATION NUMBER: 60/068017

R FILING DATE: 1997-12-18
 R FILING DATE: 1998-03-10
R APPLICATION NUMBER: 60/077632
R APPLICATION NUMBER: 60/077649
R APPLICATION NUMBER: 60/077649
R FILING DATE: 1998-03-11
R APPLICATION NUMBER: 60/078886
R FILING DATE: 1998-03-20
R APPLICATION NUMBER: 60/078999
 R FILING DATE: 1998-03-31

R APPLICATION NUMBER: 60/080194

R APPLICATION NUMBER: 60/080327

R FILING DATE: 1998-04-01

R FILING DATE: 1998-04-01

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R APPLICATION NUMBER: 60/08033
 R FILING DATE: 1998-04-15
R APPLICATION NUMBER: 60/082568
R FILING DATE: 1998-04-21
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R FILING DATE: 1998-04-21
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R FILING DATE: 1998-04-22
R APPLICATION NUMBER: 60/082797
 R FILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083499
R FILING DATE: 1998-04-29
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R RFILING DATE: 1998-04-29
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R RAPLICATION DATE: 1998-05-05
 FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-09
APPLICATION NUMBER: 60/081838
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APPLICATION UNDHER: 60/084639
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
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APPLICATION NUMBER: 60/066120
 FILING DATE: 1997-11-21
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APPLICATION NUMBER: 60/065311
 APPLICATION NUMBER: 60/066772
 FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/079664
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 Sequence 34, Application US/1017543

Sequence 34, Application US/1017543

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
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APPLICANTON NUMBER: GO/G6320
PRIOR PILING DATE: 1997-10-24
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PRIOR PILING DATE: 1997-10-22
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PRIOR APPLICANTON NUMBER: GO/G63870
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 TCEAIGKPOPVMVTWVRVDDEMPOHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 FAMLCLIIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
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R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/08553
R FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/08559
R FILING DATE: 1998-05-15
R APPLICATION NUMBER: 60/085580
 R FILING DATE: 1998-06-10
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R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
R APLILOS DATE: 1998-06-10
R APPLICATION NUMBER: 60/08861
R APPLICATION DATE: 1998-06-11
 APPLICATION NUMBER: 60/088863
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088976
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APPLICATION NUMBER: 60/089090
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APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
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APPLICATION NUMBER: 60/087098
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APPLICATION NUMBER: 60/088025
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APPLICATION NUMBER: 60/087208
 APPLICATION NUMBER: 60/087609
 FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088202
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 FILING DATE: 1998-05-28
 FILING DATE: 1998-06-05
 FILING DATE: 1998-06-10
DATE: 1998-05-07
 1998-06-02
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 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 203
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTILTITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 83
 386 FAMLCLLILGRYFARHKGTVFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDAIINAEGGQNNSEEKKEYFI 440
 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P343.0R1C119
CURRENT APPLICATION NUMBER: US/10/176,488
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH 440
TYPE: PRT
ORGANISM: Homo Sapien
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 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRILLILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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 DB 14; Length 440;
 Indels
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 Query Match
94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
 PRIOR FILING DATE: 1998-06-16
RRIOR APPLICATION NUMBER: 60/089514
PRIOR PILING DATE: 1998-06-16
RRIOR APPLICATION NUMBER: 60/089538
RRIOR FILING DATE: 1998-06-17
PRIOR PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
PRIOR PILING DATE: 1998-06-17
 Sequence 34, Application US/10176488 Publication No. US20030027271A1 GENERAL INFORMATION:
APPLICATION NUMBER: 60/089512
FILING DATE: 1998-06-16
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 Pan, James
 RESULT 58
US-10-176-488-34
 US-10-176-488-34
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
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APPLICANT:
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94.3%; Score 417; DB 14; Length 440;

Query Match

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APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Ban, James
APPLICANT: Pan, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Along, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDE ENCODING THE SAME
FILE REFERENCE: P3430R1C92
CURRENT APPLICATION NUMBER: US/10/176,747
CURRENT APPLICATION NUMBER: US/10/176,747
CURRENT APPLICATION NUMBER: US/2-06-20
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLIILGRYFARHKGTYFTHEAKGADDAADDAIINAEGGQNNSEEKKEYFI 440
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDALEL
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
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 24 LRLLLLFSAAALIPTGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Query Match
94.3%; Score 417; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
 Sequence 34, Application US/10176747
Publication No. US20030027273A1
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 GENERAL INFORMATION:
 US-10-176-747-34
 US-10-176-747-34
 APPLICANT:
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 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: SEGRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C107
CURRENT APPLICATION: MUMBER: US/10/176, 492
CURRENT FILING DATE: 2002-06-21
Frior Application removed - See File Wrapper or Palm
NUMBER: OF SEQ ID NOS: 612
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 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 NEMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 383
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 24 IRLILLIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
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 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 LRLLLLLFSAAALI PTGDGQNLFTKDVTVI EGEVATI SCQVNKSDDSVI QLLNPNRQTIY
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 FAMLCLLI ILGRYFARHKGTYFTHEAKGADDAADADTAI INAEGGONNSEEKKEYFI
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 DB 14; Length 440;
 0; Indels
 0; Indels
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 ; Pred. No. 0; 0; Mismatches
 ; Sequence 34, Application US/10176492; Publication No. US20030027272A1; GENERAL INFORMATION:
100.0%;
 Matches 417; Conservative
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-492-34
 Best Local Similarity
 RESULT 59
US-10-176-492-34
 SEQ ID NO 34
 324
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 APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Smith, Victoria
APPLICANT: Wood, William I.
APPLICANT: Town August Colin K.
APPLICANT: APPLICANT: Smith, Victoria
APPLICANT: APPLICANT: Smith, Victoria
APPLICANT: APPLICANT: Smith, Victoria
APPLICANT: APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P34390RICIO3
CURRENT APPLICATION NUMBER: US/10/176,750
CURRENT FILING DATE: 2002-06-21
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 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTBBRAGEEGSIRAVDHAVIGGVVAVVV 385
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTT383
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 440
 | FAMLCLLILGRYFARHKGTYFTHEAKGADDAADAADINAEGGQNNSEEKKBYF| 442
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 PAMLCLIILGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 440
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
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 DB 14; Length 440;
 0; Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 ; Sequence 34, Application US/10176750; Publication No. US20030027274A1; GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-750-34
 SEQ ID NO 34
 56
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APPLICANT: Watanabe, Colin-K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C99
CURRENT APPLICATION NUMBER: US/10/176, 985
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
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 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
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 266 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 83
 PAMLCLIIIGRYFARHKGTYFTHEAKGADDAADAAIINAEGGQNNSEEKKEYFI 440
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 DB 14; Length 440;
 Indels
 ö
 Query Match 94.3%; Score 417; DB Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
Sequence 34, Application US/10176985
Publication No. US20030027277A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
 ; Sequence 34, Application US/10176987; Publication No. US20030027278A1; GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
 Pan, James
Smith, Victoria
 ; ORGANISM: Homo Sapien
US-10-176-985-34
 US-10-176-987-34
 APPLICANT:
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26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 US-10-176-993-34
; Sequence 34, Application US/10176993
; Publication No. US20030027280A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
 APPLICANT: Pan, James

APPLICANT: Smith, Victoria

APPLICANT: Watanabe, Colin K.

APPLICANT: Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
 TYPE: PRT
ORGANISM: Homo Sapien
 ORGANISM: Homo Sapien
 US-10-176-992-34
 US-10-176-993-34
 LENGTH: 440
 APPLICANT:
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APPLICANT:
SEQ ID NO 34
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 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 TCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTLTITTDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 83
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: APOLYPEPTIDES AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE REPERBENCE: 29430R.C93
CURRENT APPLICATION NUMBER: US/10/176,987
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 APPLICANT: Wood, William I.

PEPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C100
CURRENT APPLICATION NUMBER: US/10/176, 992
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 ö
 Length 440;
 0; Indels
 DB 14;
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10176992
Publication No. US20030027279A1
GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Matanabe, Colin
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
Smith, Victoria
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-176-987-34
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 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVWVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 82
 83
 384 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 440
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACCESTED SUCODING THE SAME
FILE REFERENCE: P3430R1089
CURRENT PILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 24 LRILILLFSAAALIPTGDGQNLFTKDVIVIEGEVATISCQVNKSDDSVIQLINPNRQTIY
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 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 Gaps
 26 LRLLLLLFSAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIY
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI
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 Query Match
94.3%; Score 417; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0; Indels
 DB 14; Length 440;
 Indels
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Query Match
94.3%; Score 417; DB
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches
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APPLICANT:
APPLICANT:
Goddard, Audrey
APPLICANT:
Goddowki, Paul J.
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Goddowki, Paul J.
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Goddowki, Paul J.
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Goddowki, Paul J.
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Matanabe, Colin K.
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTT3185
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKKGNTELKGKSEVEEWSDMYTVTSQL 203
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCBAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTLTITTDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD
 24 LRILILIFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 FAMLCLI ILGRY FARHKGTY FTHEAKGADDAADADTAI INAEGGONNSEEKKEY FI
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 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB 100.0%; Pred. No. 0; ive 0; Mismatches
 Sequence 34, Application US/10176991; Publication No. US20030027324A1; GENERAL INFORMATION:
 Query Match 94.3*
Best Local Similarity 100.0
Matches 417; Conservative
 APPLICANT: Baker, Kevin P.
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 Chen, Jian
 US-10-176-991-34
 206
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 266
 264
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 APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Abag, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C228
CURRENT APPLICATION NUMBER: US/10/184,658
CURRENT FILING DATE: 2002-06-28
FILIC APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVGISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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 MIKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
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 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTJJJBSRAGEEGSIRAVDHAVIGGVVAVVV 385
 24 LKLLLLEFSAAALIPTGDGQNEFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 FAMLCLIIILGRYFARHKGTYFTHBAKGADDAADATAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLLIILGRYPARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
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 LRLLLLLFSAAALI PTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 ö
 Length 440;
 0; Indels
 DB 14;
 94.3%; Score 417; DB 100.0%; Pred. No. 0; cive 0; Mismatches
 ; Sequence 34, Application US/10184658; Publication No. US20030027281A1; GENERAL INFORMATION:
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-184-658-34
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 SEQ ID NO 34
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 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 144 NLMIDIQXDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTSRAGEEGSIRAVDHAVIGGVVAVVV 385
 324 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTDSRAGEEGSIRAVDHAVIGGVVAVVV 383
 83
 440
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 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 26 LRLLLLLPSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADIAIINAEGGONNSEEKKEYFI
 .;
0
 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
:ive 0; Mismatches
 US-10-173-697-34
; Sequence 34, Application US/10173697
; Publication No. US20030032102A1
; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-173-695-34
 98
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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Gurney, Austin L.
APPLICANT: Watenabe, Colin K.
APPLICANT: Watenabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
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 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 143
 205
 203
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTT3385
 83
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 440
 24 LRILILLFSAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 144 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 Gaps
 0
 Length 440;
 Indels
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 Query Match 94.3%; Score 417; DB 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 417; Conservative 0; Mismatches 0;
 Sequence 34, Application US/10173705; Publication No. US20030032103A1; GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gonowski, Paul J
APPLICANT: Gurney, Austin L
APPLICANT: Watanabe, Colin J
APPLICANT: Watanabe, Colin J
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Santh, Zanag, Zemin
Baker, Kevin P.
 ORGANISM: Homo Sapien
 Chen, Jian
 US-10-173-705-34
 LENGTH: 440
TYPE: PRT
 US-10-173-697-34
 APPLICANT:
APPLICANT:
APPLICANT:
 326
 386
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US-10-174-576-34
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 144 NIMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 203
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNINKTDNGTYRCEASNIVGKAHSD 323
 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTT338S
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY 83
 FAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKKEYFI 442
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC FITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C18 CURRENT APPLICATION NUMBER: US/10/173,705
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NOS: 612
 APPLICANT: GOGOWSKI, Paul J.
APPLICANT: GOGOWSKI, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Ban, James
APPLICANT: Matanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: APPLICANT: ALION SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC23
CURRENT APPLICATION NUMBER: US/10/174,576
CURRENT FILING DATE: 2002-06-18
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 26 LRLLLLFSAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIOLLNPNROTIY
 Gaps
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 Length 440;
 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 DB 14;
 94.3%; Score ...,
100.0%; Pred. No. 0;
...e. 0; Mismatches
 ; Sequence 34, Application US/10174576; Publication No. US20030032104A1; GENERAL INFORMATION:
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 Goddard, Audrey
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P.
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-173-705-34
 TYPE: PRT
ORGANISM: Homo Sapien
 LENGTH: 440
 SEQ ID NO 34
 204
 324
 84
 146
 206
 266
 264
 326
 386
 384
 APPLICANT:
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 86 PRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 265
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
 144 NLMIDIOKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSOL 203
 83
 83
 PAMLCLIIIGRYFARHKGTYFTHEAKGADDAADATAIINAEGGONNSEEKKEYFI 440
 386 PAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R.C37
CURRENT APPLICATION NUMBER: US/10/174,585
CURRENT FILING DATE: 2002-06-18
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 24 LRLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 146 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL
 MLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
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 Length 440;
 Length 440;
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 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
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 DB 14;
 14;
 94.3%; Scor.
100.0%; Pred. No. v,
... 0; Mismatches
 <u> 18</u>
Query Match 94.3%; Score 417; DE Best Local Similarity 100.0%; Pred. No. 0; Matches 417; Conservative 0; Mismatches
 Sequence 34, Application US/10174585
Publication No. US20030032105A1
GENERAL INFORMATION:
 Watanabe, Colin K.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Wood, William I.
 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 Pan,James
Smith,Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 ORGANISM: Homo Sapien
 RESULT 72
US-10-174-585-34
 US-10-174-585-34
 APPLICANT:
APPLICANT:
 206
 266
 326
 384
 APPLICANT:
APPLICANT:
 56
 APPLICANT:
APPLICANT:
 APPLICANT
 APPLICANT
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TITLE OF INVENTION: SECRETED AND TRANSMERRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430R1C4.

CURRENT FILING DATE: 1005-06-19
PRIOR PELICATION NUMBER: 00/69266
PRIOR PELICATION NUMBER: 60/69263
PRIOR PELICATION NUMBER: 60/69266
PRIOR PELICATION NUMBER: 60/69266
PRIOR PELICATION NUMBER: 60/69266
PRIOR PELICATION NUMBER: 60/69266
PRIOR PELICATION NUMBER: 60/69266
PRIOR PELICATION NUMBER: 60/69260
PRIOR PELICATION NUMBER: 60/66320
PRIOR PELICATION NUMBER: 60/66320
PRIOR PELICATION NUMBER: 60/66321
PRIOR PELICATION NUMBER: 60/66341
PRIOR PELICATION NUMBER: 60/66341
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PRIOR PELICATION NUMBER: 60/66311
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PRIOR PELICATION NUMBER: 60/66366
PRIOR PELICATION NUMBER: 60/66366
PRIOR PELICATION NUMBER: 60/66391
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 326 YMLYVYDPPTTIPPPTTTTTTTTTTTTTTTILTITDSRAGEEGSIRAVDHAVIGGVVAVVV 385
 266 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 384 FAMLCLIIIGRYFARHKGTYFTHEAKGADDAADATAIINAEGGQNNSEEKKEYFI 440
 386 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 Sequence 34, Application US/10175747
Publication No. US20030032107A1
GENERAL INFORMATION:
 APPLICATION NUMBER: 60/069335
FILING DATE: 1997-12-11
APPLICATION NUMBER: 60/069425
 APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 US-10-175-747-34
 APPLICANT:
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 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Godwarki, Paul J.
APPLICANT: Godwwrki, Paul J.
APPLICANT: Ban, James
APPLICANT: Ban, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: SEGRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430R1C24
CURRENT APPLICATION: NUMBER: US/10/174,586
CURRENT FILING DATE: 2002-06-18
FILE REPERENCE: P3430R1C24
CURRENT APPLICATION NUMBER: US/10/174,586
WUMBER: OF SEQ ID NOS: 612
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 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
 NLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNTELKGKSEVEEWSDMYTVTSQL 205
 206 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 325
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
 83
 384 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADDTAIINAEGGQNNSEEKKEYFI 440
 FAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKKEYFI 442
 24 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR
 26 LRLLLLLFSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIY
 Gaps
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0
 DB 14; Length 440;
 0; Indels
 94.3%; Score 417; DB
100.0%; Pred. No. 0;
:ive 0; Mismatches
 Sequence 34, Application US/10174586; Publication No. US20030032106A1; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.
Matches 417; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
US-10-174-586-34
 SEQ ID NO 34
 266
 386
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 96
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 TYPE: PRT
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| 1997-12-12<br>NUMBER: 60/069870<br>1997-12-18<br>NUMBER: 60/077450<br>1998-03-10<br>NUMBER: 60/077450<br>1998-03-11<br>NUMBER: 60/077632<br>1998-03-11<br>NUMBER: 60/077649<br>1998-03-11<br>NUMBER: 60/077649<br>1998-03-11<br>NUMBER: 60/077649                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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                                                                                                               | 44-28<br>60/08349<br>60/08349<br>44-29<br>60/08349<br>60/08355<br>44-29<br>60/08441<br>60/08441<br>60/08463<br>60/08463<br>60/08463<br>60/08464<br>60/08463<br>60/08558<br>60/08558<br>60/08558<br>60/08558<br>60/08558                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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| PILLING DATE: APPLICATION FILLING DATE:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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APPLICANT: Smith, Victoria
APPLICANT: Matanabe, Colin K.
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APPLICANT: Chang, Zemin
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 US-09-270-767-49730
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Sequence 1, Application US/09930803
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| Patent No. 6556493
| GENERAL INFORMATION:
| APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
| APPLICANT: WOSHINORI, Muramaki
| TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
| FILE REFERENCE: JUH1770-1
| CURRENT APPLICATION NUMBER: US/09/930,803
| CURRENT RELING DATE: 2001-08-15
| SOFTWARE: Patentin Version 3.0
| SOFTWARE: Patentin Version 3.0
| STOATMANE | SALOR OF TUMO
 TISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEG 120
 360
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 181 KGNTELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQ 240
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 DB 4; Length 442;
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100.0%; Pred. No. 0;
ive 0; Mismatches
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100.0%; Pred. No. 0;
Live 0; Mismatches
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Matches 442; Conservative
 Query Match
Best Local Similarity 100.
Matches 442; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1
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US-09-778-510-20
 442
 RESULT 2
US-09-930-803-1
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PILING DATE: December 11, 1997
PRIOR PILING DATE: December 11, 1997
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PRIOR PILING DATE: December 17, 1997
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 FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
 Sequence 61, Application US/09944457
Patent No. 6734288
 FILING DATE: February 9, 1998
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
 Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Goddard, Audrey
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
 Kljavin, Ivar
Napier, Mary
Roy, Margaret
 Tumas, Daniel
Wood, William
 Eaton, Dan
 GENERAL INFORMATION:
 APPLICANT:
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 86 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 145
241 YKPQVHIQMTYPLQGLTREGDALELICEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLF1 300
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2548PIC1
 24 LRLLLLFSAAALIPFGGGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNDNRQTIY
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 CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
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 Sequence 61, Application US/09866028
Patent No. 6642360
 Grimaldi, Christopher
 Eaton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
 Gurney, Austin
Hillan, Kenneth
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Godowski, Paul
 Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
 TYPE: PRT
ORGANISM: Homo Sapien
 INFORMATION:
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 APPLICANT:
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GENERAL INCORMATION:
GENERAL INFORMATION:
APPLICANT: Well, Gary
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION: H. capsulatum
FILE REFERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT FILING DATE: 1998-04-15
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
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 204 MLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 263
 264 TCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSD 323
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 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 423;
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 APPLICATION

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TITLE OF INVENTION: Molecules Designated B711

FILE REPERENCE: 2844-08

CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE: 2001-02-07

PRIOR PILING DATE: 1999-08-05

PRIOR PILING DATE: 1999-08-05

PRIOR FILING DATE: 06/095,663

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN VET: 2.0

SEQ ID NO 22

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ilarity 100.0%; Pred. No. 8.3e-135;
Conservative 0; Mismatches 0;
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Sequence 22, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
 US-09-060-767B-5; Sequence 5, Application US/09060767B; Patent No. 6720152
 ; ORGANISM: Mus musculus US-09-778-510-22
 Query Match
Best Local Similarity
Matches 150; Conser
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 MLKVHKEDDGVPVICQVEHPAVTGNLGTQRYLEVQYKPQVHIQMTYPLQGLTREGDALEL 265
 84 FRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPR 143
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 PRIOR PILING DATE: Pebruary 9, 1998
PRIOR PILING DATE: Pebruary 9, 1998
PRIOR APPLICATION NUMBER: 60/10; 956
PRIOR APPLICATION NUMBER: 60/112, 956
PRIOR FILING DATE: December 16, 1998
PRIOR FILING DATE: December 22, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: December 16, 1998
PRIOR PILING DATE: JOSEPHER: 60/1146,222
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR PILING DATE: September 16, 1998
PRIOR PILING DATE: December 1, 1998
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PRIOR PILING DATE: December 16, 1998
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PRIOR PILING DATE: December 30, 1999
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 Query Match 94.3
Best Local Similarity 100.
Matches 417; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-944-457-61
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JITLE OF INVENTION:
JENERAL SADDICATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
JITLE OF INVENTION:
JITLE OF INVENTION:
JENERAL SERVICES:
JENERAL SERVICES:
JENERAL APPLICATION NUMBER: US/09/58,95A
CURRENT FILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: 08/928,361
FRIOR FILING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: 08/10,651
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARER: PARCELLIN VET. 2.1
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 DB 4; Length 130;
2.2e-05;
hes 0; Indels
 Length 130;
 Score 14; DB 3; Lo
Pred. No. 2.2e-05;
 Query Match 3.2%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 2.2 Matches 14; Conservative 0; Mismatches
 3.2%; Score 14; DB 100.0%; Pred. No. 2.2 tive 0; Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEPRAX: 650-324-1678
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-6EP-1996
ATTORNEY AGENT INFORMATION:
NAME: Verny, Hana
 US-09-588-995A-14; Sequence 14, Application US/09588995A; Patent No. 6514697
 ; Sequence 12, Application US/08700651B
 , ORGANISM: Cryptosporidium parvum US-09-588-995A-14
 INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 340 PITITITITIT 353
 340 PITITITITIT 353
 48 PITITITITIT 61
 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 GENERAL INFORMATION:
 US-08-928-361B-14
 RESULT 10
US-08-700-651-12
 SEQ ID NO 14
LENGTH: 130
 48
 TYPE: PRT
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 RESULT 7

US-08-100-651-9

i Sequence 9, Application US/08700651B

patent No. 6015882

i GENERAL INFORMATION:

APPLICANT: BEERSEN, CAROLYN

APPLICANT: BEERSEN, SICHARD, C.

APPLICANT: GUT, JIRI

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

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TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTIONS

 Sequence 14, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL WITANTS, VARIANTS, ANALOGS AND FRAGMENTS:
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
 DNAS AND RNAS
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 3.2%; Score 14; DB 3; Length 130;
100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0; Indels
 3.4%; Score 15; DB 4; Length 41;
100.0%; Pred. No. 8.2e-07;
tive 0; Mismatches 0; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
 , OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-9
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 339 PPTTTTTTTTTT 353
 340 PTTTTTTTTTT 353
 Query Match 3.4
Best Local Similarity 100.
Matches 15; Conservative
 Best Local Similarity 100. Matches 14; Conservative
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
; ORGANISM: Leishmania
US-09-060-7678-5
 USA
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 US-08-928-361B-14
 STATE: CA
 Query Match
 FEATURE:
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us-10-622-237-2.oligo.rai

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Sequence 21069, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
WUMBER OF SEQ ID NOS: 28208
SEQ ID NO 21069
LENGTH: 197
 GENERAL INFORMATION:

APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: MISLSON, RICHARD C.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: 180.19-5
CURRENT APPLICATION NUMBER: U8/09/588,995A
CURRENT APPLICATION NUMBER: U8/28,361
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1995-04-03
NUMBER: OF SEQ ID NOS: 115
SEQ ID NO 17
LEMCTH: 175
TYPE: PRT
CANADALICATION NUMBER: U8/415,751
FRIOR FILING DATE: 1995-04-03
NUMBER: OF SEQ ID NOS: 115
SEQ ID NO 17
LEMCTH: 175
TYPE: PRT
CANADALICATION DATE: 1995-04-03
NUMBER: OF SEQ ID NOS: 115
SEQ ID NO 17
CANADATEM: CYNADARICM: DATE: 1995-04-03
NUMBER: PRT
CANADATEM: CYNADARICM: DATE: 1995-04-03
NUMBER: PRT
CANADATEM: TYPE: PRT
CANADATEM: TYPE: PRT
CANADATEM: CYNADARICM: DATE: UBWATH: 175
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 3.2%; Score 14; DB 3; Length 175; 100.0%; Pred. No. 2.9e-05; tive 0; Mismatches 0; Indels
 3.2%; Score 14; DB 4; Length 175; 100.0%; Pred. No. 2.9e-05; ve 0; Mismatches 0; Indels
 Query Match
Best Local Similarity 100.0%; Pred. No. ...
Marches 14; Conservative 0; Mismatches
 Sequence 17, Application US/09588995A Patent No. 6514697
 ORGANISM: Cryptosporidium parvum US-09-588-995A-17
 87 PTTTTTTTTTT 100
 340 PITITITITIT 353
 340 PTTTTTTTTTT 353
 Query Match 3.2%
Best Local Similarity 100.0°
Matches 14; Conservative
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-928-361B-17
 GENERAL INFORMATION:
 RESULT 13
US-09-248-796A-21069
 US-09-588-995A-17
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 GENERAL INFORMATION:
APPLICANT: PECETSEN, CATOLYN
APPLICANT: PECETSEN, CATOLYN
TITLE OF INVENTION: PERTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PERTIDES, POLYPEPTIDES, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 GLYCOPROTEINS, DNAS AND RNAS
 ö
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: PETERSEN, CAROLYN
APPLICANT: DESCH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT PILING DATE: 1997-08-14
EARLIER PILING DATE: 1997-08-14
EARLIER PILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
 Gaps
 ;
0
 Query Match 3.2%; Score 14; DB 3; Length 175; Best Local Similarity 100.0%; Pred. No. 2.9e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 94306-1840

ZIP: 94306-1840

COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/026,062
ATPLICATION NUMBER: US 60/026,062
PILING DATE: 13-SEP-1996
ATPLICATION NUMBER: US 60/026,062
PILING DATE: 13-SEP-1996
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-12
 480.76-1 (HV)
 ; Sequence 17, Application US/08928361B
; Patent No. 6071518
 ATTOKNEI/ rocest.
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
 Prirrirririr 100
 340 PTTTTTTTTTT 353
 175 amino acids
 ð
 RESULT 11
US-08-928-361B-17
 SEQ ID NO 12
 STATE:
 87
 TYPE: PRT
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, Carolyn PEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
 GENERAL INFOGRATION:
APPLICANT: BERRES., DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BUESON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: 08/827,171
PRIOR PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1997-09-12
PRIOR PILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
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 3.2%; Score 14; DB 3; Length 216; 100.0%; Pred. No. 3.5e-05;
 CUNTAIL: 0.5.

ZIP: 94306-1840

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: Patent: PC-DOS/MS-DOS

SOFTWARE: Patent: Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,361B

FILING DATE: 12-SEP-1997
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: FOR TREATMENT AND DETECT
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 0; Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 Sequence 8, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
 340 PTTTTTTTTTT 353
 LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
 Best Local Similarity 100.
Matches 14; Conservative
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 650-324-1678
 TOPOLOGY: linear
MOLECULE TYPE: protein
 USA
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 US-08-928-361B-27
 RESULT 16
US-09-588-995A-8
 COUNTRY:
 Query Match
 ઠે
 g
 APPLICANT: Petersen, Carolyn

TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
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 Score 14; DB 4; Length 197;
Pred. No. 3.2e-05;
 Score 14; DB 3; Length 216;
Pred. No. 3.5e-05;
 0; Indels
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPREATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 12-SEP-1997
CLASSIFICATION:
 3.2%; Scor.
100.0%; Pred. No. 3....
0, Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
 0; Mismatches
 Sequence 27, Application US/08928361B Patent No. 6071518 GENERAL INFORMATION:
 Sequence 8, Application US/08928361B
Patent No. 607151B
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
 100.08;
 3.28;
 113 TTTTTTTTTTT 126
 341 TTTTTTTTTT 354
 340 PTTTTTTTTTT 353
 70 PITITITITI 83
 216 amino acids
 TYPE: PRT ORGANISM: Candida albicans
 Ouery Match
Best Local Similarity 100.0
Matches 14; Conservative
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 Best Local Similarity 100.
Matches 14; Conservative
 MOLECULE TYPE: protein US-08-928-3618-8
 CITA.
STATE: CA
COUNTRY: USA
TO: 94306-1840
 TYPE: amino acid
STRANDEDNESS:
 linear
 ; ORGANISM: Candles
US-09-248-796A-21069
 US-08-928-361B-27
 TOPOLOGY:
 US-08-928-361B-8
 LENGTH:
 Query Match
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Sequence 20, Application US/09588995A

Sequence 20, Application US/09588995A

Sequence 20, Application US/09588995A

GENERAL INFORMATION:

APPLICANT: PETERSEN, CARCLYN

APPLICANT: BARNES, DEBRA A.

APPLICANT: MILSON, RICHARD C.

APPLICANT: NILSON, RICHARD C.

TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: 1800.19-5

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT FILING DATE: 1997-03-27

PRIOR FILING DATE: 1997-03-27

PRIOR FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 115

SEQ ID NO 20

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SEQ ID NO 20

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 Query Match 3.2%; Score 14; DB 4; Length 249; Best Local Similarity 100.0%; Pred. No. 4e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 3.2%; Score 14; DB 3; Length 249;
100.0%; Pred. No. 4e-05;
tive 0; Mismatches 0; Indels
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEFHONE: 650-324-1677
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-20
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
 340 PTTTTTTTTTT 353
 165 Pririririririr 178
 340 PTTTTTTTTT 353
 LENGTH: 249 amino acids
TYPE: amino acid
STRANDEDNESS:
 Query Match 3.2%
Best Local Similarity 100.0
Matches 14; Conservative
 MOLECULE TYPE: protein
 linear
 US-08-928-361B-20
 US-09-588-995A-20
 TOPOLOGY:
 Best Local
Matches
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 Sequence 15, Application US/08700651B
Fatent No. 601582
Fatent No. 601582
Fatent No. 601582
Fatent No. 601582
FAPLICANT: DETERBEN, CAROLYN
APPLICANT: DEECH, JAMES
FAPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: PREPAIRED
FILE REFERENCE: 480.194 (41V)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
FEARLIER APPLICATION NUMBER: 08/415,751
FEARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
 RESULT 18
US-08-928-361B-20
i Sequence 20, Application US/08928361B
i Patent No. 6071518
i GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
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0
 3.2%; Score 14; DB 3; Length 249; llarity 100.0%; Pred. No. 4e-05; Conservative 0; Mismatches 0; Indels
 Score 14; DB 4; Length 216;
Pred. No. 3.5e-05;
 0; Indels
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-15
 3.2%; scc...
100.0%; Pred. No. ...
0; Mismatches
 3: PETERS, VERNY, JONES & BIKSA
385 Sherman Avenue, Suite 6
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
 340 PTTTTTTTTTTT 353
 340 PTTTTTTTTTT 353
 165 PTTTTTTTTTTT 178
 SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
LENGTH: 216
 Best Local Similarity 100.
Matches 14; Conservative
 NUMBER OF SEQ ID NOS: 115
 Local Similarity
ses 14; Conservat
 COUNTRY: USA
ZIP: 94306-1840
 CITY: Palo Alto
 RESULT 17
US-08-700-651-15
 US-09-588-995A-8
 SEQ ID NO 15
LENGTH: 249
 STREET:
 20
 Query Match
 Query Match
 FEATURE:
 Best Loca
Matches
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Patent No. 60,1210:
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PHEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INPECTIONS
 Gaps
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 Query Match 3.2%; Score 14; DB 3; Length 1721; Best Local Similarity 100.0%; Pred. No. 0.00024; Matches 14; Conservative 0; Mismatches 0; Indels
 3.2%; Score 14; DB 3; Length 1721; 100.0%; Pred. No. 0.00024;
 Indels
 SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-5EP-1997
 TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES TITLE OF INVENTION: THEIR FUNCTIONAL MUTAN TITLE OF INVENTION: FOR TREATMENT AND DETE TITLE OF INVENTION: SPECIES INFECTIONS NUMBER OF SEQUENCES: 30 CORRESPONDERSS: ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
 0; Mismatches
 480.76-1 (HV)
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13.5EP-1996
ATTORNEY/AGENT INFORMATION:
 PC-DOS/MS-DOS
 Sequence 6, Application US/08928361B
Patent No. 6071518
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-08-700-651-5
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 48
TELECOMMUNICATION INFORMATION:
 100.08;
 307 PTTTTTTTTT 320
 340 Primiring 353
 340 PITITITITIT 353
 Priririririri 320
 TELEPHONE: 650-324-1677
 Best Local Similarity 100. Matches 14; Conservative
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
 MOLECULE TYPE: protein
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. ?
 TYPE: amino acid STRANDEDNESS:
 linear
 CITY: Palo Alto
 USA
 ð
 TOPOLOGY:
 SEQ ID NO 5
LENGTH: 1721
 RESULT 22
US-08-928-361B-6
 US-08-928-361B-6
 COUNTRY:
 LENGTH:
 307
 Query Match
 RESULT 23
 ð
 g
 ð
 셤
 DNAS AND RNAS
 ö
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: POR PROPHILAXIS AND TREATMENT OF Cryptosporidium parvum FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
 Gaps
 GENERAL INFORMATION:
APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
 ö
 Score 14; DB 1; Length 887;
Pred. No. 0.00013;
 0; Indels
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
PRIOR APPLICATION NUMBER: PCT/AU90/00530
PILING DATE: 02-NOV-1989
APPLICATION NUMBER: PCT/AU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: SIS-568-1100
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
 Mismatches
 Sequence 5, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
 3.2.
100.0%; F1.
 Sequence 3, Application US/07867106
Patent No. 5389526
 TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
 250 PTTTTTTTTT 263
 340 PTTTTTTTTTT 353
 : 887 amino acids
AMINO ACID
 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 ZIP: 19103
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 MOLECULE TYPE: protein
 Philadelphia
 linear
 USA
 TOPOLOGY:
 COUNTRY:
 US-07-867-106-3
 US-08-700-651-5
 US-07-867-106-3
 LENGTH:
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APPLICANY: ELENGANY. CLANCIAN,
APPLICANY: BARNES, DEBRA A.
APPLICANY: BARNES, DEBRA C.
APPLICANY: BARNES, RICHARD C.
APPLICANY: MELSON, RICHARD C.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION UNMBER: US/09/588,995A
CURRENT FILING DATE: 1997-09-06-06
FRIOR APPLICATION NUMBER: 08/928,361
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1995-08-14
FRIOR PILING DATE: 1995-04-03
FRIOR PILING DATE: 1995-04-03
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR FILING DATE: 1995-04-03
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR FILING DATE: 1995-04-03
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR FILING DATE: 1995-04-03
FRIOR APPLICATION NUMBER: 08/415,751
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FRIOR APPLICATION NUMBER: 08/415,751
FRIOR APPLICATION NUMBER: 08/415,751
FRIOR APPLICATI
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 3.2%; Score 14; DB 3; Length 1837;
100.0%; Pred. No. 0.00026;
ive 0; Mismatches 0; Indels
 Length 1837;
 ; DB 4; ne...
n. 0.00026;
0; Indels
 US-05-258-953
Sequence 953.
Sequence 953.
Application US/09205258
Fatent No. 6525174
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT PAPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER FILING DATE: 1998-06-04
 Query Match 3.2%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
 Sequence 5, Application US/09588995A Patent No. 6514697
 ORGANISM: Cryptosporidium parvum
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650-324-1677
FIZEFRAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 340 PTTTTTTTTT 353
 LENGTH: 1837 amino acids
 340 PTTTTTTTTTT 353
 378 PTTTTTTTTTTT 391
 378 Prirrirririr 391
 GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
 3.2%
Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-3618-5
 TYPE: amino acid
STRANDEDNESS:
 US-09-588-995A-5
 US-09-588-995A-5
 RESULT 26
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 PETERED, CATOLYN
VENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
VENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
FENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
SPECIES INFECTIONS
 GENERAL INC. 03.1403/1

APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DERA A.
APPLICANT: BARNES, DERA A.
APPLICANT: MEANOR, RICHARD C.
APPLICANT: MEANING, METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIOS AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: INFECTION SPECIES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT FILING DATE: 1097-03-27
FRIOR RILING DATE: 1097-09-12
FRIOR FILING DATE: 1997-09-12
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1996-08-14
FRIOR FILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NOS: 115
SEQ ID NO 6
FRIOM PAPELICATION NUMBER: 08/415,751
FRIOR PRILOR DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 6
FRIOR PAPELICATION NUMBER: 08/415,751
FRIOR PAPELICATION NUMBER: 08/415,751
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FRIOR PAPELICATION NUMBER: 08/415,751
FRIOR PAPELICATION NUMBER: 08/415,751
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0
 Score 14; DB 4; Length 1721; Pred. No. 0.00024;
 Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: STEM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
AURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES,
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: FOR TREATMENT AND DETECT:
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
 Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 US-08-928-361B-5; Sequence 5, Application US/08928361B; Patent No. 6071518
 Sequence 6, Application US/09588995A
Patent No. 6514697
 3.2%; Sco
llarity 100.0%; Pr
Conservative 0;
 : Cryptosporidium parvum
 TT 353
 307 Pritritritriti 320
 Local Similarity
tes 14; Conserv
 ZIP: 94306-1840
 USA
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 STATE: CA
 LENGTH: 1721
US-09-588-995A-6
 US-09-588-995A-6
 340
 TYPE: PRT
 Query Match
 ORGANISM
 Matches
 RESULT 24
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BARLIER APPLICATION NUMBER: 60/046,985
BEALLIER APPLICATION NUMBER: 60/046,375
BEALLIER APPLICATION NUMBER: 60/046,881
BEALLIER APPLICATION NUMBER: 60/046,881
BEALLIER APPLICATION NUMBER: 60/046,886
BEALLIER APPLICATION NUMBER: 60/046,886
BEALLIER APPLICATION NUMBER: 60/046,896
BEALLIER APPLICATION NUMBER: 60/046,976
BEALLIER APPLICATION NUMBER: 60/046,976
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BEALLIER APPLICATION NUMBER: 60/046,976
BEALLIER APPLICATION NUMBER: 60/046,971
BEALLIER APPLICATION NUMBER: 60/046,994
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BEALLIER PAPLICATION NUMBER: 60/046,915
BEALLIER PAPLICATION NUMBER: 60/046,915
BEALLIER APPLICATION NUMBER: 60/046,915
BEALLIER PILING DATE: 1997-06-06
BEALLIER APPLICATION NUMBER: 60/046,915
BEALLIER PILING DATE: 1997-06-06
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BEALLIER PILING DATE: 1997-06-06
BEALLIER PILING DATE: 19
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 US-08-900-230-59
Sequence 59, Application US/08900230
Sequence 59, Application US/08900230
Sequence 59, Application US/08900230
GENERAL INFORMATION:
APPLICANT: Bard, Jonathan A.
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham Lip
 Length 44;
 Length 57;
 Indels
 IndelB
 CORRESPONDENCE ADDRESS:
ADDRESSES:
COOPER & Dunham Lip
STREET: 1185 Avenue of The Americas
CITRET: 1185 Avenue of The Americas
CITRET: 108 VOTK
COUNTRY: U.S.A.
ZIP: 1100.
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 DB 4; Le
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 2.9%; Score 13; DB 3; Le
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 7.1 Matches 13; Conservative 0; Mismatches
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 9.1 Matches *13; Conservative 0; Mismatches
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SEQ ID NO 953
; LENGTH: 44
 419 DADTAIINAEGGQ 431
 341 TTTTTTTTTT 353
 21 DADTAIINAEGGO 33
 ; ORGANISM: Homo sapiens
US-09-205-258-953
 TYPE: amino acid
STRANDEDNESS: si
 linear
 ; ANTI-SENSE:
US-08-900-230-59
 TOPOLOGY:
 LENGTH: 44
TYPE: PRT
 RESULT 27
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Sequence 19, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
CORRESPONDENCES: 30
CORRESPONDENCES: PETERS, VERNY, JONES & BIKSA
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
 DNAS AND RNAS
 APPLICANT: BETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: MICHARD, C.
APPLICANT: GUT, JIRI
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: MIPPER: US/08/700, 651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: US/08/415, 751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTION OF: 2.0
SOFTWARE: PATENTION OF: 2.0
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 DB 4; Length 75;
0.00012;
hes 0; Indels
 Score 13; DB 3; Length 91;
; Pred. No. 0.00014;
0; Mismatches 0; Indels
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-14
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 Query Match 2.9%; Score 13;
Best Local Similarity 100.0%; Pred. No.
Matches 13; Conservative 0; Mismatch
 PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25289
LENGTH: 75
 Sequence 14, Application US/08700651B Patent No. 6015882
 TYPE: PRT ORGANISM: Cryptosporidium parvum
1999-02-12
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 TYPE: PRT ORGANISM: Candida albicans
 7 ritiritiritii 19
 CURRENT FILING DATE:
 CITY: Palo Alto
 GENERAL INFORMATION:
 US-09-248-796A-25289
 US-08-928-361B-19
 US-08-700-651-14
 STATE:
 RESULT 32
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 US-09-248-796A-23083

Sequence 23083, Application US/09248796A

Sequence 23083, Application US/09248796A

Sequence 23083, Application US/09248796A

GENERAL INCORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248, 796A

CURRENT FILING DATE: 1998-02-13

PRIOR PRILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096, 409

PRIOR APPLICATION NUMBER: US 60/096, 409

SEQ ID NO 23083
 Sequence 25289, Application US/09248796A

Sequence 25289, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT Reith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: POR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A
 ö
 ö
 APPLICANT: Weil, Gary
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
FILE REPERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
PRIOR APPLICATION NUMBER: 60/43,332
PRIOR APPLICATION NUMBER: 60/43,332
NUMBER OF SEQ ID NOS: 9
SCPTWARE: PATENTH Version 3.0
SEQ ID NO 9
LENGTH: S7
 Gaps
 Gaps
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 Score 13; DB 4; Length 63;
Pred. No. 0.0001;
0; Mismatches 0; Indels
 Length 57;
 0; Indels
 Score 13; DB 4; Le
Pred. No. 9.1e-05;
 100.0%; Prec. ...
 2.9%; Score 13; DB
llarity 100.0%; Pred. No. 9.1
Conservative 0; Mismatches
 Sequence 9, Application US/09060767B; Patent No. 6720152; GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Histoplasma Capsulatum
US-09-060-7678-9
 2.9%;
 340 PTTTTTTTTT 352
 338 PPPTTTTTTT 350
 16 peptititititi 28
 TYPE: PRT
ORGANISM: Candida albicans
 Priririririr 48
 Best Local Similarity 100.
Matches 13; Conservative
 Query Match
Best Local Similarity
 RESULT 30
US-09-248-796A-25289
 US-09-248-796A-23083
 RESULT 28
US-09-060-767B-9
 13;
 36
 Query Match
 Matches
 8
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US-08-700-651-11; Sequence 11, Application US/08700651B; Patent No. 6015882; GENERAL INFORMATION:
 ; ORGANISM: Drosophila melanogaster US-09-270-767-51409
 ; ORGANISM: Drosophila melanogaster US-09-270-767-36192
 341 TTTTTTTTTT 353
 341 TTTTTTTTTTT 353
 341 TTTTTTTTTT 353
 18 riririririri 30
 US-09-270-767-36192
 TYPE: PRT
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 Sequence 19, Application US/09588995A

Sequence 19, Application US/09588995A

Sequence 19, Application US/09588995A

GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: GIV, JIRI
TITLE OF INVENTION: INFECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: 10PECTIONS
TITLE OF INVENTION: 10PECTIONS
TITLE OF INVENTION: 10PECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: 08/929, 171
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-03-12
PRIOR PELLING DATE: 1995-08-14
PRIOR FILING DATE: 1995-08-14
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 Gaps
 ;
0
 2.9%; Score 13; DB 4; Length 91; 100.0%; Pred. No. 0.00014; Live 0; Mismatches 0; Indels
 2.9%; Score 13; DB 3; Length 91; 100.0%; Pred. No. 0.00014;
 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 91 amino acids
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-19
 341 TTTTTTTTTT 353
 Query Match 2.9
Best Local Similarity 100.
Matches 13; Conservative
 MOLECULE TYPE: protein
 TYPE: amino acid STRANDEDNESS:
 TOPOLOGY: linear
 US-08-928-361B-19
COUNTRY:
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APPLICANT: PETEREN, CAROLYN
APPLICANT: DEEGH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF CRYPCOSPOCIATIUM PARVUM TITLE OF INVENTION: INFECTIONS
PILE REFERENCE: 480.19-4(HV)
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 Sequence 51409, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094

CURRENT FILING DATE: 1999-013-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 51409

LENGTH: 106

TYPE: PRT
Sequence 36192, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PILING NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 36192
LENGTH: 106
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 Query Match 2.9%; Score 13; DB 4; Length 106; Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 2.9%; Score 13; DB 4; Length 106; Best Local Similarity 100.0%; Pred. No. 0.00016; Matches 13; Conservative 0; Mismatches 0; Indels
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RESULT 38
US-09-588-995A-16
Sequence 16, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
 Sequence 7, Application US/08700651B Patent No. 6015882
GENERAL INFORMATION:
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-16
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
PEATURE:
 341 TTTTTTTTTT 353
 341 TTTTTTTTT 353
 33 TTTTTTTTTTTT
 RESULT 39
US-08-700-651-7
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 8
 Sequence 16, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
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 Query Match 2.9%; Score 13; DB 3; Length 124; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 13; Conservative 0; Mismatches 0; Indels
 2.9%; Score 13; DB 3; Length 124;
100.0%; Pred. No. 0.00019;
tive 0; Mismatches 0; Indels
 CUDNIKX: USA

ZIP: 94306-1840

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Eloppy disk

COMPUTER: IBM PC compatible

COPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/928,361B

FILING DATE: 12-SEP-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 60/026,062

FILING DATE: 13-SEP-1996

ATTONENY/AGENT INFORMATION:
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
LENGTH: 124
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
 LENGTH: 124 amino acids
TYPE: amino acid
STRANDEDNESS:
 341 TTTTTTTTTT 353
 rrrrrrrrrr 45
 Best Local Similarity 100.
Matches 13; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 CITY: Palo Alto
STATE: CA
 USA
 US-08-928-361B-16
 US-08-700-651-11
 COUNTRY:
 33
 Query Match
 FEATURE:
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APPLICANT: PETERERSH, CAROLYN
APPLICANT: DELECH, JAMES
APPLICANT: DELECH, JAMES
APPLICANT: MELSON, RICHARD, C.
APPLICANT: MELSON, RICHARD, C.
APPLICANT: MELSON, RICHARD, C.
APPLICANT: MELSON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF CRYPCOSPOCIATIUM PARCHER FILE REPERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
GRALIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 7
LENGTH: 128
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: GUT, JIKI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM ITTLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM ITTLE OF INVENTION: INFECTIONS
FILLE REPERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILLING DATE: 1997-08-6-6
FRIOR FILLING DATE: 1997-09-12
FRIOR APPLICATION NUMBER: 08/27,171
FRIOR FILLING DATE: 1996-08-14
FRIOR FILLING DATE: 1996-08-14
FRIOR FILLING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 16
LENGTH: 124
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 DB 3; Length 128;
 Length 124;
 Indels
 Query Match 2.9%; Score 13; DB 4; Le Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 13; Conservative 0; Mismatches 0;
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-7
 2.9%; Score 13;
 Query Match
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APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: NELSON, RICHARD, C.
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND
TITLE OF INVENTION: NPECTIONS
TITLE OF INVENTION: NPECTIONS
TITLE OF INVENTION: NPECTIONS
TITLE OF INVENTION: UNPER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/15,751
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-6
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 2000-06-06
PRIOR PAPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATENTION VUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
SOFTWARE: PATENTION NUMBER: 08/105,751
PRIOR PILING DATE: 1995-04-03
SOFTWARE: PATENTION VUMBER: 08/115,751
PRIOR PILING DATE: 1995-04-03
SOFTWARE: PATENTION VUMBER: 08/115,751
PRIOR PILING DATE: 1995-04-03
SOFTWARE: PATENTION VUMBER: 08/115,751
PRIOR PILING DATE: 1995-04-03
SOFTWARE: PATENTIN VET: 2.1
 APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
 DB 4; Length 128; 0.00019;
 Length 130;
 Query Match 2.9%; Score 13; DB 3; Length 130 Best Local Similarity 100.0%; Pred. No. 0.0002; Matches 13; Conservative 0; Mismatches 0; Indels
 Indels
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-8
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 US-08-928-361B-13
; Sequence 13, Application US/08928361B
; Patent No. 6071518
; GENERAL INFORMATION:
 Sequence 8, Application US/08700651B Patent No. 6015882 GENERAL INFORMATION:
 ORGANISM: Cryptosporidium parvum
 ORGANISM: Cryptosporidium parvum
 341 TITITITITIT 353
 SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 130
 341 TTTTTTTTTT 353
 37 rirririririri 49
 39 TTTTTTTTT 51
 US-09-588-995A-12
 JS-08-700-651-8
 TYPE: PRT
 TYPE: PRT
 RESULT 43
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), Carolyn, PEPTIDES, GLYCOPROTEINS, PEPTIDES, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INPECTIONS
 ô
 Sequence 12, Application US/09588995A
PREENT NO. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLIN
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELGON, RICHARD C.
APPLICANT: NELGON, RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND
 Gaps
 Gaps
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 2.9%; Score 13; DB 3; Length 128; 100.0%; Pred. No. 0.00019;
 0; Indels
 0; Indels
 COMPUTAY: USA

ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATORNEY AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30.518
FEGISTRATION NUMBER: 30.518
 100.0%; Pred. No. 0.00019; tive 0; Mismatches 0;
 RETERS, VERNY, JONES & BIKSA 385 Sherman Avenue, Suite 6
 REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 Sequence 12, Application US/08928361B
Patent No. 6071518
 341 TTTTTTTTTT 353
 LENGTH: 128 amino acids TYPE: amino acid
 341 TTTTTTTTTT 353
 Best Local Similarity 100.
Matches 13; Conservative
 37 rrrrrrrrrrr 49
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 TTTTTTTTT 49
 TITLE OF INVENTION: PEPTITLE OF INVENTION: THEI TITLE OF INVENTION: SPECIAL OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
 13; Conservative
 MOLECULE TYPE: protein
 TOPOLOGY: linear
 Best Local Similarity
Matches 13; Conserv
 GENERAL INFORMATION:
APPLICANT: Peters
 Palo.Alto
 USA
 STRANDEDNESS
 ADDRESSEE:
 RESULT 41
US-09-588-995A-12
 RESULT 40
US-08-928-361B-12
 US-08-928-361B-12
 COUNTRY:
 STREET:
 37
 STATE:
 Query Match
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DNAS AND RNAS

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Gaps

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Gaps

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COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 TYPE: PRT; ORGANISM: Cryptosporidium parvum
US-09-588-995A-13
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 341 TTTTTTTTT 353
 341 TTTTTTTTTT 353
 47 TTTTTTTTTT 59
 39 ritititititit 51
 S
 US-08-700-651-10
 LENGTH: 130
 SEQ ID NO 13
 CITY: 1
STATE:
 RESULT 45
 RESULT 46
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 THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
 Sequence 13, Application US/09588995A
Fatent No. 614697
GENERAL INFORMATION:
APPLICANT: BARNES. DEBRA A.
APPLICANT: BARNES. DEBRA A.
APPLICANT: BARNES. DEBRA A.
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INSCITUNS
TITLE OF INVENTION: INSCITUNS
TITLE OF INVENTION: INSCITUNS
TITLE OF INVENTION: UNMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT APPLICATION NUMBER: 08/827,171
PRIOR APPLICATION NUMBER: 08/922,361
PRIOR APPLICATION NUMBER: 08/700-666
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115

SOFTWARE: PATENTIN UNBER: 08/100,651
NUMBER OF SEQ ID NOS: 115
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 Gaps
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 2.9%; Score 13; DB 3; Length 130;
100.0%; Pred. No. 0.0002;
lve 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: R10ppy disk
COMPUTER: R10ppy disk
COMPUTER: R10ppy disk
COMPUTER: R10ppy disk
COMPUTER: R10ppy disk
COMPUTER: R10ppy disk
COMPUTER: R2 PATENTION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FLING DATE: 12-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING APPLICATION NUMBER: US 60/026,062
ATTONENTATION NUMBER: US 60/026,062
ATTONENTATION NUMBER: US 60/026,062
ATTONENTATION NUMBER: US 60/026,062
ATTONENTATION NUMBER: US 60/026,062
TITLE OF INVENTION: THEIR FUNCTIONAL MUTAN TITLE OF INVENTION: FOR TREATMENT AND DETE TITLE OF INVENTION: SPECIES INFECTIONS NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESS: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
 Best Local Similarity 100.0%; Pred. No. 0.0
Matches 13; Conservative 0; Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 13:
 LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 341 TTTTTTTTTT 353
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 39 rrrrrrrrrrr 51
 MOLECULE TYPE: protein
 linear
 STREET: 385 Sher
CITY: Palo Alto
 USA
 S
 US-08-928-361B-13
 US-09-588-995A-13
 TOPOLOGY:
 STATE: C. COUNTRY:
 Query Match
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Sequence 10, Application US/08700651B

Patent No. 6015802

GENERAL INPORMATION:
APPLICANT: DETERSEN, CAROLYN
APPLICANT: DETERSEN, CAROLYN
APPLICANT: DETERSEN, RICHARD, C.
APPLICANT: DETERSEN, RICHARD, C.
APPLICANT: OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
FILE REFERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTING DATE: 1995-04-03
SOFTWARE: PALENTING DATE: 1395-04-03
SEQ ID NO 10
LENGTH: 138
 SEQUENCE 15. Application US/08928361B

| Sequence 15. Application US/08928361B
| Patent No. 6071518
| Patent No. 6071518
| GENERAL INFORMATION:
| APPLICANT: PETERS. CATOLYN
| TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, TITLE OF INVENTION: PRACMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: SPECIES INFECTIONS
| TITLE OF INVENTION: SPECIES INFECTIONS | TITLE OF INVENTION: SPECIES INFECTIONS | NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
| ADDRESSES: PETERS, VERNY, JONES & BIKSA | STREET: 385 Sherman Avenue, Suite 6 | CITY: Palo Alto
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o. 0.0002;
0. Indels
 Query Match 2.9%; Score 13; DB 3; Length 138; Best Local Similarity 100.0%; Pred. No. 0.00021; Matches 13; Conservative 0; Mismatches 0; Indels
 Length 130;
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-10
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
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Gaps
 ;
 Length 150;
 0; Indels
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
 2.9%; Score 13; DB 3; L. 100:0%; Pred. No. 0.00022; ive 0; Mismatches 0;
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 PRIOR APPLICATION NUMBER: 08/827,171
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
 INFORMATION FOR SEQ ID NO: 18:
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS:
 LITIT 353
 Query Match
Best Local Similarity 100:0
Matches 13; Conservative
 62 ririririririr 74
 650-324-1678
 SEQUENCE CHARACTERISTICS
 TOPOLOGY: linear
MOLECULE TYPE: protein
 341 TTTTTTT
 CLASSIFICATION:
 USA
 JS-08-928-361B-18
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 US-08-928-361B-18
 US-09-588-995A-18
 COUNTRY:
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 US-09-588-995A-15

i Sequence 15, Application US/09588995A

j Sequence 15, Application US/09588995A

j GENERAL INFORMATION:

j APPLICANT: PETERSEN, CAROLYN

APPLICANT: BANES, DEBRA A.

APPLICANT: BANES, DEBRA A.

APPLICANT: GUT, JIRI

TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

FILE REPERBECE: 480.19-5

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT FILING DATE: 1997-03-27

PRIOR PELLING DATE: 1997-03-12

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

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PRIOR APPLICATION NUMBER: 08/700,651

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PRIOR APPLICATION NUMBER: 08/700,651

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PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651

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PRIOR APPLICATION NUMBER: 08/700,651

PRIOR APPLICATION NUMBER: 08/700,651
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 2.9%; Score 13; DB 3; Length 138;
100.0%; Pred. No. 0.00021;
iive 0; Mismatches 0; Indels
 Length 138;
 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
 Query Match
2.9%; Score 13; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 13; Conservative 0; Mismatches 0;
 REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 138 amino acids
TYPE: amino acids
STRANDEDNESS:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY, AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
 ; ORGANISM: Cryptosporidium parvum
US-09-588-995A-15
 341 TTTTTTTTT 353
 341 TITITITITIT 353
 47 TTTTTTTTT 59
 47 TITITITITI 59
 TOPOLOGY: linear MOLECULE TYPE: protein
 US-08-928-361B-15
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Sequence 18, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL WITANTS, VARIANTS, ANALOGS AND FRAGMENTS;
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 ö
 Patent No. 6514697

GENERAL INFORMATION:
FALCH NO. 6514697

GENERAL INFORMATION:
APPLICANT: BATENES, DEBRA A.
APPLICANT: BATENES, DEBRA A.
APPLICANT: GUT, JIRI
APPLICANT: GUT, JIRI
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT APPLICATION NUMBER: US/09-6-06
CURRENT APPLICATION NUMBER: OS/00-06-06
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US-09-248-796A-16058
Sequence 16058, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/248,796A
TITLE OF INVENTION: WUMBER: US/09/248,796A
TITLE OF INVENTION: WUMBER: US/09/248,796A
TITLE OF INVENTION: WUMBER: US/09/248,796A
TITLE REPLEMENCE: 107196,132
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER: OF SEQ ID NOS: 28208
SEQ ID NO 16058
LENGTH: 207
 LOCATION: (204)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknow
US-09-248-796A-16058
 GENERAL INFORMATION:
APPLICANT: Well, Gary
APPLICANT: Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
TITLE OF INVENTION NUMBER: US/09/060,767B
CURRENT APPLICATION NUMBER: 60/043,332
PRIOR APPLICATION NUMBER: 60/043,332
PRIOR FILING DATE: 1997-04-15
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.0
LENGTH: 211
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 Query Match

2.9%; Score 13; DB 3; Length 162;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 2.9%; Score 13; DB 4; Length 207; Best Local Similarity 100.0%; Pred. No. 0.0003; Matches 13; Conservative 0; Mismatches 0; Indels
 ; FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-13
 Sequence 3, Application US/09060767B Patent No. 6720152
 TYPE: PRT ORGANISM: Cryptosporidium parvum
) ORGANISM: Histoplasma capsulatum US-09-060-767B-3
 341 TTTTTTTTTT 353
 TTTT 353
 76 TTTTTTTTTT 88
 ORGANISM: Candida albicans
 61 ririririririr 73
 341 TTTTTTT
 NAME/KEY: UNSURE
 RESULT 53
US-09-060-767B-3
 LENGTH: 162
 TYPE: PRT
 FEATURE:
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 US-09-248-796A-21631

Sequence 2161, Application US/09248796A

Sequence 2161, Application US/09248796A

Sequence 2161, Application US/09248796A

Sequence 2161, Application US/09248796A

SETEM TO THE NO. THORNATION:

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196_132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PLING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 21631

LENGTH: 159

LENGTH: 159
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 2.9%; Score 13; DB 4; Length 150;
100.0%; Pred. No. 0.00022;
ive 0; Mismatches 0; Indels
 Length 159;
 0; Indels
 Score 13; DB 4; Lot
Pred. No. 0.00024;
 Mismatches
PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR PILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.1
LENGTH: 150
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-18
 Query Match
Best Local Similarity 100.0%; P:
Matches 13; Conservative 0;
 342 TITTITITITI 354
 341 TITITITITI 353
 Query Match 2.9%
Best Local Similarity 100.0
Matches 13; Conservative
 62 rrrrrrrrrrrrr 74
 ORGANISM: Candida albicans
 52 rrrrrrrrrii 64
 US-09-248-796A-21631
 SEQ ID NO 13
 TYPE: PRT
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Sequence 341, Application US/09216393B

Sequence 341, Application US/09216393B

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INTENTION:
TOTAL OF THE OFFICE ACID MOLECULES, AND USES THERE
FILE REFERENCE:
TITLE OF INTENTION:
TOTAL OF THE OFFICE ACID MOLECULES, AND USES THERE
PRIOR FILING DATE: 1997-12-19
PRIOR FILING DATE: 1997-12-19
SEQ ID NO 341

LENGTH: 288
 GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
TILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR PILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PATENTIN VERSION 3.1
 GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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 Length 288;
 2.9%; Score 13; DB 4; Length 288; 100.0%; Pred. No. 0.00041;
 0; Indels
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 Score 13; DB 4; Le
Pred. No. 0.00041;
 Query Match
2.9%; Score 13; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 13; Conservative 0; Mismatches
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 US-09-248-796A-25055
; Sequence 25055, Application US/09248796A
; Patent No. 6747137
 CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
 Sequence 344, Application US/09216393B Patent No. 6514694
 ; SEQ ID NO 344

; LENGTH: 288

; TYPE: PRT

; ORGANISM: Toxoplasma gondii

US-09-216-393B-344
 341 TTTTTTTTTT 353
 164 TTTTTTTTTTT 176
 164 TTTTTTTTTTTT 176
 ORGANISM: Toxoplasma gondii
 341 TTTTTTTTTT 353
 RESULT 57
US-09-216-393B-344
 US-09-216-393B-341
 TYPE: PRT
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 Sequence 17391, Application US/09248796A
Patent No. 6747137
Patent No. 6747137
Patent No. 6747137
Patent No. 6747137
Patent No. 6747137
Patent No. 6747137
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17391
LENGTH: 216
 US-09-248-796A-24111

Sequence 24111, Application US/09248796A

Sequence 24111, Application US/09248796A

Sequence 24111, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR REPLICATION NUMBER: US 60/036,409

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
 ; NAME/KEY: UNSURE
; LOCATION: (212)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknq
US-09-248-796A-17391
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Query Match 2.9%; Score 13; DB 4; Length 211; Best Local Similarity 100.0%; Pred. No. 0.00031; Matches 13; Conservative 0; Mismatches 0; Indels
 2.9%; Score 13; DB 4; Length 247; 100.0%; Pred. No. 0.00036; Live 0; Mismatches 0; Indels
 Length 216;
 0; Indels
 Query Match
2.9%; Score 13; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 0.00032;
Matches 13; Conservative 0; Mismatches 0;
 338 PPPTTTTTTT 350
 341 TTTTTTTTTT 353
 341 TTTTTTTTTT 353
 37 ppiririririr 49
 TYPE: PRT
ORGANISM: Candida albicans
 74 rrrrrrrrrrr 86
 : Candida albicans
 Query Match 2.9
Best Local Similarity 100.
Matches 13; Conservative
 RESULT 54
US-09-248-796A-17391
 US-09-248-796A-24111
 ORGANISM
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APPLICANT: Milaul, Ivar.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION WUMBER: US 60/143,048
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
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PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
 Gaps
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 2.9%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00056; ative 0; Mismatches 0; Indels
 PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
 PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
 PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
 PRIOR APPLICATION NUMBER: PCT/US99/28214
 Gerritsen, Mary E.
Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 US-09-907-794A-84; Sequence 84, Application US/09907794A; Patent No. 6635468
 Ferrara, Napoleone
Filvaroff, Ellen
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
 FILING DATE: 1999-10-05
 375 DADTAIINAEGGQ 387
 419 DADTAIINAEGGQ 431
 Query Match
Best Local Similarity 100.0
Matches 13; Conservative
 US-09-778-510-6
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 NAME/KEY: UNSURE 1 LOCATION: (288), (289) 1 LOCATION: (287), (288), (289) 1 LOCATION: (287), (288), (289) 2 LOCATION: USPERVATION: Identity of amino acid sequences at the above locations are unknotus-09-248-7968-25055
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 Length 398;
 2.9%; Score 13; DB 4; Length 292; 100.0%; Pred. No. 0.00042; ive 0; Mismatches 0; Indels
 0; Indels
 Score 13; DB 4; L Pred. No. 0.00056;
 Baum, Peter
IION: Molecules Designated B7L1
 Molecules Designated B7L1
 APPLICANT:
TITLE OF INVENTION:
FILE REFERENCE:
CURRENT APPLICATION WHERE:
CURRENT APPLICATION WHERE:
FRIOR APPLICATION WHERE:
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FRIOR FILING DATE:
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FRIOR FILING DATE
 Sequence 4, Application US/09778510
Fatent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B71;
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-08-05
FRIOR FILING DATE: 1999-08-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.0
 Query Match 2.9%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25055
LENGTH: 292
 US-09-778-510-6; Sequence 6, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION:
 375 DADTAIINAEGGQ 387
 341 TITITITITI 353
 419 DADTAIINAEGGQ 431
 TYPE: PRT
ORGANISM: Candida albicans
 Best Local Similarity 100.
Matches 13; Conservative
 TYPE: PRT
ORGANISM: Mus musculus
US-09-778-510-4
 TYPE: PRT
ORGANISM: Homo sapien
 SEQ ID NO 4
LENGTH: 398
 RESULT 59
US-09-778-510-4
 Query Match
 FEATURE:
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 ö
 2.9%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00056;
 100.0%; Prec. ...
 PRIOR FILING DATE: 1999-10-05
PRIOR PLILING DATE: 1999-10-05
PRIOR PELLING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR PILLING DATE: 1999-11-30
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR PLILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30910
PRIOR APPLICATION NUMBER: PCT/US99/30910
 CURRENT APPLICATION NUMBER: US/09/902,775A CURRENT FILING DATE: 2001-07-10
 PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/USOO/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
 Sequence 84, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
 Hillan, Kenneth, J
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerber, Hanspeter
Gerritsen, Mary E.
 Paoni, Nicholas F.
 Gurney, Austin L.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 419 DADTAIINAEGGQ 431
 375 DADTAIINAEGGQ 387
 13; Conservative
 Wei-Qiang
 Desnoyers, Lu
Eaton, Dan L.
 TYPE: PRT
ORGANISM: Homo sapiens
 Goddard, A.
 Query Match
Best Local Similarity
Matches 13; Conserv
 JS-09-902-775A-84
 US-09-905-125A-84
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 ITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLE OF INVENTION: Acids Encoding the Same
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 Query Match 2.9%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00056; Matches 13; Conservative 0; Mismatches 0; Indels
 PILER REPERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT FILING DATE: 2001-07-12
PRIOR PAPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
 PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
 FILING DATE: 1999-09-13
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: 1999-09-08
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-12-16.
APPLICATION NUMBER: PCT/US99/30911
 Sequence 84, Application US/09905125A
Patent No. 6664376
 Godowski, Paul J.
Grimaldi, Christopher J.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Gurney, Austin L.
Hillan, Kenneth, J.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Timothy A.
 Gerritsen, Mary E.
Goddard, A.
 Roy, Margaret Ann
Stewart, Timothy 1
Tumas, Daniel
 Gerber, Hanspeter
 419 DADTAIINAEGGQ 431
 375 DADTAIINAEGGQ 387
 Desnoyers, Luc
Eaton, Dan L.
 LENGTH: 398
TYPE: PRT
CRGANISM: Homo sapiens
US-09-907-794A-84
 -09-905-125A-84
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APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Wood, William.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE SPERRENCE: 10466-144
CURRENT APPLICATION WOMBER: US/09/906,700
CURRENT APPLICATION WOMBER: US/04/44
PRIOR APLIACATION WOMBER: US/04/44,048
PRIOR APLIACATION WOMBER: US/04/46,222
PRIOR PILING DATE: 1999-07-26
PRIOR APLIACATION WOMBER: US/04/46,222
PRIOR APPLICATION WOMBER: US/04/46,222
PRIOR APPLICATION WOMBER: US/08/20594
PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION WOMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-10-05
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 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Stewart, Timothy A.
 419 DADTAIINAEGGQ 431
 375 DADTAIINAEGGO 387
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 Fong, Sherman
Gao, Wei-Qiang
 APPLICANT: Genentech, Inc
 ; ORGANISM: Homo sapiens
US-09-906-700-84
 US-09-903-603A-84
 APPLICANT:
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 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
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 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
 Gerritsen, Mary E.
 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
 Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
 419 DADTAIINAEGGQ 431
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 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84
 Goddard, A.
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APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: William, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/904,920A
CURRENT FILLING DATE: 2001-07-13
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PRIOR PLLING DATE: 1999-11-29
PRIOR PLLING DATE: 1999-11-30
PRIOR PLLING DATE: 1999-12-02
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NUMBER OF SEQ ID NOS: 423
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TYPE: PRT
TYPE: PRT
ORGANISM: HOMO Sapiens
US-09-904-920A-84
 PRIOR APPLICATION NUMBER: 2017/USOU/04414
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR PLING DATE: 1999-07-07
PRIOR PELING DATE: 1999-07-07
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 PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
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 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
 Sequence 84, Application US/09904920A
 errara, Napoleone
 Kenneth, J
 Paoni, Nicholas F.
 Gerritsen, Mary E
 Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
 Goddard, A.
 Pan, James
 Hillan,
 ## PPPLICANTY Wood, william, I TITLE OF INVENTION: Sected and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same PLIER ENERGIES. GNS. 161882CLS.
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT PELING DATE: 2001-07-11
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1099-07-07
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100.0%; Pred. No. 0.00056;
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Grimaldi, Christopher
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Roy, Margaret Ann
Stewart, Timothy A.
 Pan, James
Paoni, Nicholas F.
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Gerber, Hanspeter
 419 DADTAIINAEGGQ 431
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Matches 13; Conservative
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-903-603A-84
 Query Match
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375 DADTAIINAEGGQ 387

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RESULT 66 US-09-904-920A-84

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APPLICANT: Stewart, Timothy A. APPLICANT: Stewart, Timothy A. APPLICANT: Tumas, Daniel APPLICANT: Williams, P. Mickey APPLICANT: Williams, P. Mickey APPLICANT: Wood, William, I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-11 CURRENT APPLICATION NUMBER: US/09/905,381A CURRENT FILING DATE: 2001-07-13
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PRIOR FILING DATE: 2000-01-05
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FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/30911
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 Sequence 84, Application US/09905381A
Patent No. 6818746
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Paoni, Nicholas F.
Roy, Margaret Ann
 Gerritsen, Mary E.
 Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
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 Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 TYPE: PRT
CRGANISM: Homo sapiens
US-09-909-064-84
 Goddard, A.
 GENERAL INFORMATION
 Gao,
 US-09-905-381A-84
 APPLICANT:
 APPLICANT:
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 APPLICANT:
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Pred. No. 0.00056;
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FILING DATE: 1999-12-16
 Sequence 84, Application US/09909064
Patent No. 681849
GENERAL INFORMATION:
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Baton, Dan L.
 419 DADTAIINAEGGO 431
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 US-09-909-064-84
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 Sequence 1, Application US/08659984A
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; Patent No. 5942400
; GRUERAL INFORMATION:
; APPLICANT: Ancheron, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Gacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Inhibition
; TITLE OF INVENTION: Inhibition
; NUMERR OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townseend and Townseend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; ITY: San Francisco
; STATE: California
; COUNTRY: USA
; CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
; COMPUTER: IEM PC compatible Dos
 2.9%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00056;
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 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-UW-1996
CLASSIFICATION: 436
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Matches 13; Conservative 0; Mismatches
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PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
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 FILING DATE: 1999-07-28
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 , ORGANISM: Homo sapiens
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 US-08-659-984A-1
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 APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, Wicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: PCT/US99/23089;
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CURRENT APPLICATION NUMBER: US/09/906,618

CURRENT FILING DATE: 2001-07-16

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR FILING DATE: 1999-07-07
 Godowski, Paul J.
Grimaldi, Christopher J.
 Sequence 84, Application US/09906618
Patent No. 6828146
GENERAL INFORMATION:
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
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 Ashkenazi, Avi
Botstein, David
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 Eaton, Dan L.
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; ORGANISM: Homo sapiens
US-09-905-381A-84
 Goddard, A.
 -09-906-618-84
 APPLICANT:
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 Sequence 5, Application US/08659984A

Sequence 5, Application US/08659984A

Patent No. 594240

GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Sinha, Sukanto
APPLICANT: Inhab, Sukanto
APPLICANT: Inhab, Sukanto
APPLICANT: Inhab, Sukanto
APPLICANT: Inhabition
ITILE OF INVENTION: Inhabition
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CONTRY: San Francisco
STATE: California
COUNTRY: USA
 Query Match 2.9%; Score 13; DB 3; Length 421; Best Local Similarity 100.0%; Pred. No. 0.00059; Matches 13; Conservative 0; Mismatches 0; Indels
 2.9%; Score 13; DB 4; Length 432;
100.0%; Pred. No. 0.0006;
 0; Indels
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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SOFTWARE: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENT: NS-08/659,984A
FILING DATE: 07-010N-1996
CLASSIFICATION NUMBER: US 08/485,152
ATTORNEY/AGENT: INFORMATION:
APPLICATION NUMBER: US 08/485,152
ATTORNEY/AGENT: INFORMATION:
 JENGTH CALLE AND PETER TITLE OF INVENTION: Molecules Designated B7L1 FILE REFERENCE: 2844-08; CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN VOICE: 20
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SOFTWARE: PATENTIN VOICE: 20
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 Sequence 2, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION:
 303 LNKTDNGTYRCEA 315
 409 DADTAIINAEGGQ 421
 272 LNKTDNGTYRCEA 284
 419 DADTAIINAEGGQ 431
 NAME: Heslin, James M.
 TYPE: PRT
ORGANISM: Homo sapien
 RESULT 73
US-08-659-984A-5
 RESULT 72
US-09-778-510-2
 US-09-778-510-2
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 Score 13; DB 2; Length 421;
Pred. No. 0.00059;
0; Mismatches 0; Indels
 APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
 REGISTRATION NUMBER: 29,541
REGISTRATION NUMBER: 29,541
REFRENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2402
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INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
 ; Sequence 1, Application US/08660531; Patent No. 6221645
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
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 LENGTH: 421 amino acids
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 MOLECULE TYPE: protein US-08-659-984A-1
 MOLECULE TYPE: protein
 COUNTRY: USA
ZIP: 94111-3834
 GENERAL INFORMATION:
APPLICANT: Chrysle
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 US-08-660-531-1
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 APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIR: 94111-3834
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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 FILING DATE:
CLASSIFICATION 135
PRIOR PAPLICATION DATA
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUM-195
ATTORNEY/AGENT INFORMATION:
NAME: Heelin, James M.
REGISTRATION NUMBER: 29,541
REPRENCE/DOCKET UNBER: 15270-002210US
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TELEPHONE: 415-326-2400
REGISTRATION NUMBER: 29,541
REPRENCE/POCKET NUMBER: 15270-002810US
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TELEPHONE: 415-326-2400
 Sequence 5, Application US/08660531; Patent No. 6221645; GENERAL INFORMATION:
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 295 LNKTDNGTYRCEA 307
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LENGTH: 444 amino acic
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TOPOLOGY: linear
 TOPOLOGY: linear
MOLECULE TYPE: protein
 single
 MOLECULE TYPE: protein US-08-659-984A-5
 TYPE: amino acid
STRANDEDNESS: sir
 US-08-660-531-5
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US-09-248-796A-22504

US-09-248-796A-22504

Sequence 22504, Application US/09248796A

Fatent No. 6747137

GENERAL INFORMATION:
FAPILICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUMBER: US/09/248,796A

TITLE OF INVENTION: UNMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

FRIOR FEDERACE 1998-02-13

FRIOR FILING DATE: 1998-02-13

FRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 22504

LENGTH: 543
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Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 13; Conservative 0; Mismatches 0; Indels
 Search completed: June 28, 2005, 10:22:30 Job time: 34.659 secs
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 341 TITTTTTTTT 353
 , ORGANISM: Candida albicans
US-09-248-796A-22504
 TYPE: PRT
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| chitinase (EC 3.2. sensory transducti unconventional myo 1-phosphaticallyinos hypothetical prote hypothetical prote nemo, form I - fru homeotic protein s hypothetical prote alkaline phosphata hypothetical prote | hypothetical prote<br>regularory protein<br>xylanase, beta(1,3<br>hypothetical prote<br>major surface glyc<br>laminin alpha-1 ch<br>ankyrin 3, long sp<br>probable auxin-ind<br>hypothetical prote<br>merozoite surface<br>hypothetical prote<br>merozoite surface<br>hypothetical prote<br>salivary glue prot<br>RAD 238 protein - | hypothetical prote G protein-coupled nuclear pore glyco nuclear pore compl translocated intim probable transloca gp88 protein - mur hypothetical prote mucin PIM-C.1 - Af hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote | hypothetical prote elastic titin - hu nitrilase associat larval glue protei salivary glue protei salivary glue protei hypothetical prote protein T25N20.9 [hypothetical prote protein kinase (BC hypothetical protein kypothetical protein protein kinase (BC hypothetical protein protein kinase (BC hypothetical protein kinase (BC gelatinase B (BC 3 hypothetical protein and or surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface glycmajor surface protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothe |
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| Seconds<br>)<br>11 updates/sec                                                                                                                                                                                     | 423                                                                                                                                                                                                                                                                                                                                 | ave a<br>g printed,                                                                                                                                                                                                                                                                                                                                                     | Description  hypothetical prote promastigate surfa hypothetical prote probable WRKY-type 1-aminocyclopropan rep protein elim mucin-like glycopr alkaline phosphata salivary glue prote hypothetical prote merozoite surface merozoite surface merozoite surface mypothetical prote hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote probable zinc meta hypothetical prote call surface glyc glutactin - fruit major surface glyc call surface glyc glycoprotein A - m cell surface prote                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. tein search, using sw model June 28, 2005, 10:07:28; Search time 25.4289 (without alignments 1600.529 Million ce                                     | APPGLRLRLLLLLLSAAALTAIINAEG 30 pp 60.0 , Gapext 60.0 416 seqs, 96216763 residues 8 satisfying chosen parameters: th: 0 th: 0 th: 0                                                                                                                                                                                                  | isting first 150 summaries  IR 79:*                                                                                                                                                                                                                                                                                                                                     | Amatch Length DB ID  3.5 108 2 726880 3.3 3.27 2 820074 3.3 3.4 2 7252074 3.3 512 2 715922 3.3 516 2 519252 3.3 889 2 731113 3.1 247 2 A55688 3.1 274 2 A55632 3.1 274 2 A55632 3.1 274 2 A55632 3.1 274 2 A55632 3.1 274 2 A55632 3.1 276 2 7122649 3.1 278 2 7122949 3.1 560 2 7122661 3.1 560 2 7127561 3.1 651 2 721755 3.1 1023 2 512519 3.1 1023 2 712156 3.1 1023 2 712157 3.1 1083 2 712157 3.1 1083 2 712157 3.1 1083 2 712157 3.1 1083 2 712157 3.1 1083 2 712157 3.1 1083 2 712157 3.1 1083 2 712157 3.1 1083 2 712157                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
| ein - pro                                                                                                                                                                                                          | ance: 1 Ing table: 01 Ing table: 02 Shed: 28 Size: 0 I number of hi mum DB seg ler                                                                                                                                                                                                                                                  | Post-processing: Li Database : 1: 2: 2: 3: 3: 4: 8: 6: 6: 6: 6: 6: 6: 6: 6: 6: 6: 6: 6: 6:                                                                                                                                                                                                                                                                              | No. No. No. No. No. No. No. No. No. No.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

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Indels

2.4e-06; 0

Pred. No.

100.08;

Mismatches

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15; Conservative 321 PPTTTTTTTTTT

Best Local Similarity

Matches

335

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| DB 2;       |  |
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| core 15;    |  |
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Length 108;

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33.2K hypothetical
 protein F28K19.18
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Promastigote surface antigen P2 (clone 4.6) precursor - Leishmania major (fragment) C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Species: Leishmania major C;Accession: S20074; Da1710 R;Murray, P.J.; Spithill, T.W.
J. Biol. Chem. 266, 24477-24484, 1991
A,Title: Variants of a Leishmania surface antigen derived from a multigenic family. A,Reference number: A41710; MUID:92105105; PMID:1761547
A,Rocession: S20074
A,Rocession: S20074
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Gaps

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DB 2; Length 327; 6e-06; hes 0; Indels

Mismatches

Score 15; Pred. No.

3.5%; Scc. 100.0%; Pre

Query Match 3.5% Best Local Similarity 100.0 Matches 15; Conservative

335

321 PPTTTTTTTTTTT

183 PPTTTTTTTTT 197

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RESULT 3

ALIGNMENTS

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probable WRKX-type DNA binding protein At2g38470 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein T19C21.4 C;Species: Arabidopsis thaliana (mouse-ear cress) C;pacies: Arabidopsis thaliana (mouse-ear cress) C;pacies: Arabidopsis thaliana (mouse-ear cress) C;Accession: T0498; Bequence_revision 05-Mar-1999 #text_change 09-Jul-2004 C;Accession: T0498; D84805 R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul,
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 14; Conservative
 Best Local Similarity
Matches 14; Conserv
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A;Introns: 27/1; 242/2
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 Query Match
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26B80
R;Ainscough, R.
Submitted to the EMBL Data Library, October 1998
A;Reference number: Z20279
A;Reference number: Z20279
A;Reference number: D108 A;Accession: T26B80
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C;Genetics:

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C;Accession: A3-Ept 202; 518-81
R;Leiting, B.; Lindner, 1.J.; Noegel, A.A.
Mol. cell. Biol. 10, 3727-3736, 1990
A;Title: The extrachromosomal replication of Dictyostelium plasmid Ddp2 requires a cis-a-A;Reference number: A3-E679; MUID:90287164; PMID:2192261
 A;Molecule type: DNA
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Kycross-references: UNIPROT:Q23895; GB:M55298; NID:g167727; PIDN:AAA33191.1; PID:g167728
R;Slade, M.B.; Chang, A.C.M.; Williams, K.L.
Plasmid 24, 195-207, 1990
 Cjaccession: T31113
R;Barnes, D.A.; Bonnin, A.; Huang, J.X.; Gousset, L.; Wu, J.; Gut, J.; Doyle, P.; Dubrem Mol. Biochem. Parasitol. 96, 93-110, 1998
A;Title: Avovel multi-domain mucin-like glycoprotein of Cryptosporidium parvum mediates A;Reference number: 220989; MUID:99066935; PMID:9851610
A;Accession: T31113
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A,Reference number: S14202; MUID:91172902; PMID:2077544
 mucin-like glycoprotein 900 - Cryptosporidium parvum
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A;Cross-references: EMBL:X51478; NID:g7307; PIDN:CAA35843.1; PID:g7308
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 rep protein - slime mold (Dictyostelium discoideum) plasmid Ddp2
 Length 518;
 Length 889
 0; Indels
 Indels
 DB 2; Le
 Score 14; DB 2; Le
Pred. No. 0.00012;
 Residues: 1-141,'I',143-780,'E',782-885,'GY' <SLA1>
 A,Status: preliminary, translated from GB/EMBL/DDBJ
A,Molecule type: DNA
 submitted to the EMBL Data Library, January 1990
A;Reference number: $15811
A;Accession: $15811
 100.0%; Pred. ...
 100.0%; Prec. ...
 3.3%; Score 14;
00.0%; Pred. No.
 3.3%;
 322 PITITITITIT 335
 250 PTTTTTTTTT 263
 323 TITITITITII 336
 TTTTTTTTTTTT 472
 A; Cross-references: EMBL:X51478
 3.3%
Best Local Similarity 100.0
Matches 14; Conservative
 Conservative
 Query Match
Best Local Similarity
Matches 14; Conserv
 Status: preliminary
 A; Molecule type: mRNA
 ,Molecule type: DNA
 Accession: A35679
 Accession: S14202
 A; Genome: plasmid
 459
 C.Genetics:
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 A;Accession: S19252
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-516 <PAR>
A;Residues: 1-516 <PAR>
A;Cross-references: UNIPROT: P27486; EMBL: W66619
C;Superfamily: 1-aminocyclopropane1-1-carboxylate synthase
C;Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph
F;276/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - clove pink C.Species: Diahrbus caryophyllus (clove pink) C.Species: Diahrbus caryophyllus (clove pink) C.Space: B.J.Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 C.Accession: S19252 R.Park, K.Y.; Drory, A.; Woodson, W.R. Blant Mol. Biol. 18, 377-386, 1992 A.Title: Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase from senesci A.Reference number: S19252; MUID:92119258; PMID:1731995
 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - clove pink
C;Species: Dianthus caryophyllus (clove pink)
C;Species: Dianthus caryophyllus (clove pink)
C;Date: 0.2-bec-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004.,
C;Accession: S31442
R;Michael, M.Z.
Submitted to the EMBL Data Library, December 1992
A;Description: Isolation of petal senescence-associated cDNA clones encoding 1-aminocycl A;Reference number: S31442
 A.Accession: T02498
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Status: translated from GB/EMBL/DDBJ
A.Residues: 1-512 «ROU">
A.Cross-references: UNIPROT: Q8S8P5; EMBL: AC004683; NID: G3395421; PID: G3395425
A.Experimental source: cultivar Columbia
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. avix on, H.; Moffat, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Aritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A.Reference number: A84420; MUID: 20083487; PMID: 10617197
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submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence.
A;Reference number: 214676
 A, Cross-references: GB: AE002093; NID: 96598471; PIDN: AAC67339.2; GSPDB: GN00139
 Gaps
 Gaps
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 3.3%; Score 14; DB 2; Length 516;
100.0%; Pred. No. 7.7e-05;
tive 0; Mismatches 0; Indels
 3.3%; Score 14; DB 2; Length 512;
100.0%; Pred. No. 7.6e-05;
tive 0; Mismatches 0; Indels
 A;Gene: At2g38470; T19C21.4
A;Map position: 2
A;Introns: 74/3; 143/3; 321/2; 375/2
 323 TITITITITI 336
 457 Trititititii 470
 122 PTTTTTTTTT 135
 322 PTTTTTTTTT 335
 Query Match
Best Local Similarity 100..
 Query Match
Best Local Similarity 100.
Matches 14; Conservative
 A Status: preliminary
A Molecule type: DNA
A Residues: 1-512 <STO>
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RESULT 6

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Gaps

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Indels

Length 245;

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C;Accession: S39310
R;Ramasamy, R.; Ranasinghe, C.
Bubmitted to the EMBL Data Library, November 1993
A;Description: Cycle ds DNA sequencing of a malaria parasite protein from infected blood A;Reference number: S39310
A;Accession: S39310
 R;Marshall, V.M.; Coppel, R.L.; Anders, R.F.; Kemp, D.J.
Mol. Biochem. Parasitol. 50, 181-184, 1992
A;Title: Two novel alleles within subfamilies of the merozoite surface antigen 2 (MSA-2)
A;Reference number: A45632; MUID:92178286; PMID:1542312
A;Contents: KF1916
 A,Reference number: 220279
A,Accession: T26868
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-245 <WIL>
A,Residues: 1-245 <WIL>
A,Cross-references: UNIPROT:Q9XWP2; EMBL:AL032637; PIDN:CAA21609.1; CESP:Y43F8C.5
A,Experimental source: clone Y43F8C
C,Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T26868
R;Ainscough, R.
submitted to the EMBL Data Library, October 1998
 merozoite surface antigen 2 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 merozoite surface antigen - malaria parasite (Plasmodium falciparum)
C,Species: Plasmodium falciparum
C,Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 A;Residues: 1-278 <RAM>
A;Cross-references: UNIPROT:Q25862; EMBL:X76087; NID:g434996; PID:g836639
C;Superfamily: Epstein-Barr virus nuclear antigen
 A;Cross-references: UNIPROT:P50497; GB:M73810; NID:g160484; PID:g160485 A;Note: sequence extracted from NCBI backbone (NCBIN:85252, NCBIP:85257) C;Superfamily: Epstein-Barr virus nuclear antigen C;Keywords: surface antigen
 3.1%; Score 13; DB 2; Length 278;
 3.1%; Score 13; DB 2; Le:
100.0%; Pred. No. 0.00035;
ive 0; Mismatches 0;
 DB 2; Le
0.00039;
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 ilarity 100.0%; P
Conservative 0;
 197 PPTTTTTTT 209
 97 TTTTTTTTT 109
 321 PPTTTTTTT 333
 323 TTTTTTTTTTT 335
 C; Keywords: surface antigen
 Local Similarity
ses 13; Conserv
 A; Molecule type: DNA
A; Residues: 1-274 < MAR>
 A; Gene: CESP:Y43F8C.5
A; Introns: 69/3; 163/2
 A;Status: preliminary A;Molecule type: DNA
 A; Status: preliminary
 A; Accession: A45632
 C; Accession: A45632
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Matches
 C; Genetics:
 RESULT 13
 A45632
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 B56888

alkaline phosphatase (EC 3.1.3.1), intestinal type II - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004

C;Accession: B56888

C;Accession: B56888

C;Accession: B56888

A;Title: The two mRNAs encoding rat intestinal alkaline phosphatase represent two distin

A;Reference number: A56888; MUID:93092310; PMID:1458592

A;Accession: B56888
A,Cross-references: UNIPROT:096503; EMBL:AF068065; NID:94063041; PID:94063042; PIDN:AAC$
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 Solises
salivary glue protein sgs-3 precursor - fruit fly (Drosophila simulans)
(Species: Drosophila simulans
(Species: Drosophila simulans
(Spaces: Soliss) A29988
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(Spaces: Soliss) A2988
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(Spaces: Soliss) A388
(Spaces: Soliss) A388
 A.Experimental source: duodenal mucosa
A.Note: sequence extracted from NCBI backbone (NCBIN:121249, NCBIP:121252)
C.Superfamily: Alkaline phosphatase
C.Keywords: intestine; membrane protein; phosphoric monoester hydrolase
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 A;Cross-references: FlyBase:FBgn0012853
C;Superfamily: salivary glue protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-217/Product: salivary glue protein sgs-3 #status predicted
 Length 1832;
 Score 13; DB 2; Length 217;
Pred. No. 0.00032;
0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 67; larity 100.0%; Pred. No. 0.00012; Conservative 0; Mismatches 0; Indels
 Indels
 RESULT 11
T26868
hypothetical protein Y43F8C.5 - Caenorhabditis elegans
 Score 14; DB 2; L. Pred. No. 0.00022;
 100.0%; Prec. ...
 Query Match 3.3%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 14; Conservative 0; Mismatches
 A,Residues: 1-217 <MAR>
A,Cross-references: UNIPROT:P13729
C,Genetics:
 PTTTTTTTTTT 335
 373 Priririririri 386
 TTTTTTTTTT 335
 323 TTTTTTTTTTT 335
 rrrrrrrrrrr 61
 Best Local Similarity 100.
Matches 13; Conservative
 Local Similarity
nes 13; Conserv
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-67 <ENG>
 A, Molecule type:
 322
 323
 27
 Query Match
 A;Gene: Sgs-3
 Query Match
 49
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Matches
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0; Indels

Length 274;

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-517 <MIL>
A;Crose-references: UNIPROT:Q19269; EMBL:Z73896; PIDN:CAA98057.1; GSPDB:GN00022; CESP:F0
A;Experimental source: clone F09E8
 alkaline phosphatase (EC 3.1.3.1) - rat
N;Alternate names: phytase
C;Species: Rattum norvegicus (Norway rat)
C;Accession: S18408; S175.6
R;Strom, M.; Krisinger, J.; DeLuca, H.F.
R;Strom, M.; Krisinger, J.; DeLuca, H.F.
A;Title: Isolation of a mRNA that encodes a putative intestinal alkaline phosphatase reg
A;Reference number: S18408; MUID:92062729; PMID:1954251
 A;Cross-references: UNIPROT:P51740
A;Note: the correct sequence of residues 144-160 is shown in Fig. 2; the corresponding c
R;Yang, W.J.; Matsuda, Y.; Sano, S.; Masutani, H.; Nakagawa, H.
Biochim. Biophys. Acta 1075, 75-82, 1991
 A;Cross-references: UNIPROT:Q09592; EMBL:Z46935; PIDN:CAA87049.1; GSPDB:GN00020; CESP:M1
A;Experimental source: clone M106
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 C./Species: Caenorhabditis elegans
C./Bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 Gaps
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 A;Map position: 2
A;Introns: 47/2; 110/3; 185/2; 231/2; 270/2; 321/2; 347/3; 411/3; 452/3
C;Superfamily: Caenorhabditis elegans hypothetical protein M106.2
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 Length 517;
 Query Match 3.1%; Score 13; DB 2; Length 519; Best Local Similarity 100.0%; Pred. No. 0.00066; Matches 13; Conservative 0; Mismatches 0; Indels
 0; Indels
 A;Map position: 4
A;Introns: 40/1; 110/3; 141/2; 219/3; 393/1
C;Superfamily: probable zinc metalloproteinase T04G9.2
 Query Match
3.1%; Score 13; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00066;
Matches 13; Conservative 0; Mismatches 0;
 hypothetical protein M106.2 - Caenorhabditis elegans
 R;Palmer, S. submitted to the EMBL Data Library, December 1994 abunditted to the EMBL Data Library, December 1994 A;Reference number: Z19792 A;Accession: T23739 A;Accession: T23739 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-519 <WIL.>
 R;Percy, C.
submitted to the EMBL Data Library, May 1996
 323 TTTTTTTTTTT 335
 323 TITITITITI 335
 334 TTTTTTTTTT 346
 A;Reference number: Z19307
A;Accession: T20658
 A;Molecule type: mRNA
A;Residues: 1-551 <STR>
 A;Status: preliminary
 A; Gene: CESP: F09E8.6
 C; Accession: T23739
 A; Gene: CESP:M106.2
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 RESULT 18
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 Submitted to the EMBL Data Library, Pebruary 1996
A;Reference number: 219503
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Accession: T22023
A;Cross-references: UNIPROT: Q20202; EMBL: Z69792; PIDN: CAA93666.1; GSPDB: GN00028; CESP:F4
A;Experimental source: clone F40E10
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 A;Residues: 1-341 «KEM»
A;Cross-references: EMBL:AF045635; PIDN:AAC02556.1; GSPDB:GN00022; CESP:C05G6.3
A;Experimental source: strain Bristol N2; clone C05G6
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 hypothetical protein C05G6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T3299 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
R;Kemp, K.
submitted to the EMBL Data Library, February 1998
A;Description: The sequence of C. elegans cosmid C05G6.
A;Reference number: Z21252
A;Accession: T32949
 hypothetical protein F40E10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;bacies: L3-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22023
R;Smye, R.
 probable zinc metalloproteinase F09E8.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T20658
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 Query Match 3.1%; Score 13; DB 2; Length 284; Best Local Similarity 100.0%; Pred. No. 0.0004; Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 341; 100.0%; Pred. No. 0.00047; tive 0; Mismatches 0; Indels
 0; Indels
 100.0%; Pred. No. 0.00039;
tive 0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 A; Introns: 52/2; 110/1; 151/3; 195/1; 254/3; 295/3
 A,Map position: X
A,Introns: 34/3; 76/2; 141/3; 183/3; 240/3
 101 TTTTTTTTTT 113
 323 TTTTTTTTTT 335
 323 TTTTTTTTT 335
 323 TITITITITIT 335
 214 ririririririr 226
 Query Match 3.18
Best Local Similarity 100.
Matches 13; Conservative
Best Local Similarity 100.
Matches 13; Conservative
 C,Genetics:
A,Gene: CESP:F40E10.5
 A;Gene: CESP:C05G6.3
A;Map position: 4
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Length 651;

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C;Species: Ruminococcus flavefaciens
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
Mol. Gen. Genet. 245, 260-264, 1994
A;Title: Identification of non-catalytic conserved regions in xylanases encoded by the xy
A;Reference number: S51592; MUID:95115675; PMID:7816035
 A;Cross-references: UNIPROT:052753; EMBL:235226; NID:g516273; PIDN:CAA84537.1; PID:g51627: P;42-239/Domain: endo-1,4-beta-xylanase homology <XYL>F;258-401/Domain: Thermotoga xylanase A amino-terminal repeat homology <TXA>
 A;Map position: 1
A;Introns: 29/2; 54/3; 93/3; 180/2; 236/1; 264/2; 471/3; 486/3; 583/3
 Query Match
3.1%; Score 13; DB 2; Les
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 13; Conservative 0; Mismatches 0;
 KynB precursor - Ruminococcus flavefaciens
 323 TITITITITI 335
 323 TITITITITIT 335
 323 TITITITITI 335
 672 ririririririr 684
 Query Match
Best Local Similarity 100.0
Matches 13; Conservative
 A;Reference number: Z16456
 Local Similarity
Les 13; Conserv
 A;Residues: 1-781 <ZHA>
 A, Gene: CESP: F55D12.5
 A;Status: preliminary A;Molecule type: DNA
 A; Accession: T08611
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 Query Match
 C;Genetics:
A;Gene: docA
 Best Loc
Matches
 RESULT 23
 RESULT 21
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 RESULT 20
T721175
hypothetical protein F55D12.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21175; T22735
R;McMurray, A.
submitted to the EMBL Data Library, June 1996
A;Reference number: Z19385
A;Accession: T21175
A;Accession: T21175
A;Accession: T21175
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-651 <WIL>
A;Residues: 1-651 <WIL>
A;Residues: UNIPROT:Q19659; EMBL:Z75538; PIDN:CAA99842.1; GSPDB:GN00019; CESP:F5
A;Experimental source: clone F20G4
B;McMurray, A.
A;Title: Purification and characterization of phytase from rat intestinal mucosa. A;Reference number: $17576; MUID:91370007; PMID:1654110
A;Accession: $17576
A;Accession: $17576
A;Molecule type: protein
A;Residues: $20-29 < XAN>
A;Note: 10-Val was also found
C;Superfamily: alkaline phosphatase
C;Keywords: phosphoric monoester hydrolase
 Pypothetical protein K11D12.1 - Caenorhabditis elegans
(Species: Caenorhabditis elegans
(Species: Caenorhabditis elegans
(Species: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
(SACcession: T1266)
(S. Henkhaus, J.; Wohldmann, P.; Gillam, B.
Sthenkhaus, J.; Wohldmann, P.; Gillam, B.
A.; Description: The sequence of C. elegans cosmid K11D12.
A. Reference number: Z21207
A. Reference number: Z21207
A. Reference number: A. Reference of C. A. Reference number: A. Referenc
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 submitted to the EMBL Data Library, June 1996
A;Reference number: 219606
A;Reference number: 219606
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: DNA
A;Residues: 1-651 <WI2>
A;Creassreferences: EMBL:275542; PIDN:CAA99864.1; GSPDB:GN00019; CESP:F55D12.5
A;Experimental source: clone F55D12
C;Genetics:
 C;Genetics:
A;Gene: CESP:K11D12.1
A;Map position: 5
A;Introns: 5/3; 48/3; 90/3; 127/3; 149/3; 190/1; 207/1; 233/3; 264/1; 480/1
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 Length 551;
 / Match 3.1%; Score 13; DB 2; Length 560; Local Similarity 100.0%; Pred. No. 0.00071; nes 13; Conservative 0; Mismatches 0; Indels
 0; Indels
 Query Match 3.1%; Score 13; DB 2; I Best Local Similarity 100.0%; Pred. No. 0.0007; Matches 13; Conservative 0; Mismatches 0;
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 345 rrrrrrrrrrr 357
 Query Match
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protein phosphatase 2C-like protein Spalten - slime mold (Dictyostelium discoideum) C;Species: Dictyostelium discoideum C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004 C;Accession: T08606
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 A;Residues: 1-831 <AUB>
A;Cross-references: UNIPROT:O15756; EMBL:AF020409; NID:g2425146; PID:g2425147
A;Experimental source: strain AX4
 hypothetical protein DocA - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: 108611
R;Aubry, L.; Firtel, R.A.; Iranfar, N.
submitted to the EMBL Data Library, August 1997
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3.1%; Score 13; DB 2; Length 781;
100.0%; Pred. No. 0.00094;
ative 0; Mismatches 0; Indels
 Length 831;
 Indels
 3.1%; Score 13; DB 2; Le
ilarity 100.0%; Pred. No. 0.00099;
Conservative 0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
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A;Molecule type: DNA
A;Residues: 1-1083 <WAD>
A;Cross-references: UNIPROT:Q12075; GB:D31909; GB:D17441; NID:g559718; PIDN:BAA06705.1; F
 phospholipase C - yeast (Candida albicans)
C;Species: Candida albicans
C;Species: Candida albicans
C;Species: Candida albicans
C;Accession: T18257
R;Bennett, D.E.; Mccreary, C.E.; Coleman, D.C.
R;Bennett, D.E.; Mccreary, C.E.; Coleman, D.C.
A;Title: Genetic characterization of a phospholipase C gene from Candida albicans: preser A;Reference number: Z18844; MUID:98129081; PMID:9467900
 A; Residues: 1-1099 <BEN>
A; Cross-references: UNIPROT:013433; EMBL:Y13975; NID:g2462981; PIDN:CAA74308.1; PID:g246
 glycoprotein A - mouse
C.Species: Mus musculus (house mouse)
C.Species: Oz-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 15-Jun-2001
C.Accession: JE0120
R.Haidaris, C.G.; Medzihradsky, O.F.; Gigliotti, P.; Simpson-haidaris, P.J.
DNA Res. S. 77-85, 1998
À;Title: Molecular characterization of mouse Pneumocystis carinii surface glycoprotein A
A;Reference number: JE0120; MUID:98344138; PMID:9679195
 A,Gene: PLC1
F;566-726/Domain: 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase domain X hom
 C;Accession: JC2300
R;Wada, M.; Nakamura, Y.
A)Title: MSG gene cluster encoding major cell surface glycoproteins of rat Pneumocystis
A;Reference number: JC2299; MUID:96051989; PMID:8535973
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 C;Species: Pneumocystis carinii
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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 C, Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
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 Length 1083;
 Length 1099;
 Indels
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 C; Comment: This protein is a surface antigen of pneumonia.
 - Pneumocystis carinii
 3.1%; Score 13; DB 2; Le ilarity 100.0%; Pred. No. 0.0012; Conservative 0; Mismatches 0;
 3.1%; Score 13; DB 2; Le
100.0%; Pred. No. 0.0012;
ative 0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 glycoprotein MSG100
 A,Molecule type: mRNA
A,Residues: 1-1282 <HAI>
A,Cross-references: GB:AF143102
 323 TTTTTTTTT 335
 323 TTTTTTTTTT 335
 Trrrrrrrrrrr 758
 959 ririririririr 971
 Conservative
 C, Keywords: glycoprotein
 Query Match
Best Local Similarity
Matches 13; Conserv
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es 13; Conserv
 A; Accession: JE0120
 A;Gene: MSG100
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Best Local S
Matches 13
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 cell surface
 C;Genetics:
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 Glutactin - fruit fly (Drosophila melanogaster)

Cispecies: Drosophila melanogaster

Cispecies: Drosophila melanogaster

Cispecies: Drosophila melanogaster

Cispecies: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

Cispecies: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

Cispecies: Drosophila Dr
 A;Residues: 1-1023 <OLS>
A;Cross-references: UNIPROT:P33438; EMBL:X53286; NID:g297084; PIDN:CAA37380.1; PID:g2970
C;Geneticons: 390/3
A;Introns: 390/3
 major surface glycoprotein 5 - Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Species: Pneumocystis carinii
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C;Accession: JC2217
R;Kitada, K.; Wada, M.; Nakamura, Y.
B)NA Res. 1, 57-66, 1994
A;Title: Multi-gene family of major surface glycoproteins of Pneumocystis carinii: full-A;Reference number: JC2217; MUID:96051981; PMID:7584029
A;Accession: JC2217
 A;Molecule type: mRNA
A;Residues: 1-1076 <KIT>
A;Residues: 1-1076 <KIT>
A;Cross-references: UNIPROT:Q01830; DDBJ:D21827; NID:g425784; PIDN:BAA04851.1; PID:d1005
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
 F;245,471,574,804,837/Binding site: carbohydrate (Asn) (covalent) #status predicted
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R;Aubry, L.; Firtel, R.A.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z16454
A;Accession: T08606
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-975
A;Cross-references: UNIPROT:015743; EMBL:AF019985; NID:g2425120; PID:g2425121
A;Genetics:
A;Genetics:
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 3.1%; Score 13; DB 2; Length 1023; 100.0%; Pred. No. 0.0012; ive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 1076;
100.0%; Pred. No. 0.0012;
iive 0; Mismatches 0; Indels
 Length 975;
 0; Indels
 3.1%; Score 13; DB 2; I 100.0%; Pred. No. 0.0011; Live 0; Mismatches 0;
 322 PTTTTTTTTTT 334
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560 PTTTTTTTTT 572
 603 rrrrrrrrrrr 615
 323 TITITITITIT 335
 323 TTTTTTTTTTT 335
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 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
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C;Accession: S71628; S78068 — S. S. S. Simon, M.I. Schuster, S.C.; Neegell, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I. EMBO J. 15, 3880-3889; 1996 — S. S. Simon, M.I. S. Shaloster, S.C.; Neegell, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I. Saso-3889; 1996 — A;Title: The hybrid histidine kinase DokA is part of the osmotic response system of Dict, A;Teference number: S71628; MUID:96324396; PMID:8670893 — A;Status: nucleic acid sequence not shown
 A; Residues: 1-1670 - SCH>
A; Cross-references: UNIPROT: Q23901; EMBL: X96869
A; Experimental source: strain AX2; substrain 214
R; Experimental source: strain AX2; substrain 214
B; Excluster, S.C.; Noegel, A.A.; Oehme, F.; Gerisch, G.; Simon, M.I.
B; Coluster, S.C.; Noegel, A.A.; Noeme, F.; Gerisch, G.; Simon, M.I.
A; Pescription: The hybrid histidine kinase DoKA is part of the osmotic response system of A; Reference number: S78068
 A; Description: modulates cell response to changes in osmolarity; involved in spore format CxGwywords: phosphoprotein; signal transduction F;1520-1629/Domain: response regulator homology <RRH2> F;1520-1629/Domain: phosphate (Asp) (covalent) #status predicted
 A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-1737 <GEI>
A;Cross-references: UNIRROT:09TW28; GB:AF090533; NID:g5714395; PIDN:AAD47903.1; PID:g5714?
 R;Geissler, H.; Schwarz, E.C.; Soldati, T.
submitted to GenBank, September 1998
A;Description: Identification of two novel and highly divergent myosins in Dictyostellum
A;Reference number: A59235
 transduction histidine kinase dokA - slime mold (Dictyostelium discoideum)
 unconventional myosin heavy chain MyoM - slime mold (Dictyostelium discoideum)
 A;Molecule type: DNA
A;Residues: 1-149,'E',151-219,'TRVLKLIQSTNNWIYWY',238-1671 <SCW>
A;Cross-references: EMBL:X96869; NID:g1237201; PIDN:CAA65612.1; PID:g1237202
 C;Species: Dictyostelium discoideum
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
 C.Species: Dictyostelium discoideum
C.Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C.Accession: A59235
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 Query Match 3.1%; Score 13; DB 2; Length 1671; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 13; Conservative 0; Mismatches 0; Indels
 Ouery Match 3.1%; Score 13; DB 2; Length 1737; Best Local Similarity 100.0%; Pred. No. 0.0018; Matches 13; Conservative 0; Mismatches 0; Indels
 A;Map position: 6, aldB-cabA2
F;62-874/Domain: myosin motor domain homology #status atypical
 323 TTTTTTTTTT 335
 323 TITITITITI 335
 399 TTTTTTTTT 411
 A;Accession: S78068
 A; Accession: A59235
 C;Genetics:
A;Gene: dokA
 A; Gene: myoM
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 Species: Dictyostelium discoideum
(Species: Dictyostelium discoideum)
(Species: Dictyostelium discoideum
(Species: Dictyostelium discoideum
(Species: Ob-Jun-2000 #sequence_revision O9-Jun-2000 #text_change O9-Jul-2004
(SACCESSION: T17456
A.Fitle: A novel Dictyostelium cell surface protein important for both cell adhesion and A.Reference number: 218798; MUID:98359946; PMID:9693138
A.Accession: T17456
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A.Accession: T17456
A.Residues: preliminary; translated from GB/EMBL/DDBJ
A.Residues: 1-1402 <GIN>
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 A;Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
A;Residues: 1-1635 <DBL>
A;Cross-references: UNIPROT:017412; EMBL:AF026492; NID:g2564720; PID:g2564721; PIDN:AAB8
C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100
C;Keywords: glycoprotein
F;248,612,717,779,1063/Binding site: carbohydrate (Asn) (covalent) #status predicted
 chitinase (EC 3.2.1.14) - yellow fever mosquito (5/Species: Aedes aegypti (yellow fever mosquito) (5/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 (5/Accession: T14075 (7/Accession: T14075 (7/A.) (1/A.) (1
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 Query Match 3.1%; Score 13; DB 2; Length 1282; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 2; Length 1402; Best Local Similarity 100.0%; Pred. No. 0.0015; Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 2; Length 1635; 100.0%; Pred. No. 0.0017; ive 0; Mismatches 0; Indels
 C;Genetics:
A;Gene: CHT2
A;Introns: 462/3; 524/3; 618/1; 951/3; 1151/2
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
 C,Genetics:
A,Gene: dtfA
C,Function:
A,Description: involved in the cell adhesion and cell sorting
 323 TTTTTTTTTT 335
 217 TTTTTTTTTT 229
 323 TITITITITE 335
 323 TTTTTTTTTT 335
 TTTTTTTTTTT 86
 Conservative
 Best Local Similarity
Matches 13; Conserv
 A; Accession: T14075
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1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 2 - slime mold (Dictyostelium discoideum)

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RESULT

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A; Cross-references: FlyBase: FBgn0011817
 A; Introns: 8/3; 54/3; 112/3; 151/1
 134 TTTTTTTTTT 145
 421 rrrrrrrrrr 432
 275 PTTTTTTTT 286
 Best Local Similarity 100.
Matches 12; Conservative
 323 TTTTTTTTTT 334
 323 TTTTTTTTTT 334
 $33640 homeotic protein smox-2,
 C;Genetics:
A;Gene: CESP:Y57A10A.i
 A; Status: preliminary
 A; Accession: A54843
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 Query Match
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C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
Mol. Cell. Biol. 15, 5645-5656, 1995
Mol. Cell. Biol. 15, 5645-5656, 1995
A;Title: A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Bio A;Accession: T18273
A;Accession: T18273
A;Accession: T18273
A;Accession: T18273
A;Accession: Dreliminary; translated from GB/EMBL/DDBJ
A;Accession: L19873
A;Accession: L1888 AZHO
A;Accessivererences: UNIPROT:P54674; EMBL:U23477; NID:g733521; PID:g733522; PIDN:AAA85722
 hypothetical protein (clone AAC1) - slime mold (Dictyostelium discoideum) (fragment)
C;Species: Dictyostellum discoideum
C;Species: Janar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: S05358
R;Shaw, D.R.; Richter, H.; Giorda, R.; Ohmachi, T.; Ennis, H.L.
Mol. Gen. Genet. 218, 453-459, 1989
A;Fitle: Nucleotide sequences of Dictyostelium discoideum developmentally regulated cDNA
A;Reference number: S05355; MUID:90066348; PMID:2511421
A;Accession: S05358
 A;Molecule type: mRNA
A;Residues: 1-183 <SHA>
A;Cross-references: UNIPROT:P14195; EMBL:X16525; NID:g7172; PIDN:CAA34532.1; PID:g930011
 A;Residues: 1-342 <GAT>
A;Cross-references: UNIPROT:Q22902; EMBL:U64858; PIDN:AAB18288.1; GSPDB:GN00023; CESP:C1
A;Experimental source: strain Bristol N2; clone C16D9
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 hyporhetical protein C16D9.1 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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 Score 13; DB 2; Length 1858;
Pred. No. 0.0019;
 2.8%; Score 12; DB 2; Length 342;
100.0%; Pred. No. 0.004;
ive 0; Mismatches 0; Indels
 2.8%; Score 12; DB 2; Length 183; 100.0%; Pred. No. 0.0024; ive 0; Mismatches 0; Indels
 0; Indels
 C;Accession: T29557
R;Gattung, S.; Le, T.T.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C16D9.
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 323 TTTTTTTTTT 335
 A;Gene: PIK2
C;Keywords: phosphotransferase
 TTTTTTTTTT 334
 Query Match 2.8
Best Local Similarity 100.
Matches 12; Conservative
 Conservative
 A;Reference number: Z20640
A;Accession: T29557
 Local Similarity
les 12; Conserv
 A; Map position: 5
A; Introns: 59/2; 316/3
 A; Gene: CESP:C16D9.1
 323
 Query Match
 C, Genetics:
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A;Cross-references: UNIPROT:Q9NA83; EMBL:AL117195; NID:e1549729; PIDN:CAB55014.1; CESP:Y!
A;Experimental source: clone Y57A10A
 R;Choi, K.W.; Benzer, S.
Cell 78, 125-136, 1994
A;Title: Rotation of photoreceptor clusters in the developing Drosophila eye requires the
A;Reference number: A54843; MUID:94306509; PMID:8033204
 C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo: C;Keywords: alternative splicing; ATP
F;38-301/Domain: protein kinase homology <KIN>
F;46-54/Region: protein kinase ATP-binding motif
 A;Molecule type: mRNÅ
A;Residues: 1-477 <CHO>
A;Cross-references: UNIPROT:Q23993; GB:U12009; NID:g515669; PIDN:AAA21124.1; PID:g532558
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hypothetical protein Y57A10A.i - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T31631
R;Smye, R.
 C;Species: Schistosoma mansoni
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 16-Aug-2004
C;Accession: S3340; S27841
R;Webster, P.J.; Mansour, T.E.
 nemo, form I - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A54843
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 engrailed-like - fluke (Schistosoma mansoni)
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 Length 477;
 Length 458;
 Query Match 2.8%; Score 12; DB 2; Length 477 Best Local Similarity 100.0%; Pred. No. 0.0053; Matches 12; Conservative 0; Mismatches 0; Indels
 0; Indels
 2.8%; Score 12; DB 2; 1
100.0%; Pred. No. 0.0052;
 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA
A;Residues: 1-458 <WIL>
 submitted to the EMBL Data Library, September 1999
A;Reference number: Z21048
A;Accession: T31631
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 C;Genetics:
 C; Genetics
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Mech. Dev. 38, 25-32, 1992

A,Title: Conserved classes of homeodomains in Schistosoma mansoni, an early bilateral me
A,Reference number: S33640; MUID:92399260; PMID:1356008

A,Rocession: S33640

A,Rolecule type: mRNA
A,Residues: 1-524 <WEB>
A,Cross-references: UNIPROT:Q26601; EMBL:S44191; EMBL:M85305; NID:g161103; PIDN:AAA29929
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-530 cGAT>
A;Cross-references: UNIPROT:O61209; EMBL:AP040646; PIDN:AAB94986.1; GSPDB:GN00020; CESP:
A;Experimental source: strain Bristol N2; clone H17B01
 alkaline phosphatase (EC 3.1.3.1), intestinal - mouse C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Species: Mus musculus (house mouse) C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 16-Aug-2004 C;Accession: B36307 K; Ziomek, C.A.; Millan, J.L. Genomics B, 541-554, 1990 A;Title: Genomic structure and comparison of mouse tissue-specific alkaline phosphatase A;Reference number: A36307; MUID:91139124; PMID:2286375 A;Accession: B36307 A;Status: preliminary
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 hypothetical protein H17B01.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32B12
R;Gattung, S.; Maggi, L.
R;Gattung, S.; Maggi, L.
R;Description: The sequence of C. elegans cosmid H17B01.
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 A;Gene: smox-2
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;424-480/Domain: homeobox homology <HOX>
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 A;Map position: 2
A;Introns: 42/3; 58/1; 173/3; 268/2; 308/2; 340/1; 364/2; 387/3
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 2.8%; Score 12; DB 2; Length 530; llarity 100.0%; Pred. No. 0.0058; Conservative 0; Mismatches 0; Indels
 Query Match 2.8%; Score 12; DB 2; Length 559; Best Local Similarity 100.0%; Pred. No. 0.0061; Matches 12; Conservative 0; Mismatches 0; Indels
 323 TTTTTTTTTT 334
 323 TTTTTTTTTT 334
 Query Match
Best Local Similarity
Matches 12; Conserva
 A, Gene: CESP: H17B01.2
 A; Accession: T32812
 C, Genetics:
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-680 c wHLb.
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A;Experimental source: clone C44
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A;Experimental source: clone K08E3
 C,Accession: A54796
R;Insall, R.; Kuspa, A.; Lilly, P.J.; Shaulsky, G.; Levin, L.R.; Loomis, W.F.; Devreotes, J. Cell Biol. 126, 1537-1545, 1994
A;Tltle: CRAC, a cytosolic protein containing a pleckstrin homology domain, is required i
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 hypothetical protein C44H4.3 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 hypothetical protein KO8E3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23454
 regulatory protein CRAC - slime mold (Dictyostelium discoideum)
C,Species: Dictyostelium discoideum
C,Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jul-2004
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 DB 2; Lens.
o. 0.0072;
0; Indels
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A,Molecule type: DNA
 A;Map position: X
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 R;McMurray, A. submitted to the EMBL Data Library, November 1996 A;Reference number: 219743
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 R;Smye, R. submitted to the EMBL Data Library, August 1996
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A;Map position: 3
A;Introns: 36/1; 73/2; 237/3; 361/3; 612/3
513 rrrrrrrrrrr 524
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 463 TTTTTTTT 474
 325 TTTTTTTTT 336
 259 Trititiritiii 270
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 A; Gene: CESP: C44H4.3
 C; Accession: T19939
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C;Accession: T30546
R;Mei, O.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human Pneumocystis cari.
A;Reference number: Z17905; MUID:98380374; PMID:9712777
 "Molecule type: nucleic acid

"Residues: 1-3712 <KUS>

"Cross-references: UNIPPOT: Q00174; GB:M96388; NID:g157799; PIDN: AAA28662.1; PID:g157800

"Garrison, K.; MacKrell, A.J.; Pessler, J.H.

Biol. Chem. 266, 22899-22904, 1991

"Title: Drosophila laminin A chain sequence, interspecies comparison, and domain structuing the sequence number: $18253; MUID:92078147; PMID:1744083
 ;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like hr
;Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular r
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;333-400/Domain: laminin-type EGF-like homology cLEG>
;541-584/Domain: laminin-type EGF-like homology cLEGI>
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C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S28399; S18253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence.
A;Reference number: S28399; MUID:93049203; PMID:1425586
 A;Cross-references: EMBL:AF038556; NID:g3560524; PID:g3560526; PIDN:AAC34981.1
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 major surface glycoprotein - Pneumocystis carinii (fragment)
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C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
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EGF-like homology <
EGF-like homology <
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F;2017-2061/Domain: laminin-type
F;2064-2109/Domain: laminin-type
 748 TTTTTTTTTT 759
 325 TITITITITI 336
 902 Tritititii 913
 tatus: preliminary
 Gene: FlyBase:LanA
 Cross-references:
 Accession: S18253
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 Genetics:
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 A;Accession: A54796
A;Status: preliminary
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A;Residues: 1-698 <INS>
A;Cross-references: UNIPROT:P35401; GB:U06228; NID:g641960; PIDN:AAA61782.1; PID:g456398
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A;Introns: 11/3; 153/1
C;Superfamily: Dictyostelium regulatory protein CRAC
 xyjanase, beta(1,3-1,4)-glucanase - Ruminococcus flavefaciens
C;Species: Ruminococcus flavefaciens
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A36910
R;Flint, H.J.; Martin, J.; McPherson, C.A.; Daniel, A.S.; Zhang, J.X.
Bacteriol. 175, 2943-2951, 1993
A;Title: A bifunctional enzyme, with separate xylanase and beta(1,3-1,4)-glucanase domai
A;Reference number: A36910, MuID:9325938; PMID:8491715
A;Accession: A36910
A;Accession: Prellintry
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ive 0; Mismatches 0; Indels
 RiNhan, M.; Hawkins, J.
submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid C12D12.
A;Reference number: 220656
A; Reference number: A54796; MUID:94375528; PMID:8089184
 hypothetical protein C12D12.1 - Caenorhabditis elegans
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 323 TTTTTTTTT 334
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A; Residues: 1-825 <NHA>
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Chin, C.W.; Chung, M.K.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Ansen, N.F.; Hughes, B.; Huizar, L.
Anthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.S.; Schuartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Il Reference number: A86141; MulD:21016719; PMID:11130712

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C;Accession: C90029
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchana, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; FC.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
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 probable auxin-induced protein, 50455-50036 [imported] - Arabidopsis thaliana
 hypothetical protein SA2097 [imported] - Staphylococcus aureus (strain N315)
 C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C.Accession: D86417
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
C;Accession: T26561
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ive 0; Mismatches 0; Indels
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 22 Trititititi 32
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C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55575
R;Kordeli, B.; Lambert, S.; Bennett, V.
J. B;ol. Chem. 270, 2352-2359, 1995
A;Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the ax A;Reference number: A5575; MUID:95138209; PMID:7836469
A;Accession: A55575
F;2116-2697/Domain: I/II, heptad repeats <DOM2>
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F;2698-2863/Domain: repeat G2 <RG2>
F;3049-3223/Domain: repeat G3 <RG3>
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F;3079-3220/Domain: repeat G4 <RG4>
F;3134-3528/Domain: repeat G4 <RG4>
F;3134-3528/Domain: repeat G5 <RG5>
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F;3529-3712/Domain: repeat G5 <RG5>
F;3679-3720/12/Domain: repeat G5 <RG5>
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C;Keywords: alternative splicing; peripheral membrane protein
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100.0%; Pred. No. ...
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N;Alternate names: ankyrin G
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 3272 Priririririi 3283
 3967 TTTTTTTTTTT 3978
 322 PTTTTTTTT 333
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 Best Local Similarity 100.
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F;729-761/Domain:
F;762-794/Domain:
 F;795-827/Domain:
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 366-398/Domain:
 97/Domain:
 53/Domain:
 ;630-662/Domain:
 F;498-530/Domain:
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 hypothetical protein C04G6.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Cact-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29596
R;Anderson, K.; Chissoe, S.
submitted to the EMBL Data Library, April 1996
A;Description: The sequence of C. elegans cosmid C04G6.
A;Reference number: Z20648
 salivary glue protein sgs-3 precursor - fruit fly (Drosophila yakuba)
C;Species: Drosophila yakuba
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
C;Accession: S01360; C29988
 C.Species: Ictalurus punctatus (channel catfish)
C.Date: 02-Apr-2002 #sequence_revision 02-Apr-2002 #text_change 09-Jul-2004
C.Accession: JC7783
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 R;Martin, C.H.; Mayeda, C.A.; Meyerowitz, E.M.
J. Mol. Biol. 201, 273-287, 1988
A;Title: Evolution and expression of the Sgs-3 glue gene of Drosophila.
A;Reference number: S01358; MUID:88332966; PMID:3138416
 C;Superfamily: salivary glue protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-263/Product: salivary glue protein sgs-3 #status predicted <MAT>
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 RAD 23B protein - channel catfish
 175 İTTİTİTİTİ 185
 322 PITITITITE 332
 96 PTTTTTTT 106
 323 TTTTTTTT 333
 156 rrrrrrrrr 166
 323 TTTTTTTTT
 A,Gene: CESP:C04G6.2
 A;Gene: Sgs-3
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 C;Genetics:
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A, Reference number: A89758; MUD:21311952; PMID:11418146
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A, Accession: C90029
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-166 < KUR>
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 merozoite Burface antigen 2 [imported] - malaria parasite (Plasmodium falciparum) (fragm C.Species: Plasmodium falciparum
C.Species: Plasmodium falciparum
C.Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C.Accession: T46896
R.Prescott, N.; Stowers, A.W.; Cheng, Q.; Bobogare, A.; Rzepczyk, C.M.; Saul, A.
Mol. Biochem. Parasitol. 63, 203-212, 1994
A.Title: Plasmodium falciparum genetic diversity can be characterized using the polymorp
A.Reference number: 224128; MUID:94277144; PMID:8008018
 A;Reaiduea: 1-208 <PRE>
A;Cross-references: UNIPROT:Q25949; EMBL:L19048; NID:g438839; PIDN:AAC37195.1; PID:g4388
 A;Cross-references: EMBL:AL110480; NID:e1542182; PIDN:CAB54379.1; CESP:Y24F12A.c
A;Experimental source: clone Y24F12A
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 08-Sep-2000
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 C,Accession: T2660
R;Lennard, N.
Submitted to the EMBL Data Library, September 1999
A;Reference number: 220233
A;Accession: T26560
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-234 <WIL>
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C;Superfamily: Epstein-Barr virus nuclear antigen
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 99 TTTTTTTTT 109
 323 TTTTTTTTT 333
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A;Cross_references: UNIPROT:P17955; GB:X52583; NID:g57640; PIDN:CAA36813.1; PID:g57641
R;D'Onofrio, M.; Starr, C.M.; Park, M.K.; Holt, G.D.; Haltiwanger, R.S.; Hart, G.W.; Hanc Proc. Natl. Acad. Sci. U.S.A. 85, 9559-9599, 1988
A;Title: Partial CDNA sequence encoding a nuclear pore protein modified by O-linked N-ace A;Reference number: A31762; MUID:89071743; PMID:3200844
 C.Accession: AS5573
R.Cordes, V.; Waizenegger, I.; Krohne, G.
Eur. J. Cell Biol. 55, 31-47, 1991
A.Fitle: Worlear pore complex glycoprotein p62 of Xenopus laevis and mouse: cDNA cloning A.Reference number: A56573; MuID:92007945; PMID:1915419
 C;Species: Rattus norregicus (Norway rat)
C;Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 09-Jul-2004
C;Date: 09-Nov-1990 #sequence revision 09-Nov-1990 #text_change 09-Jul-2004
C;Datession: A35596; A31762; IS5336; B1666
R;Starr, C.M.; D'Onofrio, M.; Park, M.K.; Hanover, J.A.
J. Cell Biol. 110, 1861-1871, 1990
A;Title: Primary sequence and heterologous expression of nuclear pore glycoprotein p62.
A;Reference number: A35596; MUID:90277705; PMID:2190987
 A, Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1992
 nuclear pore complex glycoprotein p62 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
 RiD'čnofrio, M.; Lee, M.D.; Starr, C.M.; Miller, M.; Hanover, J.A.
J. Balol. Chem. 266, 11980-11985, 1991
Affitle: The gene encoding rat nuclear pore glycoprotein p62 is intronless.
A;Reference number: 155336; MUID:91268076; PMID:2050692
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A;Residues: 370, FR', 373-525 <DON>
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A;Experimental source: hepatic
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A;Cross-references: GB:M62992; NID:g205953; PIDN:AAA41789.1; PID:g205954
 DB 2; Lens.
 Length 525;
 Indels
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 DB 2;
0.05;
 Query Match 2.6%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
 Match 2.6%; Score 11; DB Local Similarity 100.0%; Pred. No. 0.0 es 11; Conservative 0; Mismatches
 C;Superfamily: octopamine receptor type I C;Keywords: G protein-coupled receptor
 A;Status: translated from GB/EMBL/DDBJ
 A,Introns: #status absent
C,Keywords: coiled coil; glycoprotein
 nuclear pore glycoprotein p62 - rat
 A; Experimental source: hepatic
 323 TITITITITI 333
 350 riririririr 360
 323 TTTTTTTTT 333
 274 rrrrrrrrrr 284
 A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-525 <STA>
 A;Status: preliminary
A;Molecule type: mRNA
 A; Molecule type: DNA
 A; Accession: I55336
 Query Match
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Matches
 RESULT 60
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 RESULT 58
Sp8868
G protein-coupled receptor GCR1 - migratory locust
C; Species: Locusta migratoria (migratory locust)
C; Date: 15-Pbb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
C; Date: 15-Pbb-1996 #sequence revision 01-Mar-1996 #text_change 09-Jul-2004
A; Title: Characterization of a cloned locust tyramine receptor cDNA by functional expres
A; Title: Characterization of a cloned locust tyramine receptor cDNA by functional expres
A; Accession: S58868
A; Estatus: preliminary
A; Dolecule type: mRNA
A; Estatus: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: mRNA
A; Residues: 1-307, 'D', 309-338, 'K', 340-484 *VA2>
A; Cross-references: EMBL:X69521; NID:g871406; PIDN:CAA49269.1; PID:g871407
Riliu, Z.; Li, P.; Kocabas, A.; Karsi, A.; Ju, Z.
Blochem. Biophys. Res. Commun. 289, 317-324, 2001
Arritle: Microsatellite-containing genes from the channel catfish brain: Evidence of tri
A; Reference number: JC7783
A; Contents: Brain
A; Accession: JC7783
A; Molecule type: mRNA
A; Residues: 1-385 < LIU>A; Coss-references: UNIPROT:Q7LZR8
C; Comment: This protein with a polythreonine tract, has importance in the nucleotide exc
 A;Cross-references: UNIPROT:Q9GZH9; EMBL:AF026212; PIDN:AAB71300.1; GSPDB:GN00028; CESP.
A;Experimental source: strain Bristol N2; clone F52G3
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 hypothetical protein F52G3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T32467
R;Blanchard, M.; Gattung, S.; Sansone, J.
Submitted to the BmEL Data Library, September 1997
A;Description: The sequence of C. elegans cosmid F52G3.
A;Reference number: Z21173
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-415 < PBLA>
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 A;Gene: CESP:P52G3.5
A;Map position: X
A;Introns: 31/1; 49/1; 104/1; 117/1; 220/1; 241/2; 307/1; 370/3
 Length 415;
 2.6%; Score 11; DB 2; Length 385;
100.0%; Pred. No. 0.038;
ive 0; Mismatches 0; Indels
 0; Indels
 Query Match 2.6%; Score 11; DB 2;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 11; Conservative 0; Mismatches 0
 11; Conservative
 203 TTTTTTTT 213
 323 TTTTTTTTT 333
 323 TTTTTTTTT 333
 Local Similarity
 C;Genetics:
A;Gene: rad23b
A;Introns: 76/3
 Query Match
 C;Genetics:
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A;Residues: 1-569 <THA>
A;Cross-references: UNIPROT:Q83183; EMBL:X77798; NID:g535195; PIDN:CAA54825.1; PID:g5351£
C;Superfamily: murine cytomegalovirus gp88 protein
 A;Residues: 1.649 <WIL>
A;Cross-references: UNIPROT:Q22225; EMBL:Z66500; PIDN:CAA91305.1; GSPDB:GN00020; CESP:T0^c
A;Experimental source: clone T05C12
 C,Accession: A45155
R,Hauser, F.; Hoffmann, W.
Biol..Chem. 267, 24620-24624, 1992
A)Title: P-domains as shuffled cysteine-rich modules in integumentary mucin C.1 (FIM-C.1 A;Reference number: A45185; MUID:93077586; PMID:1447205
 A;Cross-references: UNIPROT:Q05049; GB:L02115; NID:g214147; PIDN:AAA74725.1; PID:g951460
RESULT 63
547277
947277
9296 protein - murine cytomegalovirus
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Arcession: S47277
B;Thaele, R.; Lucin, P.; Schneider, K.; Koszinowski, U.
Submitted to the EMBL Data Library, February 1994
A;Reference number: S47277
A;Accession: S47277
A;Status: preliminary
A;Molecule type: Dman.
 hypothetical protein T05C12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 mucin_FIM-C.1 - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 26-May_1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
 A;Map position: 2
A;Introns: 28/3; 48/3; 103/3; 156/3; 192/3; 249/3; 408/3; 495/3; 623
C;Superfamily: Caenorhabditis elegans hypothetical protein T05C12.4
 Length 649;
 Length 569;
 0; Indels
 Query Match 2.6%; Score 11; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 11; Conservative 0; Mismatches 0;
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
 DB 2;
0.06;
 RjBurton, J. submitted to the EMBL Data Library, October 1995 A;Reference number: Z19901 A;Accession: T24505
 Query Match 2.6%; Score 11; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 11; Conservative 0; Mismatches
 F;162-202/Domain: trefoil homology <TRF1>
F;307-347/Domain: trefoil homology <TRF2>
F;354-394/Domain: trefoil homology <TRF3>
 323 TTTTTTTTT 333
 473 111111111 483
 326 TTTTTTTTI 336
 355 rrrrrrrrri 365
 A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-662 <HAU>
 A; Gene: CESP: T05C12.4
 C; Accession: T24505
 C;Genetics
 RESULT 65
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 Cispeciaes: Escherichia coli
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Cispeciaes: Escherichia coli
Cispeciaes: Bscherichia coli
Cispeciaes: Bscherichia coli
Cispeciaes: Bscherichia coli
Cispeciaes: Is-Jul-2001 #sequence_revision Is-Jul-2001 #text_change 09-Jul-2004
Cispeciaes: Nable 1-2004
RiHayashi, T.: Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A;Status: preliminary
 A;Cross-references: UNIPROT:Q63850; GB:S59342; NID:g236260; PIDN:AAB19953.1; PID:g236261 A;Note: sequence extracted from NCBI Dackbone (NCBIN:59342, NCBEP:59343) C;Comment: The amino end of this protein contains O-linked N-acetylglucosamine additions C;Keywords: glycoprotein; nuclear membrane; peripheral membrane protein
 A;Cross-references: UNIPROT:Q9R396; GB:AE005174; NID:g12518449; PIDN:AAG58825.1; GSPDB:G
S;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: tir
 probable translocated intimin receptor protein tir [imported] - Escherichia coli (strain c)Species: Escherichia coli (c)Species: Escherichia (c)Species: Escherichia (c)Species: Escherichia (c)Species: Escherichia (c)Species: Escherichia coli (c)Spe
 A;Cross-references: UNIPROT:O9R396; GB:BA000007; PIDN:BAB37984.1; PID:g13364036; GSPDB:C
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: EC84561
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 Query Match 2.6%; Score 11; DB 2; Length 526; Best Local Similarity 100.0%; Pred. No. 0.05; Matches 11; Conservative 0; Mismatches 0; Indels
 Length 558;
 Length 558;
 2.6%; Score 11; DB 2; Length 558
100.0%; Pred. No. 0.053;
ive 0; Mismatches 0; Indels
 0; Indels
 Score 11; DB 2;
Pred. No. 0.053;
 100.0%; Pred. No. 0.0 tive 0; Mismatches
 . 68;
 Conservative
 Conservative
 323 TTTTTTTTT 333
 274 TTTTTTTTTT 284
 323 TTTTTTTTT 333
 393 TTTTTTTT 403
 393 TTTTTTTT 403
 Query Match
Best Local Similarity
Matches 11; Conserva
 Query Match
Best Local Similarity
Matches 11; Conserva
 A; Molecule type: DNA
A; Residues: 1-558 <HAY>
 A; Accession: E86045
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-558 <STO>
 A;Residues: 1-526 <COR>
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C;Accession: C69493
R;Klenk, H.E.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F. Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
 A, Accession: C69493
A, Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A, Residues: 1-816 < KLL>
A, Cross-references: UNIPROT:028331; GB:AE000968; GB:AE000782; NID:g2689291; PIDN:AAB8930E
 R.Pauley, A. Submitted to the EMBL Data Library, July 1995
submitted to the EMBL Data Library, July 1995
submitted to the EMBL Data Library, July 1995
A.Description: The sequence of C. elegans cosmid F32A5.
A.Reference number: 218482
A.Reference number: 218482
A.Reference number: 218482
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-97 - APAU>
A.Residues: 1-97 - APAU>
A.Cross-references: EMBL:U20864; NID:g669026; PID:g669033; PIDN:AAC46666.1; CESP:F32A5.2
A.Experimental source: strain Bristol N2
 C; Accession: T18275
R; Zhou, K.; Takegawa, K.; Emr, S.D.; Firtel, R.A.
Mol. Cell. Biol. 15, 5645-5656, 1995
A; Title. A phosphatidylinositol (PI) kinase gene family in Dictyostelium discoideum: Biol A; Reference number: Z06411
A; Accession: T18275
 A;Molecule type: DNA
A;Residues: 1-1093 <ZHO>
A;Cross-references: UNIPROT:P54677; EMBL:U23479; NID:g733527; PID:g733528; PIDN:AAA85725
 1-phosphatidylinositol 3-kinase (EC 2.7.1.137) 4 - slime mold (Dictyostelium discoideum) C,Species: Dictyostelium discoideum C,Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Genetics:
A;Gene: CESP:F32A5.2
A;Introns: 23/1; 58/3; 102/3; 136/2; 277/2; 380/2; 422/1; 502/1; 580/2; 648/1; 935/2
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 hypothetical protein AF1948 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 hypothetical protein F32A5.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16232
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 Query Match 2.6%; Score 11; DB 2; Length 816; Best Local Similarity 100.0%; Pred. No. 0.072; Matches 11; Conservative 0; Mismatches 0; Indels
 Query Match

2.6%; Score 11; DB 2; Length 977;
Best Local Similarity 100.0%; Pred. No. 0.084;
Matches 11; Conservative 0; Mismatches 0; Indels
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 322 PTTTTTTTT 332
 159 Pririririr 169
 320 PPPTTTTTT 330
 357 PPPTTTTTT 367
 C;Genetics:
 RESULT 69
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 A.Cross-references: UNIPROT: Q95Q40; EMBL: U67953; PIDN: AAB07581.1; GSPDB: GN00028; CESP: ZG A; Experimental source: strain Bristol N2; clone ZC13
C; Genetics:
A; Gene: CESP: ZC13.3
A; Map position: X
A; Introns: 19/3; 52/2; 86/1; 169/1; 301/1; 365/1; 401/3; 506/2; 528/2; 553/1; 683
 A;Cross-references: UNIPROT:Q20908; EMBL:274473; PIDN:CAA98949.1; GSPDB:GN00023; CESP:F5
A;Experimental source: clone F56H9
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 RESULT 67
T22808
Hypothetical protein F56H9.1 - Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: Caenorhabditis elegans
CjSpecies: Dect-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
CjAccession: T22808
R;Burton, J.
R;Burton, J.
R;Reference number: Z19618
A;Reference number: Z19618
A;
 hypothetical protein ZC13.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;bate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25937
R;Bradshaw, H.
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 Query Match 2.6%; Score 11; DB 2; Length 662; Best Local Similarity 100.0%; Pred. No. 0.061; Matches 11; Conservative 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 770;
100.0%; Pred. No. 0.069;
ive 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 732;
100.0%; Pred. No. 0.066;
tive 0; Mismatches 0; Indels
 C;Genetics:
A;Gene: CESP:F56H9.1
A;Map position: 5
A;Introns: 235/1; 262/2; 320/1; 367/2; 510/3; 654/1; 681/2
 submitted to the EMBL Data Library, August 1996
A;Description: The sequence of C. elegans cosmid ZC13.
A;Reference number: Z20113
A;Recession: T25937
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-732 <BRA>
F;526-566/Domain: trefoil homology <TRF4>
F;573-613/Domain: trefoil homology <TRF5>
F;621-661/Domain: trefoil homology <TRF6>
 Query Match 2.6
Best Local Similarity 100.
Matches 11; Conservative
 Best Local Similarity 100.
Matches 11; Conservative
 322 PITTITITI 332
 214 rirriririr 224
 323 TTTTTTTTT 333
 643
 323 TTTTTTTTT 333
 633
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nitrilase associated protein-like - Arabidopsis thaliana
N;Alternate names: protein T20K14_210
S;Species arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C;Accession: T51538
C;Accession: T51538
S;Sato, S; Nakamura, Y; Kaneko, T.; Kato, T.; Assmizu, E.; Kotani, H.; Tabata, S.; Mew submitted to the Protein Sequence Database, August 2000
A;Reference number: 225394
 larval glue protein Lgp-1 precursor - fruit fly (Drosophila virilis)
C;Species: Drosophila virilis
C;Species: Drosophila virilis
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C;Accession: A60095; S50126; S44060
R;Swida, U.; Lucka, L.; Kress, H.
Bestelopment 108, 269-280, 1990
A;Title: Glue protein genes in Drosophila virilis: their organization, developmental con-A;Reference number: A60095; MUID:90276249; PMID:2351069
 Cross-references: UNIPROT:Q27423; GB:X76203; NID:g433481; PIDN:CAA53796.1; PID:g433482; Lanio, W.; Swida, U.; Kress, H. Grochim. Blophys. Acta 1219, 576-580, 1994; Jritle: Molecular cloning of the Drosophila virilis larval glue protein gene Lgp-3 and Reference number: S50125; MUID:95002181; PMID:7918662
 Cross-references: EMBL:229565; NID:9450901; PIDN:CAA82672.1; PID:9450903
Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1994
 Accession: S50126
Status: preliminary; nucleic acid sequence not shown; translation not shown;
Molecule type: DNA
 C; Ke¬words: glycoprotein; salivary gland; tandem repeat
F;1-23/Domain: signal sequence #status predicted <SIG>
F;43-86,94-104/Region: 11-residue repeats (T-T-T-T-T-P-C-P-T-T-T)
F;105-160/Region: 8-residue repeats (T-T-T-T-T-T-T-D)
 2.4%; Score 10; DB 2; Length 127;
100.0%; Pred. No. 0.13;
 2.4%; Score 10; DB 2; Length 232;
100.0%; Pred. No. 0.22;
 A;Cross-references: UNIPROT:Q9LF22; EMBL:AL391143
A;Experimental source: cultivar Columbia; BAC clone T20K14
 0; Mismatches
 llarity 100.0%; Pred. No. 0.2
Conservative 0; Mismatches
 A;Gene: FlyBase:Dvir/Lgp1
A;Cross-references: FlyBase:FBgn0010305
 Superfamily: salivary glue protein
 100.08;
 10; Conservative
 323 TITITITIT 332
 322 PTTTTTTT 331
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 69
 Best Local Similarity
Matches 10; Conserv
 Local Similarity
tes 10; Conserv
 ;Molecule type: DNA ;Residues: 1-232 <SWI>
 A, Accession: T51538
A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-127 <SAT>
 Residues: 1-232 <LA2>
 A; Map position: X16A
 Accession: A60095
 A; Note: T20K14 210
 A; Map position: 5
 A; Introns: 97/3
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 Query Match
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 C;Genetics:
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 A;Residues: 1-1271 <TIGR>
A;Cross-references: UNIPROT:P47580; GB:U39716; GB:L43967; NID:g1046037; PID:g1046042; TJ
C;Genetics:
 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-7962 <RES>
A;Residues: 1-7962 <RES>
Cross-references: UNIPROT:Q10465; EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g101C)
 Cispecies: Mycoplasma genitalium
Cispecies: Mycoplasma genitalium
Cispecies: Mycoplasma genitalium
Cispecies: Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
Ciscossion: D64237
RiFraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A;Title: The minimal gene complement of Mycoplasma genitalium.
A;Reference number: A64200; MUID:96026346; PMID:7569993
A;Accession: D64237
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Residues: 1-1271 <TIGR>
 Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
Cispecession: I38346
Ribabit, S.; Kolmerer, B.
Science 270, 293-296, 1995
A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.
A;Reference number: A57430; MUID:96026330; PMID:7569978
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 2.6%; Score 11; DB 2; Length 1093; 100.0%; Pred. No. 0.092; Live 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 1271;
100.0%; Pred. No. 0.1;
ive 0; Mismatches 0; Indels
 2.6%; Score 11; DB 2; Length 7962;
100.0%; Pred. No. 0.49;
ive 0; Mismatches 0; Indels
 D64237
hypothetical protein MG338 - Mycoplasma genitalium
 A;Gene: GDB:TTN
A;Cross-references: GDB:127867; OMIM:188840
 elastic titin - human (fragment)
 C;Keywords: phosphotransferase
 Best Local Similarity 100.
Matches 11, Conservative
 11; Conservative
 323 TTTTTTTTT 333
 775 TTTTTTTTT 785
 Conservative
 158 TIRWFKGNKEL 168
 323 TTTTTTTTT 333
 354 TTTTTTTT 364
 A; Map position: 2q31-2q31
 Best Local Similarity
Matches 11; Conserva
 Local Similarity
nes 11; Conserva
 A, Genetic code: SGC3
 A; Accession: I38346
 Query Match
 Query Match
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 A; Note: PIK4
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GSFF3
salivary glue protein sgs-3 - fruit fly (Drosophila melanogaster)
C.$pecies: Drosophila melanogaster
C.Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C.Accession: A03329
R.Garfinkel, M.D.; Pruitt, R.E.; Meyerowitz, E.M.
J. Mol. Biol. 168, 765-789, 1983
A;Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila
A;Title: DNA sequences, gene regulation and modular protein evolution in the Drosophila
A;Title: DNA sequences, Gene regulation and modular protein evolution in the Drosophila
A;Reference number: A92904; MUID:83294545; PMID:6411930
A;Residues: 1.307 <GAR>
A;Residues: 1.307 <GAR>
A;Residues: 1.307 <GAR>
A;Cross-references: UNIPROT:PO2840; GB:X01918; NID:8581; PIDN:CAA25994.1; PID:g603989
C;Comment: This protein is produced by third-instar larvae.
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Map position: 3L (68C)
A;Murcons: 10/1
C;Superfamily: salivary glue protein
C;Keywords: salivary glued repeat
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 Query Match
2.4%; Score 10; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 0.27;
Matches 10; Conservative 0; Mismatches 0; Indels
 323 TTTTTTTTT 332
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45 TTTTTTTT 54
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Search completed: June 28, 2005, 10:21:29 Job time : 28.4289 secs

| P90601 trypanosoma Q6waz8 trypanosoma Q96Zw5 trypanosoma O15776 trypanosoma O61019 trypanosoma Q2s34 leishmania Q86a81 d similar t Q86a90 dictyosteli Q6tuli arttus norv O61050 trypanosoma Q96Zw6 trypanosoma Q96Zw6 trypanosoma |                                                                                                                                                 |                                                                                                                                            | 995uy4 plasmodium (955uy4 plasmodium (955uy4 plasmodium (955uy6 plasmodium (955uy6 plasmodium (955uy6 plasmodium (955uy6 plasmodium (950uy6) plasmodium (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) plasmodium (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950uy6) trypanosoma (950u                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
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| GenCore Copyright (c) 1993 in search, using sv ne 28, 2005, 09:55:                                                                                                                                                                | 423 1 AAPPGLRIRLILLISAAAL DilGO Gapop 60.0 , Gapext 60.0 1612378 seqs, 512079187 0 hits satisfying chosen p ength: 0 ength: 0 ength: 2000000000 | Uniprot 03:* Uniprot 53:* 1: uniprot sprot 2: uniprot tremt is the number of ter than or equal ived by analysis  * ? ?uery March Length DB | 100.0 445 2 Q8R4LI<br>80.9 456 2 Q8R5M8<br>74.2 417 2 QRTNLI<br>74.2 417 2 QTTNLI<br>74.0 336 2 Q8CVG4<br>74.0 336 2 Q9CVG4<br>74.0 336 2 Q9CVG4<br>53.7 476 2 Q8CMP8<br>35.5 443 2 Q9CXP6<br>27.2 295 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 299 2 Q9CYLS<br>27.2 295 2 Q9CYLS<br>27.2 295 2 Q9CYLS<br>27.2 205 2 Q9CYLS<br>27.2 205 2 Q9CYLS<br>27.2 205 2 Q9CYLS<br>27.2 205 2 Q9CYLS<br>27.2 205 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS<br>27.2 2 Q9CYLS                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| M protein -<br>un on:                                                                                                                                                                                                             | Periect score: Sequence: Scoring table: Searched: Word size: Total number of I Minimum DB seq 1 Maximum DB seq 1                                | pase :  Pred. N score g and is                                                                                                             | 1 423<br>3 3 342<br>5 4 4 3 3 3 4 4 2 3 3 3 4 4 2 3 3 3 4 4 2 3 3 3 4 4 2 3 3 3 4 4 2 3 3 3 4 4 2 3 3 3 4 4 2 3 3 3 4 3 3 4 3 3 4 3 3 4 3 3 3 3                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

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 382 GVVAVVVFAM.CLLIIIGRYFARHKGTYFTHEAKGADDAADAADTAIINAEGGQNNSEEKK 441
 121 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTTTDSRAGEEGTIGAVDHAVIG 360
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 9
 81
 SEQUENCE FROM N.A.
MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8;
MUJICA E., Soyama A., Momoi T.;
"RA175, which is the mouse ortholog of TSLC1, a tumor suppressor gene
 202 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 262 EGDAFELTCEAIGKPQPVMVTWVKVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
 22 AAPPGLRLRLILLLSAAALIPTGDGQNLFTKOVTVIEGEVATISCQVNKSDDSVIQLLN
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 142 TVLVPPRNLMIDIQKDTAVEGERIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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 Gaps
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
 R GGD; MGI:1889272; Igsf4a.
R GGO; GG:0016021; C:integral to membrane; TAS.
GG; GG:0016021; C:integral to membrane; TAS.
GG; GG:0008021; C:synapse; IDA.
R GG; GG:0008121; C:synaptic vesicle; IDA.
R GG; GG:00016318; P:calcium-independent cell-cell adhesion; IDA.
GG; GG:0007155; P:calcium-independent cell-cell adhesion; IDA.
R GG; GG:0007155; P:calcium-independent cell-cell adhesion; IDA.
R GG; GG:0007155; P:calcium-independent cell-cell adhesion; IDA.
R GG; GG:0007110; Ig-like.
R InterPro; IPR003598; Neurexin-like.
R InterPro; IPR003598; Neurexin-like.
R SMART; SM00294; 4.1m; 1.
R SMART; SM00408; IGG2; 1.
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 100.0%; Score 423; DB 2; Length 445; 100.0%; Pred. No. 0; ive 0; Mismatches 0; Indels
 PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 445 AA; 48664 MW; C5D5A070DAF70E55 CRC64;
 Last sequence update)
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 Created)
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 100.08;
 Name=Igsf4a; Synonyms=RA175;
Mus musculus (Mouse).
 01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-OCT-2003 (TrEMBLrel. 25,
 423; Conservative
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"Identification of the Tsic1 gene, a mouse orthologue of the human
Gene 295:7-12(2002).
 Mus musculus (Mouse).
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 STRAIN-C57BL/6; TISSUE-Brain; MEDLINE=22841094; PubMed=12836663; DOI=10.1074/jbc.M305387200; MEDLINE=22841094; PubMed=12836663; DOI=10.1074/jbc.M305387200; Shingai T., Ikeda W., Kakunaga S., Morimoto K., Takekuni K., Itoh S., Satoh K., Takeuchi M., Imai T., Monden M., Takai Y.; "Implications of nectin-like molecule-2/IGSF4/RA175/Sg1GSF/TSLC1/SynCAM1 in cell-cell adhesion and transmembrane protein localization in epithelial cells."; J. Biol. Chem. 278:35421-35427(2003).
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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R GO; GO:0016021; C:integral to membrane; TAS.

R GO; GO:0016021; C:integral to membrane; TAS.

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R GO; GO:0001515; P:cell adhesion; IDA.

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R GO; GO:000715; P:cell adhesion; IDA.

R GO; GO:0007116; P:synappcgenesis; IDA.

R InterPro; IPR007110; Ig-like.

R InterPro; IRR003589; Neurexin-like.

R SMART; SM00294; 4.1m; 1.

R SMART; SM00408; IGC2; 1.

R PROSITE; PSS6035; IGC2; 1.

R PROSITE; PSS6035; IGLIKE; 3.
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 01-0cr-2003 (TrEMBLrel. 25, Created)
01-0cr-2003 (TrEMBLrel. 25, Last sequence update)
25-0cr-2004 (TrEMBLrel. 28, Last annotation update)
Nectin-like molecule 2 (RA175 isoform d).
 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTT 355
 301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTT 334
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 Submitted (JUL-2004) to the BME
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EMBL; AB183399; BAD30018.1; -.
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Biederer T., Sara Y., Mozhayeva M., Atasoy D., Liu K., Kavalali B.T.,
 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 "SynCAM, a Synaptic Adhesion Molecule That Drives Synapse Assembly."; Science 297:1525-1531(2002).
 Gaps
in human lung cancer, is a cell adhesion molecule.";

Exp. Cell Res. 287.57-66(2003).

Res. Miles. BAB83501.2;

MGD; MGI.1889272; IgsE4a.

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Ol-JUN-2003 (TrEMBLrel. 24, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
A secretion form of Sq1GSF/TSLC1 (RA175 isoform e).
Name=Igsf4a; Synonyms=RA175, sSg1GSF/sTSLC1;
Musn musculus (Mootse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musniae; Mus.
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 MGD; MGI:1889272; EMCSOGILI; ...

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0016521; C:synaptic vesicle; IDA.

GO; GO:0005515; P:protein binding; IPI.

GO; GO:00165318; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0007416; P:synaptogenesis; IDA.

InterPro; IPR007110; Ig-like.
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STRAILS-G7BL/6; TISSUE-Spleen cell-derived;
ILO A., Koma Y., Nagano T.;
submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0007416; P:synaptogenesis; IDA.
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Interpro; IPR003599; IG_2.
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SMART; SM00409; IG; 3.
PROSITE; SR05035; IG LIKE; 3.
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
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R EMBL; A3513189; A003201.1; -
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GO; GO:000521; F:protein binding; IPI.
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R GO; GO:0007155; P:cell adhesion; IDA.
R GO; GO:000715; P:protein binding; IPI.
R GO; GO:000715; P:graptcogenesis; IDA.
R InterPro; IPR007110; Ig-like.
R InterPro; IPR003589; Neurexin-like.
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R SWART; SW00409; IGC2; II.
R PROSITE; PS50835; IGC2; II.
R PROSITE; PS50835; IGC2; II.
R SWART; SW00409; IGC2; II.
R SWART; SW00409; IGC2; II.
 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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 Fujita E., Aikawa K., Momoi T.;
Submitted (UUI-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AB183400; BAD30019.1; -.
GO, GO:0016021; C:BINTEGTA1 to membrane; TAS.
GO; GO:0048202; C:Synapse; IDA.
GO; GO:0008021; C:Synaptic veelicle; IDA.
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 SMART; SM00408; IC
PROSITE; PS50835;
SEQUENCE 336 AA;
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 EGDAFELTCEAIGKPOPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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STRAIN=C57BL/6J; TISSUE=Hippocampus;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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 STRAIN=C57BL/67; TISSUE-Hippocampus; MEDLINE=99279253; PLDMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; Hijashizaki Y.; Mayashizaki Y.; Mayashizaki Y.; Meliciency full-length cDNA cloning."; Meth. Enzymol. 303:19-44(1999).
 ol-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus adult male 15, Last annotation update)
Hus musculus adult male hippocampus cDNA, RIKEN full-length enriched library, clone:2900073G06 product:immunoglobulin superfamily, member 4, full insert sequence.
 Gaps
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
 "Functional annotation of a full-length mouse cDNA collection.", Nature 409:685-690(2001).
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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 336
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01-JUN-2001 (
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STRAIN=C57BL/6J; TISSUE=Hippocampus; MEDLLHB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; MEDLHB=20499374; PubMed=11042159; DOI=10.1101/gr.145100; Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M., Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
 AAPPGLRIRLLILLISAAALIPTGDGQULFTKDVTVIEGEVATISCQVNKSDDSVIQLIN
 Degration Tissus-Hippocampus;

Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,

Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,

Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,

Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshido M.,

Muramatsu M., Hayashizaki Y.;

Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii K., Aizawa K., Nagaoka S., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riki Nincegrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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MGD; MG1:1889272; Igsf4a.

MGD; MG1:1889272; Igsf4a.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:00045202; C:synaptic vesicle; IDA.

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GO; GO:000515; F:protein binding; IPI.

GO; GO:00155; F:cell adhesion; IDA.

GO; GO:0007155; P:cell adhesion; IDA.

InterPro; IPR00710; Ig-like.

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; IG LIKE; 3.
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100.0%; Pred. No. 3.6e-293;
ive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 313; Conservative
 Pfam; PF00047; ig;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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 202 YIVISQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQV
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Last annotation update)
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 Proc. Natl. Acad.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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 MGD; MGI:1889272; 19844a.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:004520; C:synappe; IDA.

GO; GO:00515; E:protein binding; IPI.

GO; GO:001515; P:protein binding; IPI.

GO; GO:001515; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0007155; P:call adhesion; IDA.

GO; GO:0007155; P:call adhesion; IDA.

InterPro; IPR007110; J=1ike.

InterPro; IPR003589; Ig c2.
 69.5%; Score 294; DB 2; Length 295; 100.0%; Pred. No. 7.1e-275; ive 0; Mismatches 0; Indels
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Zhou Y., Du G., Chen J., Yuan J., Qiang B.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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 VGKAHSDYMLYVY 313
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 Matches
 RESULT 8
Q9Z2H8
 RESULT 9
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94 DSRRQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 34 SAAALIPITGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 94 DSRFQLIANFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQ 152
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQ 134
 SECUENCE FROM N.A.
MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8;
Fujita E., Soyama A., Momoi T.,
Fujita E., Soyama A., Momoi T.,
Fujita E., Soyama A., Homos ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule.";
Exp. Cell Res. 287:57-66(2003).
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
 ó
 Query Match 28.1%; Score 119; DB 2; Length 442; Best Local Similarity 100.0%; Pred. No. 8.9e-106; Matches 119; Conservative 0; Mismatches 0; Indels
 SEQUENCE FROM N.A.

Zhou Y., Du G., Chen J., Yuan J., Qiang B.;

Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AF132811, AAF69029.1;

INTERPYO; IRR007110; Ig-1ike.

INTERPYO; IRR003598; Ig_C2.

INTERPYO; IRR003598; Neurexin-like.

PEam, PF00047; ig; 2.

SMART; SM00491; 4.1m; 1.
 PROSITE; PS50835; IG_LIKE; 3.
SEQUENCE 442 AA; 48537 MW; 68183E3238735062 CRC64;
 Created)
Last sequence update)
Last annotation update)
 Last sequence update)
Last annotation update)
 278 AA
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
 PRT;
 Adhesion protein RA175N.
Name=Igsfa; Synonyms=ra175n;
Mus musculus (Mouse).
 01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17, 01-OCT-2003 (TrEMBLrel. 25,
 PRELIMINARY;
 PRELIMINARY;
 Nectin-like protein 2.
Name=NECL2;
 Homo sapiens (Human)
 01-JUN-2001
01-JUN-2001
 090YL3
 Q9BY67
 RESULT 12
Q9BY67
 RESULT 13
Q9QYL3
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGQNLPTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 0; Gaps
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
 SEQUENCE FROM N.A.

JISSUB-Whole embryo;

Ota T., Nishikawa T., Suzuki Y., Kawai-Hio Y., Hayashi K., Ishii
Saito K., Yamanoto J., Wakamatsu A., Nagai T., Nakamura Y.,
Nagahari K., Sugano S., Isogai T.;
Nagahari K., Sugano S., Isogai T.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AKO75502; BAC1167.1;
Genew; HGNC:5951; IGSF4
 ö
 35.5%; Score 150; DB 2; Length 443; 100.0%; Pred. No. 1.1e-135; ive 0; Mismatches 0; Indels
 Score 150; DB 2; Length 333;
Pred. No. 8.3e-136;
 0; Indels
 1to A., Koma, Y., Nagano T.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AB094146; BAC66178.1; -.
InterPro; IPR001310; Ig-like.
InterPro; IPR0013598; Ig_c2.
Pfam; PR00047; ig; 2.
Pfam; PR00408; ig; 2.
PR051TE; PS0035; IGC2; 1.
PROSITE; PS0035; IGC2; 1.
SEQUENCE 333 AA; 36915 MW; D7C1102F46D08492 CRC64;
 SMART; SM00294; 4.1m; 1.
SMART; SM0408; IGc2; 1.
PROSITE; PS50835; IG LIKE; 3.
SEQUENCE 443 AA, 48648 MW; 046B43AA156F6F64 CRC64;
01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUAR-2004 (TrEMBLrel. 26, Last annotation update)
Secretory isoform of TSLC-1.
Name=sTSLC-1;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 443 AA
 100.0%; Pred. nc.
 Created)
 PRT;
 Interpro; IPR007110; Ig-like.
Interpro; IPR003598; Ig-c2.
Interpro; IPR003585; Neurexin-like.
 35.5%;
 01-OCT-2002 (TrEMBLrel, 22,
 Best Local Similarity 100.
Matches 150; Conservative
 Matches 150; Conservative
 PRELIMINARY;
 Pfam, PF00047; 19, 2.
 Homo sapiens (Human)
 Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;
 TISSUE=Lung;
 136
 Query Match
 Query Match
 Q8N2F4
 RESULT 11
Q8N2F4
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130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 1 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 60
 1 MIDIQKDTAVEGEEIEVNCTAWASKPATTIRWFKGNKELKGKKSEVEEWSDMYTVTSQLML
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 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQXKPQVHIQMTYPLQGLTREGDA 115
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175C.
Name=Igsf4a; Synonyms=ra175C;
Mus musculus (Mouse).
EMARATORIS, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae;
 Eukaryota, Metaria, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
 Length 295;
 Query Match 27.2%; Score 115; DB 2; Length 29 Best Local Similarity 100.0%; Pred. No. 4.6e-102; Matches 115; Conservative 0; Mismatches 0; Indels
 PROSITE; PS50835; IG LIKE; 2.
SEQUENCE 295 AA; 32347 MW; FDD9E8145C6B971B CRC64;
 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 295 AA
 Created)
 PRT;
 PRT;
 Adhesion protein RA175A.
Name=Igsf4a; Synonyms=ra175a;
Mus musculus (Mouse).
 (TrEMBLrel. 13,
 PRELIMINARY;
 PRELIMINARY;
 01-MAY-2000
 090YL4
 090YL6
 RESULT 15
Q9QYL6
 RESULT 16
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 DECEMBER 18 FORM N.A.

MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827 (03) 00095-8;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

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Rujita E., Soyama A., Momoi T.;

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Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

Rujita E., Soyama A., Momoi T.;

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 130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 189
 9
 1 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML
 Gaps
 Gaps
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 61 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 115
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
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 MGD; MGI:1889272; Igsf4a.

GO; GO:0016021; C:integral to membrane; TAS.

GO; GO:0045202; C:synapse; IDA.

GO; GO:0005215; C:synapse; IDA.

GO; GO:0005515; P:protein binding; IPI.

GO; GO:00155; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0007155; P:calcium-independent cell-cell adhesion; IDA.

GO; GO:0007416; P:synaptogenesis; IDA.

InterPro; IPR0031585; Neurexin-like.
 27.2%; Score 115; DB 2; Length 278; 100.0%; Pred. No. 4.4e-102; ive 0; Mismatches 0; Indels
 27.2%; Score 115; DB 2; Length 289; 100.0%; Pred. No. 4.5e-102; Live 0; Mismatches 0; Indels
 Pfam; PF00047; 19; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; 1Gc2; 1.
PROSITE; PS0835; IGc. LIKE; 2.
SEQUENCE 278 AA; 30636 MW; A295F4DEA2724B04 CRC64;
 01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Adhesion protein RA175B.
Name=Igsf4a; Synonyms=ra175b;
Mus musculus (Mouse).
 289 AA
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EMBL; AB021967; BAA87917.1; -.
 01-MAY-2000 (TrEMBLrel. 13,
 Best Local Similarity 100.0
Matches 115; Conservative
 Best Local Similarity 100.
Matches 115; Conservative
 PRELIMINARY;
 SEQUENCE FROM N.A.
 NCBI_TaxID=10090;
 Query Match
 Query Match
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Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; "The Trypanosoma cruzi mucin family is transcribed from hundreds of "The Trypanosoma cruzi mucin family is transcribed from hundreds of
 MEDLINE=98225151; pubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998).

EMBL; AF036411; AAC14222.1; -. Intererpo; IPR000458; Tryp_mucin.

Pfam; PF01456; Mucin; 1.
 3.5%; Score 15; DB 2; Length 74;
100.0%; Pred. No. 4.9e-06;
tive 0; Mismatches 0; Indels
 Length 86;
 Indels
 SEQUENCE 74 AA; 7743 MW; 734CC37663E21401 CRC64;
 86 AA; 8963 MW; 7AD26B22604E36A9 CRC64;
 01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
 Last annotation update)
 Score 15; DB 2; Ler
; Pred. No. 5.6e-06;
 Last sequence update)
 3.5%; Scc...
100.0%; Pred. No. 5...
... 0; Mismatches
 74 AA.
 genes having hypervariable regions.;
J. Biol. Chem. 273:10841-10850(1998).
BEMBL; AP0364340.1;
InterPro; IPR000458; Tryp_mucin..
Pfam; PF01456; Mucin; 1.
 Created)
 PRT;
 PRT;
 Mucin-like protein (Fragment)
Name=EMUCe-4;
 Mucin-like protein (Fragment)
 321 PPTTTTTTTTT 335
 321 PPTTTTTTTTT 335
 01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-MAR-2004 (TrEMBLrel. 26,
 PPTTTTTTTTT 73
 71 PPTTTTTTTTTT 85
 Best Local Similarity 100. Matches 15; Conservative
 Conservative
 PRELIMINARY;
 PRELIMINARY;
QNNSEEKKEYF
 Query Match
Best Local Similarity
Matches 15; Conserv
 SEQUENCE FROM N.A. STRAIN=C1-Brenner;
 SEQUENCE FROM N.A.
 NCBI_TaxID=5693;
 Name=EMUCe-12;
 NON TER
SEQUENCE
 Query Match
 061023
061023;
 Q9TVF2
 RESULT 19
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 412
 1 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLML 60
 13 AVDHAVIGGVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGG 72
 MEDLINE=22683149; PubMed=12799182; DOI=10.1016/S0014-4827(03)00095-8; Pujita E., Soyama A., Momoi T.; Ruists, which is the mouse ortholog of TSLC1, a tumor suppressor gene in human lung cancer, is a cell adhesion molecule."; Exp. Cell Res. 287:57-66(2003).
 130 MIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSOLML
 353 AVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADAAIINAEGG
 Gaps
 190 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 244
 KVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDA 115
 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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 Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BX641042; CAE46024.1; -.
 MG1: JR89272; JG954a.

GO; GO:0016021; C:integral to membrane; TAS.
GO; GO:0016021; C:synapse; IDA.
GO; GO:000515; C:synapse; IDA.
GO; GO:0016319; C:synapse; IDA.
GO; GO:0016319; P:sprotein binding; IPI.
GO; GO:001515; P:call adhesion; IDA.
GO; GO:0007155; P:call adhesion; IDA.
GO; GO:0007155; P:call adhesion; IDA.
InterPro; IPR007110; Jg-like.
InterPro; IPR003585; Ig-C2.
InterPro; IPR003585; Neurexin-like.
 Score 115; DB 2; Length 306;
Pred. No. 4.7e-102;
 16.8%; Score 71; DB 2; Length 84; ilarity 100.0%; Pred. No. 4.7e-60; Conservative 0; Mismatches 0; Indels
 0; Indels
 SMART; SM00408; 16cc, ...
PROSITE; PS50835; IG LIKE; 2.
eroTFNCE 306 AA; 33522 MW; A4CE37B0F23554D5 CRC64;
 84 AA; 8986 MW; D50A20AD25854087 CRC64;
 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 Hypothetical protein DKFZp686F1789 (Fragment)
Name=DKFZp686F1789;
 84 AA
 100.0%; Pred.
 PRT;
 TISSUE=Human retina;
The German Human cDNA Consortium;
 EMBL; AB021966; BAA87916.1; -.
 27.2%;
 Matches 115; Conservative
 Pfam; PF00047; ig; 1.
SMART; SM00294; 4.1m; 1.
SMART; SM00408; IGc2; 1.
 ONNSEEKKEYF 423
 PRELIMINARY;
 Hypothetical protein.
 Homo sapiens (Human)
 Local Similarity
nes 71; Conserv
 Best Local Similarity
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NON TER
SEQUENCE
 61
 413
 Query Match
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 Q6MZK6
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01-NOV-1999 (TrEMBLrel. 12, Created)
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01-NOV-1999 (TrEMBLrel. 24, Last annotation update)
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MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
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MEDLINE=98225151; PubMed=955657; DOI=10.1074/jbc.273.18.10843;
M. Horia J.M., D'Orso I., Aalund L., Sanchez D.O., Frasch A.C.;
"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hyper-variable regions.";
J. Biol. Chem. 273:10843-10850(1998).
EMBL, AF036450; AAC14247.1;
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STRAIN=Bristol N2;
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EMBL, ALO32637; CAA21621.1;
PIR; T26880; T26880.
 Mormbase; WBGene00012831; Y43F8C.9.
Wormbep; Y43F8C.9; CE1907.
Wptochetical protein.
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Science 282:2012-2018(1998)
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 Trypanosoma cruzi.
Bukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
NCBI_TaxID=5693;
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 MEDIJINE-98255151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998).

EMBL. AR036422; AAC14223.1; -.

InterPro; IPR000458; Tryp_mucin.
 MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998).

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InterPro; IPR00458; Tryp_mucin.
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 Freitas-Junior L.H., Briones M.R., Schenkman S.,
"Two distinct groups of mucin-like genes are differentially expressed
in the developmental stages of Trypanosoma cruzi.";
Mol. Biochem. Parasitol. 93:101-114(1998).
EMBL, AF027897.2, AAC48350.1;
Interpro; IPR000458; Tryp_mucin.
Fam: PP01456; Mucin, 1.
 Trypanosoma cruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
 PubMed=14668015; DOI=10.1016/j.molbiopara.2003.09.006; Campo V., Di Noia J.M., Buscaglia C.A., Aguero F., Sanchez D.O., Frasch A.C.C.; Uliferential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of Trypanosoma cruzi.";
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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EMBL; AY298908; AAQ74639.1; -
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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"The Trypanosoma cruzi mucin family is transcribed from hundreds of
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 Di Noia J.M., Frasch A.C.C.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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J. Biol. Chem. 273:10843-10850(1998).

EMBL, AF036413, AAC14224.1; -.

InterPro; IFRO7000458; Tryp_mucin.

Pfam; PF031456; Mucin; 1.

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Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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STRAIN=CL Brener;
MEDLINE=97113006; PubMed=8943259; DOI=10.1074/jbc.271.50.32078;
Di Noia J.M., Pollevick G.D., Xavier M.T., Previato J.O.,
Mendoca-Previato L., Sanchez D.O., Frasch A.C.;
"High diversity in mucin genes and mucin molecules in Trypanosoma
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"The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).
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MEDLINE=9825151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
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 Pubmed-14666015; DOI=10.1016/j.molbiopara.2003.09.006; Pubmed-14666015; DOI=10.1016/j.molbiopara.2003.09.006; Pubmed-14666015; DOI=10.1016/j.molbiopara.2003.09.006; Prasch A.C.C.; Prasch A.C.C.; Prasch A.C.C.; Prasch A.C.C.; Poliferential accumulation of mutations localized in particular domains of the mucin genes expressed in the vertebrate host stage of
 Trypanosoma ċruzi.
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI _TaxID=5693;
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
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 MEDLINE-9711 006; PubMed-8943259; DOI=10.1074/jbc.271.50.32078; Di Noia J.M., Pollevick G.D., Xavier M.T., Previato J.O., Mendoca-Previato L., Sanchez D.O., Frasch A.C.; "High diversity in mucin genes and mucin molecules in Trypanosoma cruzi.";
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Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
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 Mol. Biochem. Parasitol. 133:81-91(2004).
EMBL; AY298908; AAQ74640.1; -.
 izi.";
Biol. Chem. 271:32078-32083(1996).
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 Freitas Junior L.H., Briones M.R., Schenkman S.,
"Two distinct groups of mucin-like genes are differentially expressed
in the developmental stages of Trypanosoma cruzi...;
Mol. Biochem. Parasitol. 93:101-114(1998).
EMBL, AF027874; AAC48352.1;
InterPro; IPRO06458; Tryp_mucin.
 Trypanosoma cruzi.
Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
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Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Trypanosoma.
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 MEDLINE=98324409; Pubmed=9662032; DOI=10.1016/S0166-6851(98)00025-5;
 MEDLINE=98225151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843; Di Noia J.M., D'Orso I., Aslund L., Sanchez D.O., Frasch A.C.; The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions."; J. Biol. Chem. 273:10843-10850(1998).

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Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
 Gloeckner G., Bichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Ghigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
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Similar to Mus musculus (Mouse). 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3000008H23 product:hypothetical Acyl-CoA dehydrogenase/Glutamic acid-rich region containing protein, full
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-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostellum discoideum (Slime mold). Histidine kinase
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116986; AAOS1856.1; -.
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 Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
NCBL_TaxID=44689;
 Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
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 Mismatches
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100.08;
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 130 PPPTTTTTTTT 144
 183 PPTTTTTTTTTT 197
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Matches 15; Conservative
 15; Conservative
 321 PPTTTTTTTTTTT
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 Nature 418:79-85(2002).
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 SEQUENCE FROM N.A.
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 STRAIN=AX4;
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 Q86AG0
 Q86A81
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 RESULT 40
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 Trypanosoma cruzi.
Bukaryota; Buglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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 Eukaryota, Euglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
 Murray P.J., Spithill T.W.; "Variants of a Leishmania surface antigen derived from a multigenic
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 3.5%; Score 15; DB 2; Length 148; 100.0%; Pred. No. 8.8e-06; ive 0; Mismatches 0; Indels
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 Trypanosoma cruzi.";

Trypanosoma cruzi.";

Mol. Biochem. Parasitol. 133:81-91(2004).

EMBL; AX298908; AA074638.1; -.

InterPro; IPR0000458; Tryp_mucin.

Pfam; PF01456; Mucin; 1.

SEQUENCE 148 AA; 15203 MW; C7F2E02CF13554E6 CRC64;
 327 AA; 34229 MW; 2571B35B6577E715 CRC64;
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Last annotation update)
 Last sequence update)
Last annotation update)
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 327 AA.
 148 AA
 0; Mismatches
 family.",
7. Biol. Chem. 266:2447-24484 [1991).
EMBL; K57135; CAA40414.1;
PIR; S20074; S20074.
InterPro; IPR0093030; Grow fac_recept.
InterPro; IPR006210; IEGF.
InterPro; IPR001611; IRR.
InterPro; IPR007090; LRR_Plant.
Pfam; PF00560; LRR_1; 3.
SMART; SM00181; EGF; 1.
 3.5%; Score 15;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
 Created)
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 PRT;
 STRAIN=V121;
MEDLINE=92105105; PubMed=1761547;
 Surface antigen P2 (Fragment)
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 Best Local Similarity
Matches 15; Conserv
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 Leishmania major.
 05-JUL-2004
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SEQUENCE
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 Q25334
Q25334;
 Q6WB00;
 Q6WB00
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 SEQUENCE
 Query Match
 Q962W6
 RESULT 44
YOOB_CAEEL
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 RESULT 43
 0962W6
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 STRAIN-Sprague-Dawley;

Xu C.S., Chang C.F., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,

Yang K.J., Zhao L.F., Ma H., Wang L., Wang S.F., Xing X.K., Shen G.M.,

Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;

Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AY387047; AAQ91017.1;

SEQUENCE 58 AA; 6466 MW; DEA36599EB327F47 CRC64;
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
NCBI_TaxID=5693;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
 Gaps
 STRAIN=C1-Brenner;
MEDLINE=98255151; PubMed=9556557; DOI=10.1074/jbc.273.18.10843;
Di Noia J.M., D'orso I., Aslund L., Sanchez D.O., Frasch A.C.;
Di Noia J.M., D'orso I., Aslund L., Sanchez D.O., Frasch A.C.;
The Trypanosoma cruzi mucin family is transcribed from hundreds of genes having hypervariable regions.";
J. Biol. Chem. 273:10843-10850(1998).
EMBL; AR036454; AAC14251.1; -.
InterPro; IPR000498; Tryp_mucin.
Pfam; PF01456; Mucin; I.
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 3.5%; Score 15; DB 2; Length 1015; 100.0%; Pred. No. 4.6e-05; ive 0; Mismatches 0; Indels
 3.3%; Score 14; DB 2; Length 58; 100.0%; Pred. No. 3.7e-05;
 0; Indels
 SEQUENCE 1015 AA; 116816 MW; 58CF6693543381A8 CRC64;
 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases. EMBL, AC115594; AAO51537.1; -. GO; GO:0016301; P:kinase activity; IEA.
 01-AUG-1998 (TrEMBLrel. 07, Created)
01-MAR-2094 (TrEMBLrel. 07, Last sequence update)
Mucin-like protein (Fragment).
 Last sequence update)
Last annotation update)
 107 AA
 100.0%; Prea. ...
 Created)
 320 PPPTTTTTTTTT 334
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
 TTTTTTTTTT 336
 rrrrrrrrrrr 47
 Conservative
 15; Conservative
 PRELIMINARY;
 PRELIMINARY;
 Rattus norvegicus (Rat)
 Query Match
Best Local Similarity
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=10116;
 Baumgart C.;
 14;
 LRRGT00061.
 552
 323
 Query Match
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 Matches
 RESULT 41
QG TUI3
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AC QG TUI
DT 05-JU
DT 05-JU
DT 05-JU
DE LRRGT
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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 "Genome sequence of the nematode C. elegans: a platform for
 DB 2; Length 107; 6.2e-05;
 3.3%; Score 14; DB 2; Length 216; 100.0%; Pred. No. 0.00011; ive 0; Mismatches 0; Indels
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Hypothetical protein EEED8.11 in chromosome II precursor.
ORFNAMMES-EEED8.11;
 Di Noia J.M., Frasch A.C.C.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, A3198551, AAK94014.1; -.
InterPro; IPROM958; Tryp_mucin.
Pfam; PF01456; Mucin; 1.
SEQUENCE 216 AA; 21815 MW; 01C85738541BB6C6 CRC64;
 investigating biology.";
Science 282:2012-2018(1998).
-!- SIMILARITY: Some, to C.elegans R13F6.2 and R13F6.8.
 107
10986 MW; 26E2947FD6EB06D2 CRC64;
 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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Mucin-like protein MUC-loc2.
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 NCBI_TaxID=6239;
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Matches
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Adams M.D.C. Celniker S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams N.D. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G. Wortman J.R., Yandell M.D. Zahang O., Chen L.X.,

RA Abril J.F., Agbayani A., An H.J. Andrews-Pfannicch C., Baldwin D.,

RA Ballew R.M. Baau A., Baxendale J., Bayraktaroglu L., Beaaley B.M.,

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Reinert K., Remington K.A., Mixon K., Musskern D.R., Pacled J.M.,

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RA Yeh R., Zhong F.N., Zhong W., Zhon W., Zhon G., Zheng L.,

RA Sheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Zhu S., Zhu S., Zhu X., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S., Zhu S
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 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neopera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 Hypothetical protein EEED8.11.
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Last annotation update)
 341 AA.
 Potential
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EMBL; U23484; AAC46771.1; -.
PIR; T15922; T15922.
WormBase; WBGene00017139; EEED8.11.
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InterPro; IPR001304; Lectin_C.
SWART; SM00034; CLECT; 1.
Hypothetical protein; Signal.
 64 92 P
 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2004 (TrEMBLrel. 26,
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 14; Conservative
 PRELIMINARY;
 304
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 CG31439-PA.
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MEDLINE=22445070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise B., Mheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
The transposable elements of the Drosophila melanogaster euchromatin:
 SEQUENCE FROM N.A.

MEDLINE=22426065; PubMed=12537568;

MEDLINE=22426065; PubMed=12537568;

Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,

Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

Pater D.M., Park P.E., Wan K., Stapleron M., Sutton G.G., Venter C.,

Weinstrock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

"Finishing a whole-genome shotgun: Release 3 of the Drosophila
 Gaps
 MEDLINE-22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Kusso S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 Annotation of the Drosophila melanogaster euchromatic genome: a
 ó
 3.3%; Score 14; DB 2; Length 341;
100.0%; Pred. No. 0.00017;
ive 0; Mismatches 0; Indels
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GO, GO:0005576; C:extracellular; IEA.

GO; GO:0006061; F:chitin binding; IEA.

GO; GO:0006001; F:chitin metabolism; IEA.

GO; GO:0006020; P:chitin bind PerA.

InterPro; IPR002125; Chitin bind PerA.

InterPro; IPR002125; GMP/cyt_deam.

Ffam; PP01607; CEM 14; 1.

FRAM; PR01607; CEM 14; 1.

FRAM; PS01607; CHIT_BIND_II; 1.

PROSITE; PS09040; CHIT_BIND_II; 1.

PROSITE; PS00903; CYT_DCMP_DEAMINASES; UNKNOWN 1.

SEQUENCE 341 AA; 38627 MW, A935A06377895A15 CRC64;
 FlyBase;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
 01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
 350
 170 Priririririri 183
 EMBL; AE003751; AAN14054.1;
 Conservative
 PRELIMINARY;
 Local Similarity
tes 14; Conserv
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 Lewis S.E.;
 322 P
 Query Match
 FlyBase;
 Q7Q1R0
Q7Q1R0;
 4445
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Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Biking T., Engels R., Mang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nielsen M., Washburne M., Schler C., Jankiev J.A., Braun E.L., Zelter A., Schulte U., Schle G., Jedg G., Mewes W., Staben C., Marcotte E., Greenberg D., Ramal M., Kamwysselis M., Mauceli B., Bielke C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSoura C.C., Glass L., Orbech M.J., Berglund J., Voelker R., Arden C., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Arden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B., Wille G., Conne, Sequence of the Filamentous Fungus Neurospora crassa.";
 MEDLINE-22092622; PubMed-12097910; DOI-10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Plarzer M., Rosenthal A., Noegel A.A. "Sequence and analygis of chromosome 2 of Dictyostelium discoideum.";
 -1- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
 Neurospora crassa.
Eukaryota, Fungi, Ascomycota, Pezizomycotina, Sordariomycetes,
Sordariomycetidae, Sordariales, Sordariaceae, Neurospora.
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostellium discoideum (Slime mold). Histidine
 3.3%; Score 14; DB 2; Length 364;
100.0%; Pred. No. 0.00018;
iive 0; Mismatches 0; Indels
 Baumgart C.; Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 Hypothetical protein.
SEQUENCE 364 AA; 40946 MW; ECIDF588FE543738 CRC64;
 Dictyostelium discoideum (Slime mold).
Bukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 365 AA.
 EMBL; AC116957; AAOS2509.1; -.
GO; GO:0016301; F:Kinase activity; IEA.
 PRT;
 EMBL; AABX01000420; EAA29686.1; ...
InterPro; IPR008547; DUF829.
Pfam; PF05705; DUF829; 1.
 322 PITITITITITI 335
 Conservative
 PRELIMINARY;
 Nature 418:79-85(2002).
 Hypothetical protein.
 preliminary data
 Local Similarity
les 14; Conserv
 [1]
SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=5141;
 STRAIN=OR74A;
 STRAIN=AX4;
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
 Anopheles gambiae str. PEST.
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterrygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
 Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
 Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 Score 14; DB 2; Length 350;
Pred. No. 0.00017;
 Score 14; DB 2; Length 356;
Pred. No. 0.00017;
 0; Indels
 0; Indels
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356 356 386 MW; CS1B095A700DEC22 CRC64;
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 Created)
Last sequence update)
 3.3%; Scor.
100.0%; Pred. No. vo...
0; Mismatches
 AgCP8129 (Fragment).
Name-agCG53199; ORFNames=ENSANGG0000007781;
Anopheles gambiae str. PEST.
 AgCP9900 (Fragment).
Name=agCG52059; ORFNames=ENSANGG0000015451;
 356 AA.
 364 AA
 / Match 3.3%; Score 14; DB Local Similarity 100.0%; Pred. No. 0.0 nes 14; Conservative 0; Mismatches
 GO; GO:0016020; C:membrane; IEA.
InterPro; IPR002000; Lamp.
PRINTS; PR00336; LYSASSOCTDMP.
PR0031TE; PS00310; LAMP_1; UNKNOWN_1.
 01-MAR-2004 (TrEMBLrel. 26, Created)
 PRT;
 PRT;
 preliminary data.
EMBL; AAAB01008986; EAA00798.1; -.
 AAAB01008980; EAA14126.1;
 Q7S2P4;
01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 100.0
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 STRAIN=PEST
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RESULT 48 Q7S2P4 ID Q7S2P AC Q7S2P DT 01-MAI

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Gaps

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SEQUENCE FROM N.A.
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1A1C_DIACA
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 Gaps
 Name=agCG50324; ORFNames=ENSANGG0000010153;
Anophales gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
 Gaps
 UCCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last amnotation update)
Probable WRKY transcription factor 33 (WRKY DNA-binding protein 33).
Name=WRKX33; OrderedLocusNames=At2g38470; ORFNames=T19C21.4;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 Anopheles Genome Sequencing Consortium,
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Belongs to peptidase family S1.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
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 Length 365;
 3.3%; Score 14; DB 2; Length 445; 100.0%; Pred. No. 0.00021; ive 0; Mismatches 0; Indels
 0; Indels
 preliminary data.

EMBL; AAAB01008905; EAA09700.1; -.

HSSP; PO8709; LIBU.

GO; GO:0008233; F:opptidase activity; IEA.

GO; GO:0004295; F:crypsin activity; IEA.

GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

InterPro; IPR001254; Peptidase_S1.

InterPro; IPR001254; Peptidase_S1A.

InterPro; IPR001314; Peptidase_S1A.

InterPro; IPR0010314; Peptidase_S1A.
365 AA; 39409 MW; 132DEB0383959196 CRC64;
 445 AA; 48897 MW; 48A34474F5414364 CRC64;
 Last sequence update)
Last annotation update)
 Query Match
3.3%; Score 14; DB 2; Le
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 0;
 512 AA.
 PRINTS; PR00722; CHYMOTRYPSIN.
PROSITE; PS50240; TRYPSIN_DOM; 1.
PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
 Hydrolase; Protease; Serine protease.
 Created)
 PRT;
 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
 322 PTTTTTTTTTT 335
 266 Pririririririr 279
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 Local Similarity 100.
ses 14; Conservative
 Pfam; PF00089; Trypsin; 1
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 SEQUENCE FROM N.A.
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SEQUENCE
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 ö
 -!- FUNCTION: Transcription factor. Interacts specifically with the W box (5'-(T)TGAC(C/T)-3'), a frequently occurring elicitor-responsive cis-acting element (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear (Probable).
-!- SIMILARITY: Belongs to the WRKY group I family.
-!- SIMILARITY: Contains 2 WRKY domains.
 STRAIN=Cv. Columbia;
MEDLINE=20083487; bubMed=10617197; DOI=10.1038/45471;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 Gaps
 01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 24, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase (EC 4.1.14) (ACC synthase) (S-adenosyl-L-methionine methylthioadenosine-1yase).
Mame-ACS2; Synonyms-CARAC;
Dianthus caryophyllus (Carnation) (Clove pink).
Eukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; caryophyllaceae; Dianthus.
 InterPro; IPR003657; WRKY.
Pfam; PF03106; WRKY; 2.
PROSITE; PS50811; WRKY; 2.
DNA-binding; Nuclear protein; Repeat; Transcription regulation.
DOMAIN 123 Thr-rich.
DNA_BIND 171 235 WRKY 1.
DNA_BIND 349 414 WRKY 2.
 'Sequence and analysis of chromosome 2 of the plant Arabidopsis
 ö
 3.3%; Score 14; DB 1; Length 512;
100.0%; Pred. No. 0.00024;
 0; Indels
 "Arabidopsis thaliana transcription factor WRKY33.";
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
 512 AA; 56457 MW; 8F19CBE41BC18662 CRC64;
 517 AA.
 100.0%; Preu. ...
 Asn-rich
STRAIN=cv. Columbia; TISSUE=Flower;
Lippok B., Somssich I.E.;
 PRT;
 EMBL; AF509499; AAM34736.1; -.
 322 PITITITITIT 335
 122 PTTTTTTTTTT 135
 Nature 402:761-768(1999).
 Local Similarity 100.
Les 14; Conservative
 STANDARD;
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Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 Best Local Similarity 100.0
Matches 14; Conservative
 OrderedLocusNames=PF1233;
 PRELIMINARY;
 PRELIMINARY;
 Cryptosporidium parvum.
 518 AA;
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=2261;
 SEQUENCE
 Query Match
 08U1H5
 Q7YYY0
 Lyase.
 RESULT 54
Q7YYY0
 RESULT 55
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 Submitted (DEC-1992) to the EMBL/GenBank/DDBJ databases.

EMBL; Z18952; CAA7947.1; -.

EMBL; S14442; S31442.

HSSP; P18445; IAX.

GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.

GO; GO:0016829; F:1yase activity; IEA.
 Park K.Y., Drory A., Woodson W.R.;
"Molecular cloning of an 1-aminocyclopropane-1-carboxylate synthase from senescing carnation flower petals.";
Plant Mol. Biol. 18:37-38(1992).
-!- FUNCTION: Catalyzes the formation of 1-aminocyclopropane-1-carboxylate, a direct precursor of ethylene in higher plants.
-!- CATALYTIC ACTIVITY: S-adenosyl-L-methionine = 1-aminocyclopropane-1-carboxylate + methylthioadenosine.
-!- COFACTOR: Pyridoxal phosphate.
 Gaps
 -!- SIMILARITY: Belongs to the class-I pyridoxal-phosphate-dependent
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 02, Last annotation update)
1-oCT-2003 (TrEMBLrel. 25, Last annotation update)
1-aninocyclopropane 1-carboxylate synthase (EC 4.4.1.14).
Dianthus caryophyllus (Carnation) (Clove pink).
Sukaryota, Viridiplantea; Streptophyra; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllaceae; Dianthus.
 Pyridoxal phosphate (By similarity)
 PROSITE; PS00105; AA TRANSFER CLASS 1; 1.
Ethylene biosynthesië; Fruit Tipening; Lyase; Multigene family;
 ö
 PATHWAY: Bthylene biosynthesis; first (rate-limiting) step.
 3.3%; Score 14; DB 1; Length 517;
100.0%; Pred. No. 0.00024;
 0; Indels
 Poly-Thr.
C31BA10732E940AE CRC64;
 518 AA.
 100.0%; Prec. ...
 or send an email to license@isb-sib.ch)
 HSSP; P18485; 11AX.
InterPro; IPR001176; ACC_synthase.
InterPro; IPR004839; AminOtrans_I/II.
InterPro; IPR004839; NHtransf 1_BS.
Pfam; PF00155; AminOtran 1_2; 1.
 PRT;
 MEDLINE=92119258; PubMed=1731995;
 453 470 P
 PRINTS; PR00753; ACCSYNTHASE
 aminotransferase family.
 EMBL; M66619; AAA33275.1; -.
 323 TTTTTTTTTT 336
 458 TTTTTTTTTT 471
 14; Conservative
 PRELIMINARY;
 SUBUNIT: Homodimer.
 PIR; S19252; S19252.
 Pyridoxal phosphate
 Local Similarity
 SEQUENCE FROM N.A.
 SEQUENCE FROM N.A.
 NCBI_TaxID=3570;
 TISSUE=Petal;
 Michael M.Z.
 SEQUENCE
 Query Match
 BINDING
 DOMAIN
 043753
 Matches
 RESULT 53
1043753
AC 044375
AC 044375
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Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
 Bankier A.T., Spriggs H.F., Fartmann B., Konfortov B.A., Madera M., Vogel C., Teichmann S.A., Ivens A., Dear P.H.; "Integrated mapping, chromosomal sequencing and sequence analysis of Genome Res. 0:0-0(2003).
 Gaps
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 STRAIN=Vol / DSM 3638 / ATCC 43587 / JCM 8422;
Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
"The complete sequence of the Pyrococcus furiosus genome.";
 3.3%; Score 14; DB.2; Length 667;
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tive 0; Mismatches 0; Indels
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ORFNames=1MB.826;
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MEDIJINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185; RA Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Andams M.D., Celniker S.E., Richards S., Abburner M., Henderson S.N., Sutton G.G., Wortman J.R., Richards S., Abburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Blazej R.G., Champe M., Ffeiffer B.D., Man J. A., Baxer E.G., Hell G., Nelson C.R., Gabbr Gl.L., Abril J.F., Apdayani A., An H.J., Andrews-Pfannkoch C., Baldwin D., Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M., Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Besaley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhanderin D., Bolshakov S., Abrit S., Delcher A., Deng Z., Mays A.D., Delcher P., Cawley S., Dulke C., Davenport L.B., Davies P., Cherry J.M., Cawley S., Dallwe C., Davenport L.B., Davies P., Dodos N., Delcher A., Deng Z., Mays A.D., Dev. J., Platser R., Dodos N., Delcher A., Deng Z., Mays A.D., Dev. J., Platser R., Dodos N., Delcher A., Deng Z., Mays A.D., Dev. J., Platser R., Gordell J.H., Gu Z., Guban P., Harris M., J., Harvey D., Heiman T.J., Hernandez J.R., Houck J., RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Rolly D., Lai Z., Liang Y., Lin X., Mattei B.E., Kodire G.D., Krafte S., Kodire C.D., Krafte C., Kravite S., Kodire C.D., Krafte C., Kravite S., Morris J., Moshon D.L., Mount S.M., Moy M., Milshina N.V., Morshen D.R., Morshell D.R., Nelson D.R., Malazolo M., Pittman G.S., Pan S., Pollard J., Mount S.M., Moy M., Wilshin N.V., Nelson M., Stupski M. P., Shaft T., Spier E., Spradling A.C., Stapleton M., Stupski M. P., Shaft T., Shier R., Shore R., Wang S., Yao Q., Yao J., Yang S., Yao Q., Xhon W. Hang S., Yao Q., Xhon W. Wang S., Wang S., Yao Q., Yang S., Yao Q., Xhon W. Wang S., Wang S., Wang S., Wang S., Yao Q., Yang S., Yang S., Yang S., Yao Wang S., Wang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yang S., Yan
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 GO; GO:0016787; F.hydrolase activity; IEA.
GO; GO:0004553; F.hydrolase activity, hydrolyzing O-glycosyl . .; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
GO; GO:0008152; P:metabolism; IEA.
PFam; PF00553; CBM 2; 1.
SMART; SM0657; CBD_II; 1.
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 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilla.
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 MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.B., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Myers E.W., Rubin G.M., Venter J.C.; sequence of Drosophila melanogaster.";
 Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Mheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., "The transposable elements of the Drosophila melanogaster euchromatin:
 Gaps
 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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 'Annotation of the Drosophila melanogaster euchromatic genome:
 3.3%; Score 14; DB 2; Length 746;
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 to the EMBL/GenBank/DDBJ databases.
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EMBL, AE003835; AAFS9007.11; -.
FlyBase; FBGN033331; CGB181.
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 melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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MEDLINE=22426070; PubMed=12537573;
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01-MAR-2004 (TrEMBLrel. 26,
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 MEDLINE=98139494; PubMed=9472083; Shammat I.M. Gonzales C., Welker D.L.; Dammat I.M. Gonzales C., Welker D.L.; Diatryostellium discoideum nuclear plasmid Ddp6 is a new member of the Ddp2 plasmid family."; Curr. Genet. 33:77-82(1998).
 MEDLINE-99189343; PubMed=10087212; DOI=10.1006/plas.1998.1385;
Gonzales C.M., Spencer T.D., Pendley S.S., Welker D.L.;
"Dgp1 and Dfp1 are closely related plasmids in the Dictyostelium Ddp2
 MEDLINE=92390516;
Yin Y., Welker D.L.;
"Dictyostelium giganteum plasmid Dgpl is a member of the Ddp2 plasmid
 Gaps
 suppressors.";
Proc. Natl. Acad. Sci. U.S.A. 93:15260-15265(1996).

EMBL, UG0169; AAB03507.1;
R HSSP, Q13153; IP3M.

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R GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.

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MEDLINE=97140317; PubMed=8986798; DOI=10.1073/pnas.93.26.15260; Shaulsky G., Escalante R., Loomis W.F.; "Developmental signal transduction pathways uncovered by genetic
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 Length 860;
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 STRAIN=WS380B;
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Slade M.B., Chang A.C.M., Williams K.L.;
The sequence and organisation of Ddp2, a high copy number plasmid of Dictyostelium discoideum.";
Plasmid 24:195-207(1990).
 Gonzales C.M., Spencer T.D., Pendley S.S., Welker D.L.; "Dgp1 and Dfp1 are closely related plasmids in the Dictyostelium Ddp2 plasmid family.";
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tive 0; Mismatches 0;
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InterPro; IPR007778; Dict_REP.
Pfam; PF05086; Dicty_REP; I.
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EMBL; AF076279; AAC33156.1; -.

InterPro; IRR007778; Dict REP.

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01-MR-2004 (TrEWBLrel. 26, Last annotation update)
Similar to Arabidopsis thaliana (Mouse-ear cress). Hypothetical 79.2
 STRAIN=WS380B;
MEDLINE=90287164; PubMed=2192261;
Leiting B., Lindner I.J., Noegle A.A.;
"The extrachromosomal replication of Dictyostelium plasmid Ddp2
"The extrachromosomal replication of Dictyostelium plasmid Ddp2
requires a cis-acting element and a plasmid-encoded trans-acting
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 Chang A.C.M., Slade M.B., Williams K.L.; "Identification of the eukaryote Dictyostelium discoideum nuclear plasmid Ddp2.";
 3.3%; Score 14; DB 2; Length 887;
100.0%; Pred. No. 0.00038;
tive 0; Mismatches 0; Indels
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 Discription 24:08-217(1990).

EMBL; X51478; CAA35843.1; -.

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InterPro; IFR007778; Dict REP.

Ffam; PF05086; Dicty REP; I.

SEQUENCE 887 AA; 100809 MW; 478B68C4E500F470 CRC64;
 MOI. Cell. Biol. 10:3727-3736(1990).

EMBL, M55298; AAA3191.1; -.

PIR; A35679; A35679.

DictyBase; DDB00001833; Ddp2-rep.

InterPro; IPR007778; Dict REP.

Pfam; PF05086; Dicty REP; I.

SEQUENCE 889 AA; 101055 WW; 0C96F120DE30F544 CRC64;
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Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
 Dictyostellum discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBI_TaxID=44689;
 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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086A69
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
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MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
Glocckner G., Eichinger L., Szafranski K., Pachebat J., Dear P.,
Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K.,
Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
Nature 418:79-85(2002).
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ive 0; Mismatches 0; Indels
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 Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 SMART; SM0382; AAA; 1.
ATP-binding; Hypothetical protein.
SEQUENCE 937 AA; 106088 MW; 0AFD6F0123CE2967 CRC64;
 895 AA; 104485 MW; 94895D6A284E3384 CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Dictyostellum discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyostellida, Dictyostellum.
 937 AA.
 InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR000862; RFC.
Pfam; PP00004; AAA; 1.
 Submitted (MAK-2007)

EMBL; ACI16986; AAC1507.1; -.

Dictybase; DDB0168226; JC2V2.0.

Interpro; IPR006768; CWfJ.C.I.

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 RA Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Galle R.F.,
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RA Batton R.C., Rogers Y.H., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Abril J.F., Agbayani A., Am H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendal J., Bayratharoglu L., Basaley E.M.,
RA Beson K.Y. Banos P.V., Burman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottler P.,
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RA Dodson K., Evangelista C.C., Ferraz C., Ferriera S., Rieischmann W.,
RA Harris N.J., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
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Alasko M., Gong F., Gorrell J.H., Gu Z., Gelbart W., Gabrielian A.B.,
Alain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Alain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
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RA Merklivo G. Milshina N.V., Mobarry C., Morris S., Kolire C., Marshina N., Rabaner R., Sunner S.M., Moy M., Murphy B., Murphy L., Warny D.M., Nelson D.L.,
RA Reinert K., Remington K.A., Nixon K., Musskern D.R., Parl W., Rabasarband D.R., Weiner S., Wun D., Yang S., Yang
 MEDLINE=22436065; PubMed=12537568; MEDLINE=22436065; PubMed=12537568; Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A., Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a Whole-genome shotum: Release 3 of the Drosophila melanogaster euchromatic genome sequence.", George Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 01-MAR.2003 (TrEMBLrel. 23, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
CG32972-PB (RE16941p).
Mame-BG:BC01523.2.; ORFNames=CG32972;
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Mooptera; Endopterygota; Diptera; Exachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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 Science 287:2185-2195(2000).
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323
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MEDLINE=224260/70; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise B., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to Dictyostelium discoideum (Slime mold). Nucleotide exchange
 MEDLINE=22426069; PubMed=12537572;
Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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 STRAIN-Berkeley; Stapleton D., Hong L., Agbayani A., Carlson J., Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., Champe M., Choralez M., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 ;
 Lewis S.E.; ^{\prime}_{\rm A} . The Drosophila melanogaster euchromatic genome:
 Length 1166;
 1166 AA; 128893 MW; DD25F816E75F7CF9 CRC64;
 FlyBase;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases EMBL; AE003642; AAN10874.1; -- EMBL; BT010014; AAQ22483.1; --
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Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium
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 Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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Pfam; PF02469; Fasciclin; Z.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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 ORFNames=CG32972;
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 Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85(2002).
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 SEQUENCE FROM N.A.
MEDILINE=99066915; PubMed=8851610; DOI=10.1016/S0166-6851(98)00119-4;
Barnes D.A., Bonnin A., Huang J.K., Gousset L., Wu J., Gut J.,
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"A novel multi-domain mucin-like glycoprotein of Cryptosporidium
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 Score 14; DB 2; Length 1832;
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
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 parvum mediates invasion.";
Mol. Biochem. Parasitol. 96:93-110(1998).
EMBL, PAF068065; AAC98153.1; -.
PIR; 731113; T31113.
SEQUENCE 1832 AA; 192653 MW; 590E6ACB16BBE0D2 CRC64;
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 Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases
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01-MAY-1999 (TrEMBLrel. 10,
01-JUN-2003 (TrEMBLrel. 24,
 05-JUL-2004 (TrEMBLrel. 27, 05-JUL-2004 (TrEMBLrel. 27,
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 Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R., Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., Ashburner M., Celniker S.E., F. The transposable elements of the Drosophila melanogaster euchromatin:
 MEDLINE=22436065; PubMed=12537568;
MEDLINE=22436065; PubMed=12537568;
MEDLINE=22436065; PubMed=12537568;
MEDLINE=22436065; PubMed=12537568;
MEDLINE=22436065; PubMed=12537568;
Medline=1 S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
George R.A., Hoskins R.A., Laverty T., Michards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Man K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.

NCBL TaxID=7227;
 melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 Genome Biol. 3: RESEARCH0084-RESEARCH0084 (2002).
 MEDLINE=22426070; PubMed=12537573;
 a genomics perspective."
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Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
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Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
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Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A.,
Sethi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
Ziezan L.L., Rubin G.M.;
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 MEDLINE=99403001; PubMed=10471707; Ashburner M. Misra S. Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw R. Celniker S., Rubin G.M.;

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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.B., Smith C.D., Tupy J.L., Whitfied B.J., Bayraktaroglu L., Berman B.P. Bettencourt B.R., Celniker S.B., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 "Annotation of the Drosophila melanogaster euchromatic genome: a
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 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ebhydroidea, Drosophilidae, Drosophila.
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1853 AA; 201677 MW; 518684872828D53F CRC64;
 Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
 Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
 PRT; 1893 AA
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A. Nsequence and analysis of chromosome 2 of Dictyostelium discoideum." Nature 418:79-85(2002).
 -1- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family. EMBL; AC116957; AAO52538.1; -.
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 GO, GO:0004840; F:ubiquitin conjugating enzyme activity; IEA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR002083; MATH.
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Pfam; PF00917; MATH; 4.
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SMART; SM0061; UBCc; 1.
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 Length 2208;
FlyBase; FBGN0028905; CG32972.

GO; GO:0007155; P:cell adhesion; IEA.
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SEQUENCE 1893 AA; 206483 MW; 2C3152610B858A4D CRC64;
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Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
 2208 AA; 250169 MW; CF247BA9B0E2205C CRC64;
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2004 (TrEMBLrel. 26, Last annotation update)
101-MR-2004 (TrEMBLrel. 26, Last annotation update)
11-JUN-2004 (TrEMBLrel. 26, Last annotation update)
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NCBI_TaxID=10116;
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STRAIN-BN/SakHsdMcW;

A Culp D.J. Latchney L.R., Fallon M.A., Denny P.C.,
Couwenhoven R.I., Chuang S.;

I "The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
Relationship to SMGC.";

Physiol. Genomics (Online) 0:0-0(2004).

EMBL; BKO05555; DAAO5595.1; -..

InterPro; IPR006529 WGC.

R InterPro; IPR006529 WWC.out.

R InterPro; IPR001846; WWF.D.

R Pfam; PF001826; TIL; 1.

R Pfam; PF00182; WWD. 3.

R SWART; SM00215; WWD. 3.

R SWART; SM00215; WWD. 3.
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STRAIN=BN/SSNHsdMcW;
Culp D.J., Latchney L.R., Fallon M.A., Denny P.A., Denny P.C.,
Couwenhoven R.I., Chuang S.;
The Gene Encoding Mouse Muc19: cDNA, Genomic Organization and
Relationship to SMGC.";
 3.3%; Score 14; DB 2; Length 3295; 100.0%; Pred. No. 0.0012; ve 0: Mismatches 0; Indele
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25-OCT-2004 (TrEMBLrel. 28, Last amnotation update)
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Last annotation update)
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 PRT; 3550 AA.
 100.0%; Pred. w.
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EMBL, BK005556, DAA05596.1; -
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PROSITE; PS01208; VWFC 1; UNKNOWN 1.
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Name=Muc19;
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 MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847; Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tunggal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum.";
 Bukaryota, Fungi, Ascomycota, Pneumocystidomycetes; Pneumocystidaceae, Pneumocystis.
 SEQUENCE FROM N.A.
STRAINE-protocype form 1;
STRAINE-protocype form 1;
Linke M.J., Smulian A.G., Stringer J.R., Walzer P.D.;
Linke M.J., Smulian A.G., Stringer J.R., Walzer P.D.;
"Characterization of multiple unique cDNAs encoding the major surface glycoprotein of rat-derived Pneumocystis carinii.";
Parasicol. Res. 80:478-486 (1994).
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 Score 14; DB 2; Length 3550;
Pred. No. 0.0012;
0; Mismatches 0; Indels
 Length 56;
 3550 AA; 354982 MW; 108149CC5F35DBFC CRC64;
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116551; AAOS2164.1;
 56 AA; 5825 MW; AE1F4EA7718D7DF7 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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| 5.1.6<br>Compugen Ltd.                                                                                               |                                      | Search time 114.43 Seconds (without alignments) 1429.691 Million cell updates/sec | TAIINAEGGQNNSEEKKEYF 423                                                           |                                      | dues                                 |                                  | eters: 2105692                       |                                   |                                |                                                    |                                          |                                                    |                | chance to have a           | re of the result being printed,<br>l score distribution.                 | S                                | Description                      |                | Mous           | Hamis          | Nove                             | Huma                             | Abo84564 Human can<br>Aav17830 Himan PRO | Hume           | Huma           | Nove<br>Huma                     | Hume           | Hum            | Huma           | Nove<br>Hum                      | 5 Nove              |                |
| GenCore version<br>Copyright (c) 1993 - 2005                                                                         | protein search, using sw model       | June 28, 2005, 09:54:53 ; See (4                                                  | US-10-622-237-4<br>423<br>1 AAPPGLRLLLLLLLSAAAL                                    | OLIGO<br>Gapop 60.0 , Gapext 60.0    | 2105692 segs, 386760381 residues     | 0                                | of hits satisfying chosen parameters | length: 0<br>  length: 2000000000 | g: Listing first 150 summaries | a                                                  | 2: geneseqp1990s:*<br>3: geneseqp2000s:* |                                                    |                | . is the number of results | greater than or equal to the score<br>derived by analysis of the total s | SUMMARIES                        | ΟΣ                               |                | 93.6 397 8     | 35.5 364 6     | 35.5 364 8<br>35.5 370 5         | 35.5 402 4<br>35.5 414 3         | 35.5 425                                 | 35.5 440 3     | 35.5 440 6     | 35.5 440 6<br>35.5 440 6         | 35.5 440 6     | 35.5 440 6     | 35.5 440 6     | 35.5 440 6<br>35.5 440 6         | 35.5 440 6 ABU96145 | 35.5 440 6     |
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|          |          |          |          |          |              |                     |                   |              |          |              |          |              |             |              |           |          |          |          |                                         |              |             |              |               |          |              |          |              |          |             |          |              |              |          |              |            |              |             |             |              |              |              |              |              |              |              |              |                           |
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ALIGNMENTS

Lymphoid derived dendritic cell adhesion molecule; LDCAM; mouse; B7-1; B7-L1; T cell proliferation; natural killer cell; NK; tumour cell; B7-L1; T cell proliferation; control reagent; treatment; inflammation; immune system disorder; autoimmune; viral infection; infectious disease; organ transplant rejection; bone marrow; modulator; immune response. Mouse lymphoid derived dendritic cell adhesion molecule. AAY45093 standard; protein; 423 AA. (first entry) 31-MAY-2000 AAY45093; RESULT 1
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cells and displays homology to adhesion molecules, B7-1 and cytoplasmic cells and displays homology to adhesion molecules, B7-1 and cytoplasmic region of B7-L1. Mouse LDCAM is found on Mynole embryo, testes, triple negative cells murine splanic and lymph node CD8+, S49.1 and dendritic cells. LDCAM polypeptides interacts with T cell surface molecules to alter signalling and inhibits T cell proliferation, bind to themselves and B7L-1, an LDCAM binding protein and increases natural killer (NK) cell populations. It may be used to measure the biological activity and as quality control reagents of LDCAM binding proteins. LDCAM may be used for treating disorders associated with malfunctioning of immune system, inflammation, autoimmune disorders, viral infected cells, infectious diseases and for killing tumour cells. They are also useful for prevention or reducing the effect of organ and bone marrow transplant crejection and for modulating T cell immune responses. LDCAM polypeptides may also be used as carriers for delivering agents attached to T cells or cells bearing B7L-1
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 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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 ules designated LDCAM are capable of altering or modulating T
 amino acid sequence is the mouse lymphoid derived dendrtitic
 1 AAPPGLRILILILISAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
 1 AAPPGLRILILILISAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLIN
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comprising at least 10 contiguous nucleotides of any of the above-
cc ementioned nucleotide sequences, an isolated polypeptide (encoded within
an open reading frame of a Sequence selected from any of the 95
cc polynucleotide sequences as mentioned in the specification, or its
cc polynucleotide sequences as mentioned in the specification, or its
cc polynucleotide sequences as mentioned in the specification, or its
cc polynucleotide sequences as mentioned in the specification, or its
cc pulming to the above polypeptide, a hybridoma that produces the above
cc antibody and a pharmaceutical excipient, a kit for detecting the above
cc antibody and a pharmaceutical excipient, a kit for detecting cancer
cc calls (comprising the antibody cited above, methods for diagnosing cancer
cc calls (comprising the antibody cited above, methods for diagnosing cancer
cor for detecting the presence or absence of cancer cells in an
individual, a method for inhibiting growth of cancer cells in an
individual, an electronic library comprising the above
cc individual, an electronic library comprising the above
cc polynucleotide or polypeptide (or their fragments), methods of screening
cc polynucleotide or polypeptide (or their fragments), methods of a screening
cc the activity of a CA protein (CAP), methods for detecting cancer
cassociated with expression of a polypeptide in a test cell sample, a
method for treating cancers and a method for inhibiting the expression of
cd agencing preventing and treating cancer, sepecially lymphoma and
cc method for treating cancers and a method for inhibiting the expression
cd diagnosing, preventing and treating cancer, sepecially lymphoma and
cancer. The present sequence is a mouse CAP protein sequence data for this patent did not form part of the printed
cancer. The present sequence is a mouse CAP protein sequence. Note: The
sequence data for this patent did not form part of the printed
cancer. The presence sequence is a mouse cancer.

 ELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEBIEVN 120
 121 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP 180
 protein; immunosuppressant; anti-inflammatory; antiarthritic;
 AVTGNIĞTĞRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVFVDD
 1 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 ELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVN
 TTTTTTTTTIIIIIDSRAGEEGTIGAVDHAVIGGVVAVVVFAMLCLLIILGRYFARHKGT
 28 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP
 AVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDD
 EMPQHAVLSGPNLFINNLNKTDNGTYRCEASNIVGKAHSDYMLYVYDPPTTIPPPTTTTT
 Score 396; DB 8; Length 397;
 Indels
 Protein encoded by human secreted protein gene #11.
 YFTHEAKGADDAADADTAIINAEGGONNSEEKKEYF 396
 ö
 YFTHEAKGADDAADADTAIINAEGGONNSEEKKEYF
 93.6%; Sco...
100.0%; Pred. No. v,
... 0; Mismatches
 Ą
 standard; protein; 364
 (first entry)
 Matches 396; Conservative
 Query Match
Best Local Similarity
 Sequence 397 AA;
 21-NOV-2000
 88
 61
 148
 181
 241
 388
 AAB25586
 AAB25586;
 208
 268
 328
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 AAB25586
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 The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above recombinant nucleic acid or expression vector, a microarray for detecting
 240
 240
 300
 300
 360
 420
 180
 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTILTITDSRAGEEGTIGAVDHAVIG 360
 New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 TVLVPPRNLMIDIOKDTAVEGEE1EVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 GVVAVVVFAMLCLLILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK
 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI
 cancer-associated protein; cytostatic; cancer; leukaemia;
 Mouse cancer-associated protein MP16-039.1.
 English
 Malandro MS;
 ABO84563 standard; protein; 397 AA.
 disclosure; segid 419; 310pp;
 2003US-003B8B3B.
2003US-00417375.
2003US-00461862.
 15-SEP-2003; 2003US-00663431.
15-DEC-2003; 2003US-00737318.
 17-FEB-2004; 2004WO-US004730
 SAGRES DISCOVERY INC
 (first entry)
 Morris DW, Morris DW,
 WPI; 2004-652914/63.
 N-PSDB; ABD32790.
 EYF 423
 EYF 423
 WO2004074320-A2
 lymphoma; CAP
 15-APR-2003;
 Mus musculus
 14-FEB-2003;
 14-MAR-2003;
 18-NOV-2004
 02-SEP-2004
 361
 181
 301
 AB084563;
 121
 121
 181
 241
 241
 301
 361
 421
 421
 (SAGR-)
 AB084562
 RESULT
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267 240 327

hemostatic; gene therapy; cancer; inflammation; immune disorder; neurological disorder; blood clotting disorder; food additive; cytostatic; antiinflammatory; immunomodulator; neuroprotective;

preservative; human; secreted protein.

Homo sapiens.

Human novel secreted protein from cDNA HOUDJ81 #1.

(first entry)

20-NOV-2003

ADA27058;

ADA27058 standard; protein; 364 AA.

4DA27058

```
The present invention relates to 12 secreted human proteins and the nucleotide sequences encoding them. The polynucleotide sequences given in AAA80606A80623 encode the 12 secreted protein sequences given in AAA80606A80623 encode the 12 secreted proteins have various activities dependent on the tissues in which they are expressed. Examples of the cativities of the proteins include: immunosuppressant; anti-inflammatory; antiarthritic; antirhemmatic, dermaclogical; antiproliferative; antiarthritic; antirhemmatic, dermaclogical; antiproliferative; and antifungal activity. The proteins, polypeptides, agonists and antitude and conditions examples of which include: immune disorders e.g. disorders and conditions examples of which include: immune disorders e.g. Crohn's disease, rheumatoid arthritis, dermatitis, and multiple colon's disease, thenmatory disorders e.g. inflammatory bowel disease, crohn's disease, and nephritis; hyperproliferative disorders such as paraproteinaemias and purpura; cardiovascular disorders e.g. coronary atteniosclerosis and moptoratitis; canner e.g. melanoma and lymphoma. The proteins and polynucleotide sequences may also be used in wound healing and the treatment of infectious diseases. The human secreted protein gene and the treatment of infectious diseases. The human secreted protein gene
 Isolated nucleic acid molecules encoding human secreted proteins are used for the prevention, amelioration and treatment of autoimmune, inflammatory, hyperproliferative and cardiovascular disorders, cancer, wounds, and infectious diseases.
 anticancer; vulnerary; antiviral; antibacterial; antifungal; immune disorder; Addison's disease; rheumatoid arthritis; dermatitis; multiple sclerosis; inflammatory disorder; inflammatory bowel disease; Crohn's disease; nephritis; hyperproliferative disorder; cardiovascular disorder; coronary arteriosclerosis; myocarditis; cancer; melanoma; lymphoma; wound healing; human.
 antirheumatic, dermatological; antiproliferative; antiarteriosclerotic;
 χ.
 #11 and protein sequences are represented in sequences AAA80616 and AAB25586. Sequences AAA80677-A80682 represent genes related to the
 Wei
 Young PE, Kenny JJ, Moore PA,
 Claim 1; Fig 28A-B; 803pp; English.
 99WO-US025031.
 98US-0105971P.
 (HUMA-) HUMAN GENOME SCI INC.
 Ruben SM, Olsen HS,
 protein gene#11
 2000-387742/33.
 N-PSDB; AAA80616.
 Sequence 364 AA;
 WO200029435-A1
 Homo sapiens.
 27-OCT-1999;
 28-OCT-1998;
 25-MAY-2000.
 Greene JM;
 secreted
 'n
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Claim 11; Fig 28; 454pp; English.
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 93
 SAAALIPTGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 ..
0
 35.5%; Score 150; DB 3; Length 364;
 0; Indels
 6.5e-135;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 100.0%; Prec.
 Conservative
 Local Similarity
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Matches 150;

Query Match

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The invention transfer to an instance of the control of the contro
 New human secreted nucleic acid molecules and polypeptides, useful for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation, immune disorders, neurological and blood clotting
 The invention relates to an isolated nucleic molecule that is at least
 Greene JM;
 Wei Y,
 Olsen HS, Moore PA,
 Kenny JJ, O]
Crocker PR;
 27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
2000US-0CT-2000; 2001US-00835353.
 29-OCT-2001; 2001US-00984130
 2003-567103/53.
 YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
WEI Y.
GREENE J M.
 CROCKER P R
 ng PE, K
Liu D,
 RUBEN S M.
 WPI; 2003-567103/
N-PSDB; ADA27040
 US2003055231-A1.
 Young
 28-OCT-1998;
 20-MAR-2003
 Ruben SM,
 disorders.
 (RUBE/)
(LIUD/)
(CROC/)
 (/CCIN)
 KENN/)
 OLSE/)
 (MEIX/)
 GREE/)
 (MOOR/
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baving the activity). The polypeptides, nucleic acids and antibodies are useful for diagnosing a pathological condition or a susceptibility to a pathological condition, for preventing, treating, or ameliorating a medical condition, such as cancer, inflammation and other immune disorders, neurological and blood clotting disorders (many examples are given in the specification). The nucleic acids are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The polypeptides and antibodies are useful for providing immunological probes for differential identification of the rissues immunohistochemistry assays. The polypeptide, polynucleotide, agonist or antagonist may also be used as a food additive or preservative to increase or decrease storage capabilities, fat content or other intaining components. The present is a secreted protein of the
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 75
 SAAALIPTGGGONFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Greene JM;
 0; Gaps
 35.5%; Score 150; DB 6; Length 364; 100.0%; Pred. No. 6.5e-135; Live 0; Mismatches 0; Indels
 secreted protein; cancer; liver disorder; hepatitis;
 Wei Y,
 Moore PA,
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Olsen HS,
 disorder; Alzheimer's disease.
 ADE86588 standard; protein; 364 AA
 Novel human secreted protein #11.
 27-OCT-1999; 99WO-US025031.
19-APR-2000; 2000US-0198407P.
 98US-0105971P.
 18-APR-2001; 2001US-00836353
 Kenny JJ,
 29-JAN-2004 (first entry)
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 WPI; 2004-020335/02
 WEI Y. GREENE J M.
 NI J.
YOUNG P E.
KENNY J J.
OLSEN H S.
MOORE P A.
 RUBEN S M
 Young PE,
 N-PSDB; ADE86570
 Sequence 364 AA;
 US2003129685-A1
 28-OCT-1998;
 Homo sapiens
 10-JUL-2003.
 invention.
 Ruben SM:
 ADE86588;
 34
 94
 136
 96
 154
 (XOUN/)
 (WEIY/)
(GREE/)
(RUBE/)
 (KENIN/)
 neural
 (OLSE/)
 human;
 MOOR/
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 RESULT 5
 ADE86588
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prevention; immune disorder; immunodeficiency; autoimmune disorder; prevention; immune disorder; haemaclogical disorder; haemactatic disorder; thrombolytic disorder; hyperproliferative disorder; cancer; tumour; apoptotic disorder; radiovascular disorder; respiratory disorder; andiogenic disorder; neovascularisation; neurological disorder; andiogenic disorder; payetem disorder; infectious disease; gastrointestinal disorder; drug screening; tissue regeneration; chemotaxis; gene therapy; antibody therapy; drug targeting; chemotaxis; gene therapy; antibody therapy; drug targeting; chemotatic; tranquiliser; vulnerary; antiinflammatory; nephrotropic; cardiant; antiallergic; anti-HIV; antirheumatic; antiarthritic; antibactatic; immunospherseive; vasotropic; nootropic; neuroprotective; antibbacterial; dermatological; chromosome 11q23.2.
 The invention relates to an isolated nucleic acid sequence, or its atalalist variant, a fragment of the cDNA sequence, or its fragment domain, epitope or species homologue. The nucleic acid is useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g., cancer, liver disorders such as hepatitis or neural disorders such as Alzheimer's disasse. The present sequence represents the amino acid sequence of a novel human secreted protein.
 ö
 94 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 34 SAAALIPIGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 New nucleic acid molecule, useful for preparing a medicament for preventing, treating or ameliorating a medical condition e.g. cancer, liver disorders or neural disorders.
 0; Gaps
 CD-like molecule; cluster of differentiation; diagnosis;
 Length 364;
 Indels
 35.5%; Score 150; DB 8; Le
100.0%; Pred. No. 6.5e-135;
iive 0; Mismatches 0;
 Human CD-like molecule HATCZ07, SEQ ID NO:268.
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Claim 11; SEQ ID NO 39; 380pp; English
 Ź
 ADR41469 standard; protein; 370
 (HUMA-) HUMAN GENOME SCI INC.
 25-SEP-2001; 2001WO-US029838
 26-SEP-2000; 2000US-0235484P
 07-OCT-2004 (first entry)
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Birse CE
 Sequence 364 AA;
 WO200226930-A2
 Homo sapiens.
 04-APR-2002
 Rosen CA,
 16
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 136
 ADR41469;
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 Human; secreted protein, nutritional; cytokine; cell proliferation; differentiation; immune stimulating; vaccine; suppression; haematopoiesis regulation; tissue growth; activin; inhibin; chemotactic; chemokinetic; haemostatic; thrombolytic; receptor; ligand; anti-inflammatory; cadherin; tumour invasion suppressor; tumour inhibition; gene therapy.
 New polynucleotides encoding secreted human proteins, derived from adult placenta, adult retina, fetal brain, fetal.
The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 34 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Human secreted protein clone cw1000_2 protein sequence SEQ ID NO:62.
 Collins-Racie LA, Evans C;
Steininger RJ, Bowman MR;
 .;
0
 Length 402;
 Indels
 35.5%; Score 150; DB 4; Le 100.0%; Pred. No. 7.1e-135; iive 0; Mismatches 0;
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 Lavallie ER,
Agostino MJ,
 Ä.
 AAY53028 standard; protein; 414
 98US-0084564P.
98US-0087645P.
98US-0093712P.
98US-0094935P.
 98US-0095880P.
98US-0096068P.
99US-00306111.
 99WO-US009970
 (GEMY) GENETICS INST INC.
 (first entry)
 Query Match 35.5.
Best Local Similarity 100.
Matches 150; Conservative
 Treacy M, Ag
th E, Widom
 protein of the invention
 Mccoy JM,
 WPI; 2000-052937/04.
 Merberg D, Treacy
Diblasio-Smith E,
 N-PSDB; AAZ33346
 Sequence 402 AA;
 WO9957132-A1.
 07-MAY-1999;
 06-MAY-1999;
 29-FEB-2000
 07-MAY-1998
 02-JUN-1998
 10-AUG-1998
 11-NOV-1999
 22-JUL-1998
 31-JUL-1998
 Jacobs K,
Merberg D,
 94
 136
 AAY53028;
 RESULT 8
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 Novel polynucleotides and polypeptides useful for treating, preventing or ameliorating cardiovascular, renal, neurovascular, and autoimmune disorders.
 The invention relates to 167 novel human CD (cluster of differentiation) - like molecules (ADR41388-ADR41563) and to cDNAs encoding them (segid:11}-
 Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 161
 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 101
 75
 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
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 Asundi
 Length 370;
 Indels
 ъ,
 Chen
 Score 150; DB 5; Le
Pred. No. 6.6e-135;
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0
 Zhou P, Qian XB, Wang Z,
 35.5%; Scor.
100.0%; Pred. No. e...
0; Mismatches
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 191
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Human EST encoded protein SEQ ID NO: 1216.
 Claim 11; SEQ ID NO 268; 1243pp; English
 Claim 20; Page 877-878; 1275pp; English
 Z
 2000US-00491404.
2000US-00617746.
2000US-00631451.
 25-JAN-2001; 2001WO-US002687
 2000US-00663870
 AAM23691 standard; protein;
 (first entry)
 Conservative
 gene therapy; nutrition.
 Tang YT, Liu C, Zh
Cao Y, Drmanac RA,
 WPI; 2001-476164/51
N-PSDB; AAH98350.
 WPI; 2002-405050/43
 Local Similarity
 (HYSE-) HYSEQ INC.
 N-PSDB; ADR41293
 Sequence 370 AA;
 WO200154477-A2
 25-JAN-2000;
17-JUL-2000;
 Homo sapiens
 15-SEP-2000;
 03-AUG-2000;
 12-OCT-2001
 02-AUG-2001.
 150;
 AAM23691;
 42
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 102
 136
 Query Match
 162
 Matches
 AAM2369
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The present invention describes new human secreted proteins which were isolated from adult placenta, adult retina, foetal brain, foetal kidney, adult blood, adult brain, adult thyroid, adult blood, adult neural tissue, adult testes, and adult lymph node cDNA libraries. The human secreted proteins, and the polynucleotides encoding them, are predicted treating, preventing or ameliorating make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and call proliferation/differentiation activity, immune stimulating (e.g. as vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, cadherin/tumour ceptor/ligand activity, anti-inflammatory activity, cadherin/tumour incompassion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. AAX3316 to AAX3313 encode human secreted proteins, and AAX52998 to AAX5360 crepresent human secreted proteins, given in the present invention
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 Gaps
 cancer-associated protein; cytostatic; cancer; leukaemia;
 ö
 Query Match 35.5%; Score 150; DB 3; Length 414; Best Local Similarity 100.0%; Pred. No. 7.3e-135; Matches 150; Conservative 0; Mismatches 0; Indels
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Human cancer-associated protein HP16-039.1
Claim 71; Page 416-417; 492pp; English.
 Malandro MS;
 ABO84564 standard; protein; 425 AA.
 14-FEB-2003; 2003US-00367094.
14-MAR-2003; 2003US-0038B38.
15-APR-2003; 2003US-00417375.
13-JUN-2003; 2003US-00461862.
15-SEP-2003; 2003US-00663431.
 (SAGR-) SAGRES DISCOVERY INC
 17-FEB-2004; 2004WO-US004730
 2003US-00737318
 (first entry)
 Morris DW, Morris DW,
 WPI; 2004-652914/63.
 Sequence 414 AA;
 N-PSDB; ABD32792
 WO2004074320-A2
 lymphoma; CAP
 Homo sapiens.
 18-NOV-2004
 02-SEP-2004.
 94
 AB084564;
 9/
 34
 136
 Human;
 RESULT 9
 AB08456
 8XX C C C C C C C C C C C C C C C X 8
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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid or expression vector, a microarray for detecting a cenominant nucleic acid or expression vector, a microarray for detecting a cancer-associated (CA) nucleic acid comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the 35 comprising at least 10 contiguous nucleotides of any of the 35 comprising at least 10 contiguous nucleotides of any of the 35 comprising frame of a CA sequence selected from any of the 35 complement), an isolated antibody, (or its antigen binding fragment) that an open reading trame of a CA sequence selected from any of the 35 complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridoma that produces the above complement), an isolated antibody, (or its antigen binding fragment) that conformal antibody, a pharmaceutical composition comprising the above antibody and a pharmaceutical composition of cancer cells in an individual, a method for inhibiting growth of cancer cells in an individual, an electronic library comprising the above conformation of a polypeptide in a test cell sample, a secreting cancer activity or fa CA protein (CAP), methods for detecting the expression of a sociated with expression of a polypeptide in a test cell sample, and antibod for training the activity of a CA protein (CAP), methods for a benefit method for training the expression of a polypeptide in a test cell sample, and and method for inhibiting and method for training the expression of a polypeptide in a test cell sample. CAP associated with expression of a polypeptide in a test cell sample of animar cell cancer and a method for treatenting and treating cancer and a method for prese
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 cancer. The present sequence is a human CAP protein sequence. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
 New isolated cancer-associated polynucleotides and polypeptides useful for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Human, PRO protein; tumour necrosis factor family, TNF; cytokine; secreted protein; transmembrane protein; inflammation disorder.
 .;
0
 Length 425;
 Indels
 35.5%; Score 150; DB 8; Le
100.0%; Pred. No. 7.5e-135;
tive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 at ftp.wipo.int/pub/published_pct_sequences
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 claim 18; seqid 422; 310pp; English.
 AAY17830 standard; protein; 440
 Human PRO355 protein sequence.
 12-AUG-1999 (first entry)
 Conservative
 Local Similarity
les 150; Conserv
 Sequence 425 AA;
 Homo sapiens
 91
 94
 136
 154
 AAY17830;
 Query Match
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Matches
 RESULT 10
 AAY17830
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New human nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO polypeptides, useful as pharmaceutical and diagnostic
PRO715; PRO241; PRO323; PRO2299; PRO233; PRO344; PRO347; PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide; antibody; screening; detection; inhibition; probe; primer; human.
 Eaton DL, Ferrara N, Filvarol. ., A, Godowski PJ, Grimaldi CJ, Girney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
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Goddard A, Godowski
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 Claim 12; Fig 24; 187pp; English
 98WO-US025108.
98US-0112850P.
98US-0113296P.
 99WO-US028301.
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 Homo sapiens,
 01-DEC-1999;
 01-DEC-1998;
 22-DEC-1998;
 08-JUN-2000
 Peptide
 Domain
 agents
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 transmembrane proteins used therapeutically. The PRO proteins have expressed in the proteins have activity. The proteins and polynuclectiderative and immunosuppressive activity. The proteins and polynuclectides can be used in therapy, identification of homologues, raising antibodies and design of probes and primers. They can be used in a range of diseases related to proteins that they have homology with, e.g. a PRO protein having homology to complement proteins may be used in inflammatory responses
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 91
 present invention describes nucleic acids encoding PRO secreted and
 PRO; membrane bound protein; secreted protein; PRO357; PRO327; PRO243;
 Gaps
 ö
 Nucleic acids encoding PRO secreted and transmembrane proteins
 Chen J;
 35.5%; Score 150; DB 2; Length 440; 100.0%; Pred. No. 7.7e-135;
 0; Indels
 Baker KP,
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 100.0%; Prec. ...
 Yuan J,
 AAB01321 standard; protein; 440 AA
 Gurney AL,
 Claim 12; Fig 27; 123pp; English.
 97US-0069702P.
97US-0069870P.
97US-0069873P.
 97US-0069278P.
97US-0069278P.
97US-0069334P.
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 98WO-US025108
 98US-0074092P
 98US-0075945P
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Matches 150; Conservative
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 Wood WI, Goddard A,
 WPI; 1999-371118/31
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 01-DEC-1998;
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17-DEC-1997
 18-DEC-1997
 25-FEB-1998
 16
 32
 9/
 Query Match
 136
 152
 AAB01321
 RESULT 11
 AAB0132
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ABU58416 standard; protein; 440 AA
 Baker KP,
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 92
 136
 152
 ABU58416;
 Query Match
 Pan J,
 RESULT 13
 ABU58416
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New human nucleic acids encoding secreted and transmembrane polypeptides which are designated as PRO polypeptides are described The membrane-bound proteins have various industrial applications, including as pharmaceutical and diagnostic agents. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule antibodies are useful for the affinity purification of PRO from recombinant cell culture or natural sources
 PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; dog; cat; pig; goat; rabblt; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 Gaps
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 35.5%; Score 150; DB 3; Le
100.0%; Pred. No. 7.7e-135;
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2000WO-US006884.
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 2000US-0194647P.
2000US-0195975P.
2000US-0196000P.
 2000US-0187202P.
2000US-0186968P.
 2000US-0191007P.
 2000US-0193032P.
 2000US-0192655P
 2000WO-US008439
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 28-FEB-2001; 2001WO-US006520
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 RESULT 12
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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of detect the presence of a tumour in a mammal by comparing the level of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders
 Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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Watanabe CK, Wood WI, Zhang Z;
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Claim 11; Fig 34; 774pp; English.
2000US-0199397P.
2000US-0199550P.
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2000WO-US013705.
 2000WO-US014042.
2000WO-US014941.
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2000WO-US023328
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 20-DEC-2000; 2000WO-US034956
 Best Local Similarity 100.
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 WPI; 2001-602746/68.
N-PSDB; AAS45941.
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Smith V, W
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 25-APR-2000;
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 06-FEB-2003
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98US-0085579P. 98US-0085580P. 98US-0085582P.

15-MAY-1998; 15-MAY-1998; 15-MAY-1998;

ABU87964 standard; protein; 440 AA

ABU87964 ID ABU8 XX

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RESULT 15 ABU84279 ID ABU84279 standard; protein; 440 AA.

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 and transmembrane protein; PRO; TNF-alpha; factor alpha; chondrocyte cell; tumour; gene therapy;
 Human secreted/transmembrane protein (PRO) #17.
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| PR 15-MAY-1998; PR 15-MAY-1998; PR 22-MAY-1998; PR 02-UN-1998; PR 04-UN-1998; PR 04-UN-1998; PR 05-UN-1998; PR 10-UN-1998; PR 10-UN-1998; PR 10-UN-1998; PR 11-UN-1998; PR 22-UN-1998; 25-JUN-1998<br>25-JUN-1998<br>25-JUN-1998<br>25-JUN-1998<br>26-JUN-1998<br>26-JUN-1998<br>01-JUL-1998<br>01-JUL-1998<br>02-JUL-1998<br>02-JUL-1998<br>02-JUL-1998<br>02-JUL-1998<br>02-JUL-1998<br>10-AUG-1998<br>10-AUG-1998                                                                                 |

| 80S-0096867<br>80S-0096891<br>80S-0096949<br>80S-0096949<br>80S-0097954<br>80S-0097954<br>80S-0097954<br>80S-0097954<br>80S-0097954 | 00000000000000000000000000000000000000  | 80.5 - 0.0147.5 80.5 - 0.0147.5 80.5 - 0.0147.5 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173.9 80.5 - 0.0173. |
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| 7-AUG-199<br>7-AUG-199<br>7-AUG-199<br>8-AUG-199<br>8-AUG-199<br>6-AUG-199<br>6-AUG-199<br>6-AUG-199<br>6-AUG-199                   |                                         | 3.3.5.EF 199 3.4.5.EF 199 4.5.EF 199 4.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF 199 6.5.EF  |
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0; Gaps

Query Match 35.5%; Score 150; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 7.7e-135; Matches 150; Conservative 0; Mismatches 0; Indels

8 6 8 6

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The invention relates to an isolated PRO polypeptide (a secreted or transmembrane protein) comprising: (a) at least 80% sequence identity or positives when comparated to any of 15 sequences, fully defined in the specification, lacking or with its associated signal peptide; or (b) at least 80% sequence of any of 15 sequence encoded by the full-length coding sequence of a DNA deposited in the American Type Culture Collection (ATCC). Also included are: (l) an isolated mucleic acid comprising: (a) at least 80% sequence identity to a nucleotide sequence comprising: (a) at least 80% sequence identity to a nucleotide sequence or full-length coding sequence with any of 15 fully defined sequences of 957-3441 base pairs, given in the specification; or (c) at least 80% sequence identity to a full-length coding sequence of a proposited under ATCC Accession No. 209526, 209528, 209527, 209538, 209530, 209531, 209530, 209531, 209530, 209531, 2
 New isolated PRO polypeptide and encoding nucleic acid, useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS, cancer, atherosclerosis, inflammatory disease and diabetes.
 Human; PRO; secreted protein; transmembrane protein; anti-HIV; cytostatic; antiarteriosclerotic; antiinflammatory; antidiabetic; cardiant; AIDS; acquired immunodeficiency syndrome; cancer; atherosclerosis; inflammatory disease; diabetic complication; cardiac injury; organ failure.
 Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;
Gerritsen ME, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL;
Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 Human secreted/transmembrane protein PRO355.
 ABUSS930 standard; protein; 440 AA
 Claim 12; Fig 24; 178pp; English
 15-5EP-1999; 99WO-USCIL222.

30-NOV-1999; 99WO-USCIR913.

30-NOV-1999; 99WO-USCIR913.

31-NOV-1999; 99WO-USCIR913.

31-NOV-1999; 99WO-USCIR910.

31-FEB-2000; 2000WO-USCIR912.

32-FEB-2000; 2000WO-USCIR911.

32-FEB-2000; 2000WO-USCIR911.

31-MAR-2000; 2000WO-USCIR911.

32-MAR-2000; 2000WO-USCIR91.

32-MAR-2000; 2000WO-USCIR91.

32-MAR-2000; 2000WO-USCIR91.

32-MAR-2000; 2000WO-USCIR91.

32-MAR-2000; 2000WO-USCIR91.

31-FEB-2000; 2000WO-USCIR91.

31-FEB-2000; 2000WO-USCIR91.

31-FEB-2000; 2000WO-USCIR91.

31-FEB-2000; 2000WO-USCIR91.

31-FEB-2000; 2000WO-USCIR91.
 98WO-US025108.
99WO-US012252.
99WO-US021090.
 28-FEB-2001; 2001WO-US006520
25-MAY-2001; 2001US-00866028
 31-AUG-2001; 2001US-00944654
 (first entry)
 (GETH) GENENTECH INC.
 WPI; 2003-174141/17.
N-PSDB; ABX75486.
 US2002142959-A1.
 Homo sapiens
 26-MAR-2003
 03-OCT-2002
 ABUS5930;
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 75
 91
cell comprising the vector which, when cultured under conditions suitabl for expression of the PRO polypeptide, produces the PRO protein; (4) a chimeric molecule comprising PRO fused to a heterologous amino acid sequence; and (5) an anti-PRO antibody. The methods and compositions of the present invention are useful for the diagnosis and treatment of disorders associated with the PRO polypeptide, such as AIDS (acquired immunodeficiency syndrome), cancer, atherosclerosis, inflammatory disease, diabetic complications, cancer, autheroscierosis, inflammatory antibodies can also be used in the different screening, therapeutic and biological assays. The present sequence represents a PRO protein
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 Human, PRO polypeptide; secreted and transmembrane protein; tumour; chromosome mapping; gene mapping; cytostatic.
 ;
 Length 440;
 Indels
 35.5%; Score 150; DB 6; Le
100.0%; Pred. No. 7.7e-135;
tive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ABU82722 standard; protein; 440
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97US - 0059266P
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97US - 0063544P
97US - 0063544P
97US - 0063544P
97US - 0063134P
97US - 0063131P
97US - 0063712P
97US - 0063712P
97US - 0064103P
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97US - 0069425P
97US - 0069425P
97US - 0069425P
 20-JUN-2002; 2002US-00176911
 (first entry)
 Human PRO polypeptide #17.
 Conservative
 Similarity
 Sequence 440 AA;
 US2003032113-A1.
 24-007-1997;
28-007-1997;
28-007-1997;
28-007-1997;
29-007-1997;
31-007-1997;
13-007-1997;
 27-JUN-2003
 18-DEC-1997;
10-MAR-1998;
 Best Local Simi
Matches 150;
 18-SEP-1997
 997
 13-FEB-2003
 ABU82722;
 16
 32
 94
 92
 136
 152
 17-OCT-19
21-OCT-19
 24-NOV-19
11-DEC-19
 Query Match
 21-NOV-1
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 24-NOV-1
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| 98US - 0090435P. 98US - 0090444P. 98US - 0090444P. 98US - 0090444P. 98US - 009064BP. 98US - 009066BP. 98US - 009066BP. 98US - 009066BP. 98US - 009066BP. 98US - 009066BP. 98US - 009066BP. 98US - 00906BSP. 98US - 00911359P. 98US - 00911359P. 98US - 00911486P. 98US - 009144BP. 98US - 00914BBP. 98US - 00914BBP. 98US - 00915BP. 98US - 0091632P. 98US - 0091632P. 98US - 00959BBP. 98US - 00959BBP. 98US - 00959BBP. 98US - 00959BP. 98US - 00959BP. 98US - 00959BP. 98US - 00959BP. 98US - 00959BP. 98US - 00959BP. 98US - 00959BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 00999BP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP. 98US - 0099BBP.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | 98US-0101068P.<br>98US-0101471P.<br>98US-0101475P.<br>98US-0101477P.<br>98US-0101779.<br>98US-0101738P.<br>98US-0101738P.<br>98US-0101743P.<br>98US-0101743P. |
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| 24-JUN-1998; 24-JUN-1998; 24-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 25-JUN-1998; 26-JUN-1998; /u>                                                                                                                                                      |
| ***************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | % % % % % % % % % % % % % % % % % % %                                                                                                                         |
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| <u>ኛ ዊ ኛ ኛ ዊ ዊ ዊ ዊ ዊ ዊ</u>                                                           | ***************************************                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |
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100.0%; Pred. No. 7.7e-135;
tive 0; Mismatches 0;
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 98US-0101739P.
98US-0101743P.
98US-0101742P.
98US-01022P.
98US-0102240P.
98US-010231P.
98US-0102487P.
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Best Local Similarity 100.
Matches 150; Conservative
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24-SEP-1998;
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RR 22.-UN-1998, 9805-009962P.
RR 24.-UN-1998, 9805-009962P.
RR 25.-UN-1998, 9805-009962P.
RR 26.-UN-1998, 9805-009962P.
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Pred. No. 7.7e-135;
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100.0%; Pred. No. ...
0; Mismatches
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98US-0101477P
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Matches 150; Conservative
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23-SEP-1998;
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                                                                                                                                                                                                                                 35.5%; Score 150; DB 6; Le
100.0%; Pred. No. 7.7e-135;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted polypeptide PRO355, SEQ ID NO:34
                                                                                                                                                                                                                                                                                                                                                                    DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
                                                                                                                                                                                                                                                                                                                                                                               DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                             ABR94621 standard; protein; 440 AA
           98US-0101068P.
98US-0101471P.
98US-0101477P.
98US-0101477P.
98US-0101738P.
98US-0101738P.
98US-0101738P.
98US-0101738P.
98US-0101738P.
98US-0101738P.
98US-0102210P.
98US-0102210P.
98US-0102311P.
98US-0102311P.
98US-0102571P.
98US-0102571P.
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97US-0059266P.
97US-0062250P.
97US-0063120P.
97US-0063121P.
97US-0063541P.
97US-0063541P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2003 (first entry)
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2003044926-A1
18-SEP-1998;
23-SEP-1998;
23-SEP-1998;
23-SEP-1998;
24-SEP-1998;
24-SEP-1998;
24-SEP-1998;
24-SEP-1998;
25-SEP-1998;
25-SEP-1998;
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30-SEP-1998;
01-OCT-1998;
01-OCT-1998;
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Best Local Simi
Matches 150;
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18-SEP-1997;
24-0CT-1997;
24-0CT-1997;
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29-SEP-1998
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          98US-0089512P

98US-0089514P

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98US-008953BP

98US-009052BP

98US-0090545BP

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26-AUG-1998;
26-AUG-1998;
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26-AUG-1998;
26-AUG-1998;
01-SEP-1998;
01-SEP-1998;
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02-SEP-1998;
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10-SEP-1998;
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18-SEP-1998;
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25-JUN-1998
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98US-0089090P98US-0089115P98US-0089114P98US-00895114P98US-0089518P98US-0089518P98US-0089518P98US-0089518P98US-0089518P98US-0090518P98US-0099711P98US-0099711P98US-0099711P98US-0099711P98US-0099711P98US-0099711P98US-0099711P98US-0099711P98US-00099711P98US-00099711P98US-00099711P98US-00099711P98US-00099771P-

12-70N-1998 16-70N-1998 16-70N-1998 17-70N-1998 17-70N-1998 17-70N-1998 22-70N-1998 23-70N-1998 he invention relates to a human secreted and transmembrane polypeptide (PRO) and the polynucleotide encoding it. The PRO polypeptide or polynucleotide is useful in pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating cancers, inflammatory diseases, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS) and diabetic complications in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits. The sequences are also useful in biotechnological and medical research and in various polypeptides of the invention
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 New secreted and transmembrane polypeptides (e.g. PRO241, for use in pharmaceuticals, diagnostics or bioreactors, particularly for detecting or treating e.g. cancers, infertility or acquired immunodeficiency syndrome in mammals.
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Botstein D, Eaton DL, Ferrara N, Flance C, MK, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL; Kliavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;
 35.5%; Score 150; DB 6; Le
100.0%; Pred. No. 7.7e-135;
iive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Claim 1; Fig 24; 173pp; English.
 9705-0068017P

9805-007409EP

9805-007409EP

9805-0075945P

9800-005015310

9800-00216021

9805-0112850P

9805-0112850P

9805-0112850P

9905-01462252

9906-01462252
 2000WO-US014042.
2000WO-US020710.
2000WO-US032678.
2001WO-US006520.
 99WO-US028409
99WO-US028301
 99WO-US028313
 99WO-US030095
 2000WO-US005841
 2000WO-US008439
 2000WO-US003565
 2000WO-US004414
 2001US-00866028
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Gerritsen ME, Goddard A
Hillan KJ, Kljavin IJ,
 (GETH) GENENTECH INC.
 WPI; 2003-174088/17.
 N-PSDB; ABX89477
 Sequence 440 AA;
 16-DEC-1999;
11-FEB-2000;
22-FEB-2000;
 30-NOV-1999;
30-NOV-1999;
01-DEC-1999;
 02-MAR-2000;
 30-MAR-2000;
22-MAY-2000;
 01-DEC-2000;
28-FEB-2001;
 25-MAY-2001;
 16-DEC-1998
22-DEC-1998
 25-FEB-1998
16-SEP-1998
 16-DEC-1998
 22-DEC-1998
 MAR-1999
 28-JUL-1999
15-SEP-1999
 01-DEC-1998
 22-JUN-1999
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 Human; PRO; secreted polypeptide; transmembrane polypeptide; cancer; inflammatory disease; atherosclerosis; cardiac injury; AIDS; infertility; birth defect; premature aging; diabetes; dog; cat; horse; acquired immunodeficiency, syndrome; cow, sheep; pig; goat; rabbit; industry; cytostatic; antiinflammatory; cardiant; antiinfertility; anti-HIV; antiarteriosclerotic; antidiabetic.
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
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 Score 150; DB 6; Length 440;
Pred. No. 7.7e-135;
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100.0%; Pred. No....
0; Mismatches
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 ABU60240 standard; protein; 440
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98US-0101068P.
98US-0101472P.
98US-0101475P.
98US-0101477P.
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98US-0101922P
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97US-0069702P.
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98US-0102687P
 2001US-00945015
 (first entry)
 Human PRO polypeptide #11
 Best Local Similarity 100.
Matches 150; Conservative
 US2002132768-A1
 18-SEP-1998
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30-SEP-1998
30-SEP-1998
 31-AUG-2001;
 24-APR-2003
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 16-DEC-1997;
16-DEC-1997;
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 19-SEP-2002
 03-DEC-1997
 11-DEC-1997
12-DEC-1997
 01-OCT-1998
 11-DEC-1997
 16-DEC-1997
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 RESULT 29
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Length 440; Indels

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2001US-00866028.
2001WO-US017800.
2001US-00874503.
2001WO-US019692.
 2001US-00854208.
2001US-00854280.
 (first entry)
 (GETH) GENENTECH INC.
 WPI; 2003-332028/31
 Chen J,
 N-PSDB; ACA72787
 Sequence 440 AA;
 01-JUN-2001; 205-JUN-2001; 20-JUN-2001; 20
 25-MAY-2001;
 29-JUN-2001;
 18-JUL-2001;
 30-JUL-2001;
 06-AUG-2001;
 16-AUG-2001;
 28-AUG-2001;
 29-AUG-2001;
 15-JAN-2002;
 04-SEP-2001;
 01-AUG-2003
 Baker KP,
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 136
 152
 ABU98754;
 Pan J,
 RESULT 31
 ABU98754
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 polypeptide; transmembrane polypeptide;
or alpha; TNF-alpha; chondrocyte cell; tumour;
DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Z
 ABU85594 standard; protein; 440
 99WO-US020111.
99WO-US021090.
99US-00403297.
99US-00423844.
 98US-00202054.
99US-00254311.
99WO-US005028.
99US-00311832.
 99WO-US031274.
 2000WO-US005601.
 2000WO-US020710.
2000US-00644848.
 99WO-US010733.
99WO-US012252.
 99US-00380139.
 99WO-US028551
 2000WO-US004341
 2000WO-US008439
 2000WO-US013705
 2000WO-US014941
 2000WO-US015264
 2000WO-US023328
 2001WO-US006520
 99US-00380138
 99WO-US028301
 2000WO-US004342
 2000WO-US005004
 2000WO-US005841
 2000WO-US014042
 98US-00168978
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98WO-US025108
 2000WO-US004414
 2002US-00187588
 99US-00380137
 2000WO-US006884
 (first entry)
 Human PRO polypeptide #17.
 necrosis factor
 Human; PRO; secreted
 US2003036140-A1.
 20-DEC-2000; 2
20-DEC-2000; 2
28-FEB-2001; 2
 15-SEP-1999;
18-OCT-1999;
12-NOV-1999;
01-DEC-1999;
 18-FEB-2000;
18-FEB-2000;
 22-FEB-2000;
24-FEB-2000;
 01-MAR-2000;
02-MAR-2000;
 15-MAR-2000;
 17-MAY-2000;
22-MAY-2000;
 02-JUN-2000;
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06-NOV-1998;
01-DEC-1998;
07-DEC-1998;
 22-AUG-2000;
 24-AUG-2000;
 18-SEP-2000;
 38-NOV-2000;
 30-DEC-1999;
05-JAN-2000;
 30-MAY-2000;
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 02-JUL-2003
 14-MAY-1999;
02-JUN-1999;
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25-AUG-1999;
 08-MAR-1999
 25-AUG-1999
 25-AUG-1999
 01-SEP-1999
 20-FEB-2003
 cytostatic.
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 152
 tumour
 4BU85594
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 transmembrane polypeptides) and the PRO polymucloctides encoding them. The invention also relates to a method for stimulating the release of twing the ercrosis factor alpha (TNF alpha) from human blood by contacting the blood with a sequence of the invention, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide and a method for detecting the presence of a tumour in a mammal. The polypeptides and polymucleotides are useful for the manufacture of a medicament for diagnosing or treating a tumour in a mammal. Sequences ABUSSSRA represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 Three hundred and five nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor.
 Godowski PJ, Gurney AL;
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
 The invention relates to human PRO polypeptides (secreted and
 Length 440;
 0; Indels
 Novel human secreted and transmembrane protein PRO355.
 , Goddard A, Godo
Wood WI, Zhang Z;
 Query Match 35.5%; Score 150; DB 6; Le Best Local Similarity 100.0%; Pred. No. 7.7e-135; Matches 150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Claim 11; Fig 34; 707pp; English.
 Desnoyers L,
 ABU98754 standard; protein; 440
 Smith V, Watanabe CK,
2001MO-US021066.
2001MO-US021735.
2001US-00908827.
2001US-00918585.
2001US-00924419.
2001US-00931836.
 2001US-00941992.
 2002US-00052586
 2001US-00946374
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980S-0083496P.
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98US-0086392P.
 2002US-00175737
 US2003013153-A1.
 Homo sapiens
 19-JUN-2002;
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07-MAY-1998
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-NOV-1997;
-NOV-1997;
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 -APR-1998;
 16-JAN-2003
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gene therapy;
 Human; secreted and transmembrane protein; PRO; cytostatic; chondrocyte stimulator; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; dironsome identification.
 Novel human secreted and transmembrane protein PRO355
 97US-0059263P
97US-0053264P
97US-0063248P
97US-0063121P
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11-JUN-1998;
11-JUN-1998;
 12-JUN-1998
 16-JUN-1998
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 ö
 Length 440;
 Indels
 35.5%; Score 150; DB 6; Le liarity 100.0%; Pred. No. 7.7e-135; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 98US-0096959P

98US-0097052P

98US-0097052P

98US-0097971P

98US-0097971P

98US-0098014P

98US-0098014P

98US-0098014P

98US-009802P

98US-009802P

98US-009802P

98US-0099741P

98US-0099741P

98US-0099741P

98US-0099741P

98US-0100662P

98US-0100663P

98US-0100663P

98US-0100684P

98US-0100684P

98US-010073B

98US-010073B

98US-0101472P

98US-0101472P

98US-0101473P

98US-0101473P

98US-0101473P

98US-0101473P

98US-0101473P

98US-0101473P

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98US-0101473P

98US-0101473P

98US-0101473P

98US-0101473P

98US-0101474P

98US-010173BP

98US-010173BP

98US-010173BP

98US-010173BP

98US-0101743P

98US-0101743P

98US-0101747P

98US-0101747P

98US-0101747P

98US-0101747P

98US-0101747P

98US-0101747P

98US-0101747P

98US-0101747P

98US-0101747P
98US-0096949P
 Similarity
 18-AUG-1998, 18-AUG-1998, 26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 10-SEP-1998, 10-SEP-1998, 10-SEP-1998, 16-SEP-1998, 24.5EP-1998,
24.5EP-1998,
25.5EP-1998,
29.5EP-1998,
29.5EP-1998,
30.5EP-1998,
30.5EP-1998,
30.5EP-1998,
30.5EP-1998,
30.5EP-1998,
30.5EP-1998,
30.5EP-1998,
30.5EP-1998,
 23-SEP-1998;
23-SEP-1998;
24-SEP-1998;
 Query Match
Best Local Simi
Matches 150;
 18-SEP-1998;
18-SEP-1998;
 32
 9/
 92
 136
 16
 152
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Gaps

ABU86209 standard; protein; 440 AA

RESULT 35
ABU86209
ID ABU86
XX
AC ABU86

ABU86209

```
Human; immunogen; secreted protein; transmembrane protein; PRO; tumour; proliferation; differentiation; chondrocyte cells; tumour necrosis factor-alpha; TNF-alpha; blood; gene therapy.
 Human secreted/transmembrane protein (PRO) #17
 98WO-US019330
98US-00168978
 98US-00202054
99US-00254311
 99US-00423844
 98US-00187368
 98WO-US025108
 99WO-US005028
 99US-00380139
 99WO-US021090
 99WO-US028551
 2002US-00187603
 99WO-US012252
 99US-00403297
 99WO-US031274
 22-FEB-2000; 2000WO-US004414
 000WO-US005841
 2000WO-US014042
 2001WO-US021735
 01-JUL-2003 (first entry)
 99US-003
 SN-OM66
 99WO-US
 US2003036146-A1
 01-MAR-2000;
02-MAR-2000;
15-MAR-2000;
30-MAR-2000;
17-MAY-2000;
 22-MAY-2000;
30-MAY-2000;
02-JUN-2000;
28-JUL-2000;
22-AUG-2000;
 18-SEP-2000;
08-NOV-2000;
08-NOV-2000;
01-DEC-2000;
 28-FEB-2001;
22-MAR-2001;
 Homo sapiens.
 02-JUL-2002;
 20-DEC-2000;
 09-JUL-2001;
 30-DEC-1999;
 20-FEB-2003
 MAR-1999
 17-OCT-1998
 JUN-1999
 -OCT-1999
XX
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```
The invention relates to three hundred and five nucleic acids encoding CC RRO polypeptides (secreted and transmembrane), sequences 80% identical to them, or encoding a RRO polypeptide lacking its associated signal peptide cc are extracellular domain of the PRO polypeptide, with or lacking its associated signal peptide. Also included are the encoded PRO proteins, PRO expression vectors, host cells transformed with the vector (used to produce PRO proteins), a chimaric molecule comprising the PRO proteins), a chimaric molecule comprising the PRO proteins), a chimaric molecule comprising the PRO proteins), a chimaric molecule comprising the PRO proteins), a method for stimulating the release of tumor necrosis factor alpha (TNP-alpha) from human blood (by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the prosence of tumour in a mammal and an oligonucleotide probe darived from any of the nucleotide sequences cited above. The PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful on bypeptides or anti-PRO antibody. The PRO nucleoted are also useful for turn are useful in the development and screening of therapeutically useful reagents, for chromosome admitication, and animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome cited are also useful for detecting the presence of a tumour in a mammal, arimulating the transgence byping. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of a tumour in a mammal, are useful contactors, and molecular weight markers for protein or differentiation or differentiation o
 Three hundred and five nucleic acids encoding PRO polypeptides, useful in gene therapy, chromosome identification, tissue typing, and for detecting the presence of tumor in a mammal.
 76 DSRPQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SARALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 Godowski PJ, Gurney AL;
 Gaps
 ,
0
 35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135; ive 0; Mismatches 0; Indels
 , Goddard A, Godo
Wood WI, Zhang Z;
 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 165
 Desnoyers L,
 Claim 11; Fig 34; 707pp; English.
 Smith V, Watanabe CK,
 ; 2001US-00924419.
; 2001US-00929404.
; 2001US-00931836.
; 2001US-00941992.
; 2001US-00946374.
 2002US-00052586
 Best Local Similarity 100,0
Matches 150, Conservative
 (GETH) GENENTECH INC.
 WPI; 2003-332034/31.
 Chen J,
 N-PSDB; ACA73401
 Sequence 440 AA;
 28-AUG-2001;
29-AUG-2001;
04-SEP-2001;
 36-AUG-2001;
 16-AUG-2001;
 LS-JAN-2002;
 13-AUG-2001;
 Baker KP,
 92
 136
 Query Match
 Pan J,
8
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secreted and transmembrane protein; PRO; TNF-alpha; necrosis factor alpha; chondrocyte cell; tumour; gene therapy;
 Human secreted/transmembrane protein (PRO) #17.
152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 ABU67422 standard; protein; 440 AA
 30-DEC-1999, 99W0-US031274.
05-JAN-2000; 2000W0-US000219.
18-FEB-2000; 2000W0-US004342.
18-FEB-2000; 2000W0-US004342.
22-FEB-2000; 2000W0-US005004.
01-MAR-2000; 2000W0-US005601.
02-MAR-2000; 2000W0-US005884.
30-MAR-2000; 2000W0-US006884.
 99WO-US021090.
99US-00403297.
99US-00423844.
 99US-00380137.
99US-00380138.
99US-00380139.
99US-00380142.
 2000WO-US020710.
2000US-00644848.
 98WO-US019330
98US-00168978
 98US-00202054
99US-00254311
 99US-00311832
 2000WO-US015264
 98US-00187368
98WO-US025108
 99WO-US005028
 99WO-US010733
 99WO-US012252
 99WO-US020111
 99WO-US028301
 2000WO-US014042
 2000WO-US014941
 2000WO-US023328
 99WO-US028551
 2000US-00665350
 2001US-00816744
 (first entry)
 Human; secreted
 US2003036162-A1
 18-SEP-2000; 2
18-SEP-2000; 2
08-NOV-2000; 2
 20-DEC-2000; 2
28-FEB-2001; 2
22-MAR-2001; 2
 tissue typing.
 07-OCT-1998;
06-NOV-1998;
01-DEC-1998;
07-DEC-1998;
03-MAR-1999;
 22-MAY-2000;
 02-JUN-2000;
 24-AUG-2000;
 08-MAR-1999;
14-MAY-1999;
14-MAY-1999;
 15-SEP-1999;
18-OCT-1999;
12-NOV-1999;
 22-AUG-2000;
 Homo sapiens
 12-JUL-2002;
 29-MAY-2003
 01-DEC-1999;
02-DEC-1999;
 25-AUG-1999
 25-AUG-1999
 25-AUG-1999
 01-SEP-1999
 20-FEB-2003
 25-AUG-1999
 ABU67422;
 tumour
 RESULT 36
 ABU67422
ID ABU
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The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNF-alpha) from human blood by contacting the blood a PRO polypeptide, a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation of chondrocyte cells by contacting the proliferation or differentiation and the presence of a tumour in a mammal and an oligonucleotide probe derived from any of the PRO nucleotide sequences. The nucleotide sequences are useful as probes, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as chromosome identification, as chromosome markers, as therapeutic agents, for chromosome identification, as chromosome markers, as therapeutic agents, for stimulating the proliferation or differentiation of chondrocytes and electring the presence of a tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for tissue typing. The sequences presented in ABUG7100 are the PRO polypeptides of the invention
 nucleic acids, useful chromosome markers,
 92 DSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gurney AL;
 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
 Query Match 35.5%; Score 150; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 7.7e-135; Matches 150; Conservative 0; Mismatches 0; Indels
 Godowski PJ,
 New secreted and transmembrane PRO polypeptides and in gene therapy, in chromosome and gene mapping, as in tissue typing, and in chromosome identification.
 , Desnoyers L, Goddard A, Godov Watanabe CK, Wood WI, Zhang Z;
 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN
 Claim 11; Fig 34; 706pp; English.
 01-JUN-2001; 200103-0056025.

05-JUN-2001; 200105-00874503.

20-JUN-2001; 2001W0-US019692.

29-JUL-2001; 2001W0-US021066.

09-JUL-2001; 2001W0-US021056.

09-JUL-2001; 2001US-0099827.

18-JUL-2001; 2001US-00998827.

13-AUG-2001; 2001US-00929404.

13-AUG-2001; 2001US-00931836.

28-AUG-2001; 2001US-00931836.

29-AUG-2001; 2001US-00941992.

29-AUG-2001; 2001US-00941992.
 2001US-00854280.
2001US-00866028.
 2002US-00052586
 (GETH) GENENTECH INC.
 WPI; 2003-332039/31.
N-PSDB; ACA05716.
 Chen J,
 Smith V,
 Sequence 440 AA;
10-MAY-2001;
10-MAY-2001;
25-MAY-2001;
 15-JAN-2002;
 16
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 152
 Pan J,
 Baker
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75 91

RESULT 37 ABU80450

transmembrane

Gurney AL;

Godowski PJ,

, Goddard A, Godo Wood WI, Zhang Z;

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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 The invention relates to three hundred and five nucleic acids encoding PRO polypeptides (secreted and transmembrane). Methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of tumours, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumours. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human CDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The present sequence represents a human PRO polypeptide of the invention
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 Three hundred and five nucleic acids encoding secreted and transmembrand PRO polypeptides, useful for the diagnosis, prevention and/or treatment of tumors, such as adrenal, lung, colon, breast, prostate, rectal,
 KW Human, PRO, secreted protein, transmembrane protein, extracellular domain, tumour necrosis factor-alpha; TNF-alpha; chondrocyte, proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis;
 35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135;
 Human secreted polypeptide PRO355, SEQ ID NO:34.
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Best Local Similarity 100.0%; Pred. No. 7.7
Matches 150; Conservative 0; Mismatches
 ABR99368 standard; protein; 440 AA
 Claim 11; Fig 34; 708pp; English.
 Desnoyers L,
 Watanabe CK,
, 2001WO-US021066.
; 2001WS-US021735.
; 2001US-00918587.
; 2001US-00924419.
; 2001US-00924419.
; 2001US-00941992.
; 2001US-00941992.
; 2001US-00941992.
; 2001US-00941992.
 18-SEP-2003 (first entry)
 cervical or liver tumors
 (GETH) GENENTECH INC
 WPI; 2003-342038/32.
N-PSDB; ACA66550.
 Chen J,
 Smith V,
 Sequence 440 AA;
 13-AUG-2001;
16-AUG-2001;
28-AUG-2001;
 06-AUG-2001;
 29-AUG-2001;
04-SEP-2001;
 15-JAN-2002;
 Baker KP,
 16
 32
 96
 92
 136
 ABR99368;
 Query Match
 Pan J,
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 Human; tumour; adrenal; lung; colon; breast; prostate; rectal; cervical;
liver; PRO; gene therapy.
 ABU80450 standard; protein; 440 AA
 99WO-US012252.
99US-00380137.
99US-00380138.
99US-00380139.
 99US-00403297.
99US-00423844.
99WO-US028301.
 99WO-US005028.
 99WO-US010733.
 2000WO-US004341,
 2000WO-US005601
 2000US-00665350,
2000US-00709238.
 98WO-US019330
98US-00168978
 98WO-US021141
98US-00187368
 98US-00202054
 99US-00254311
 99WO-US020111
 99WO-US021090
 2000WO-US005004
 2000WO-US008439
 2000WO-US013705
 2000WO-US015264
 2000US-00664610
 2000WO-US030952
 2001WO-US019692
 2002US-00184640
 98WO-US025108
 2001US-00874503
 (first entry)
 SU-OW66
 SU-OM6
 Human PRO protein #17
 JS2003036137-A1.
 Homo sapiens.
 22-FEB-2000;
24-FEB-2000;
 08-NOV-2000;
08-NOV-2000;
 05-JUN-2001;
20-JUN-2001;
 27-JUN-2002;
 18-FEB-2000;
 -SEP-2000;
 01-MAR-2000;
 17-MAY-2000;
 -AUG-1999;
-AUG-1999;
 18-FEB-2000;
 23-JUN-2003
 06-NOV-1998
 20-FEB-2003
 07-DEC-1998
 14-MAY-1999
 12-NOV-1999
 01-DEC-1999
 30-DEC-1999
 07-OCT-1998
 JUN-1999
 01-SEP-1999
 15-SEP-1999
 18-OCT-1999
 ABU80450;
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Gaps ö

0; Indels

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98US-0088023P

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98US-0088032P

98US-0088120P

98US-0088117P

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 02-JUL-1998;
24-JUL-1998;
10-AUG-1998;
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 26-JUN-1998;
26-JUN-1998;
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01-JUL-1998;
 24-JUN-1998;
24-JUN-1998;
 24-JUN-1998;
 26-AUG-1998
26-AUG-1998
 24 - JUN - 1998
 antiarthritic; vulnerary; gene therapy
 9705-0059263P

9705-0059266P

9705-0063486P

9705-0063121P

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 2002US-00183006
 US2003040063-A1
 08-APR-1998;

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21-APR-1998;

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29-APR-1998;

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29-APR-1998;

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Human; PRO; secreted protein; transmembrane protein;

Human secreted polypeptide PRO355, SEQ ID NO:34.

(first entry)

ABR78243;

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The invention relates to human PRO secreted/transmembrane polypeptides (ABRPOS17-ABRPOS13) and nucleic acids encoding them (ACPOINO-00404). The invention also relates to sequences at least 80% identical to the PRO invention also relates to sequences at least 80% identical to the PRO nucleic acid and polypeptide sequences of the invention, recombinant vectors and host cells comprising a PRO polypeptide. Mucleic comprising a PRO polypeptide in a PRO polypeptide in And fusion proteins comprising a PRO polypeptide. Mucleic colds encoding PRO polypeptides of the invention were initially intelled the colds and fusion proteins comprising a PRO polypeptide. Mucleic colds encoding PRO polypeptides of interest were identified via man colds and characterised. The PRO polypeptides are useful for invention with a proteins containing sequences from known secreted proteins. Human cDNA incleaded and characterised. The PRO polypeptides are useful for stimulating release be tumour necrosis factor-alpha (TNF-alpha) from man blood and may thus be used in the treatment of conditions in which change of the proliferation or differentiation or differentiation of propertides may be used in the treatment of various bone and/or cartilage such may be used in the treatment of various bone and/or cartilage such may be used in the treatment of various bone and/or cartilage such may be used in the treatment of various bone and/or cartilage used in the treatment of various bone and/or cartilage used in the treatment of various bone and/or cartilage which as attribrials and sports injuries. The PRO polypeptides may be used in the treatment of various bone and/or cartilage in the test samples, where a higher transport unmour, lung tumour, colon tumour, breast tumour, profetter tumour, profetter tumour, profetter tumour, profetter of the presence of a tumour of PRO polypeptides in the test samples, where a higher language of propeptides are and control samples, where a higher language of the presence of a tumour and propertion of PRO polypeptides
 New secreted and transmembrane PRO polypeptides and nucleic acids, usefuin gene therapy, or for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody.
extracellular domain; tumour necrosis factor-alpha; TNP-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 Gurney AL;
 Godowski PJ,
 Chen J, Desnoyers L, Goddard A, Godor
th V, Watanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 700pp; English.
 Smith V, Watanabe CK,
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99US-00380137.
 22-JUL-2002; 2002US-00201530
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15-JAN-2002; 2002US-00052586
 (GETH) GENENTECH INC
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 22-JUN-1998;
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 5-AUG-1999;
 20-MAR-2003
 Baker KP,
 Pan J,
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a PRO protein
30-MAR-2000;
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 Human, PRO; secreted protein, transmembrane protein,
Cornelia de Lange syndrome; gene therapy; immune disorder;
inflammatory disease; organ failure; atherosclerosis; cardiac injury;
infertility; birth defect; premature aging; cardiac injury; AIDS; cancer;
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 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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Pred. No. 7.7e-135;
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98WO-US019330.
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98US-0113296P.
99WO-US012252.
 98WO-US025108
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 99WO-US028313
 99WO-US028409
 2000WO-US004414
2000WO-US005841
 2000WO-US003565
 31-AUG-2001; 2001US-00944944
 (first entry)
 Matches 150; Conservative
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 Similarity
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 22-FEB-2000;
02-MAR-2000;
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 21-NOV-2002.
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 22-DEC-1998
 18-DEC-1997
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 16
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 92
 136
 152
 Query Match
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The invention relates to an isolated nucleic acid encoding a secreted/
transmembrane polypeptide (designated as PRO proteins). 15 PRO
CC polypeptides and thair encoding polymuclectides are disclosed. Also
cincluded are a vector comprising the PRO nucleic acid, a host cell
comprising the vector, a process for producing a PRO polypeptide (by
CC culturing the host cell under conditions for the expression of the PRO
polypeptide, and recovering the PRO polypeptide form the cell culture, an
isolated polypeptides a chimmaeric molecule comprising PRO fused to a
cherrologous amino acid sequence and an antibody which specifically binds
cc he PRO polypeptides, a chimmaeric molecule comprising PRO fused to a
cherrologous amino acid sequence and an antibody which specifically binds
cc herrologous amino acid sequence are useful as hybridisation probes,
in chromosome and gene mapping, in generating sense and antisense RNA or
DNA, in generating transgenic or knock-out animals which can be used in
the development and screening of therapeutically useful reagents, and in
cc gene therapy. The polypeptides may be used as molecular weight markers
cc for protein abscrophoresis purposes. The PRO polypeptide and nucleic
cacids may also be used for chromosome identification, and tissue typing.
PRO241 (identified as Chordin) is a candidate gene for Cornelia de Lange
cc syndrome. Other PRO proteins are variously implicated in immune
cd isorders, inflammatory disease, organ failure, atherosclerosis, cardiac
injury, infertility, birth defects, premature aging, cardiac
injury, infertility, borth defects, premature aging, cardiac
injury, and contents and diabetic complications. The present sequence represents
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 75
 91
 chromosome
 32 SAAALIPIGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Gaps
 New transmembrane polypeptides and polynucleotides useful for chrome identification, tissue typing, gene therapy, in chromosome and gene mapping, or as molecular weight markers.
 Eaton DL, Ferrara N, Filvaroff E;
A, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
 Length 440;
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 35.5%; Score 150; DB 6; L6 100.0%; Pred. No. 7.7e-135; ive 0; Mismatches 0;
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 Claim 12; Fig 24; 172pp; English
 22-MAY-2000; 2000WO-US014042.
28-JUL-2000; 2000WO-US020710.
01-DEC-2000; 2000WO-US032678.
 28-FEB-2001; 2001WO-US006520.
25-MAY-2001; 2001US-00866028.
2000WO-US008439
 Baker KP, Botstein D, Ea
Gerritsen ME, Goddard A,
Hillan KJ, Kljavin IJ, N
 30-JUN-2003 (first entry)
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Matches 150; Conservative
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N-PSDB; ABX96814.
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16-MAY-1998

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152

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 Human; antinflammatory; antiarteriosclerotic; cardiant; gynecological; anti-HIV; cytostatic; antidiabetic; BMP-agonist; BMP-Antagonist; cytokine-agonist; gene-Therapy; cytokine-antagonist; gene-Therapy; inflammatory disease; organ failure; atherosclerosis; cardiac injury; infertility; birth defect; premature aging; AIDS; cancer; diabetic complication.
 New isolated PRO polypeptide and encoding nucleic acids, useful for the diagnosis and treatment of disorders such as inflammatory disease, atherosclerosis, cardiac injury, infertility, AIDS, cancer and diabetic complications.
 Eaton DL, Ferrara N, Filvaroff E;
,, Godowski PJ, Grimaldi JC, Gurney ,
Napier MA, Roy MA, Tumas D, Wood W
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 Novel human secreted protein PR0355
 97US-0069425P.
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 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 Human, gene therapy, chondrocyte stimulation, TNF-alpha release, chondrocyte proliferation, chondrocyte differentiation, tumour detection,
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
The invention describes a novel isolated PRO polypeptide. The methods a compositions of the present invention are useful for the diagnosis and treatment of disorders such as inflammatory disease, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, diabetic complications and mutations in general. This is the amino acid sequence of a novel human secreted PRO protein
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10-MAR-1998
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New secreted and transmembrane PRO polypeptides and nucleic acids, useful in gene therapy, chromosome identification, tissue typing, for detecting the presence of tumor in a mammal, or as hybridization probes in gene mapping.
 The invention describes a novel isolated PRO polypeptide. The PRO polypeptide or anti-PRO antibody is useful for preparing a medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody. The PRO nucleotide sequences are useful as hybridisation probes in chromosome and gene mapping, or in generating antisense RNA DNA. PRO nucleic acide are also useful in preparing PRO polypeptides, in assays to identify other proteins or molecules involved in binding
 Gurney AL;
 Godowski PJ,
 Baker KP, Chen J, Desnoyers L, Goddard A, Godo
Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 707pp; English.
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 6-JUN-1998
 reaction, to generate transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents, for chromosome identification, and tissue typing. The PRO polypeptides and nucleic acid molecules are also useful for detecting the presence of tumour in a mammal, stimulating proliferation or defection of chondrocyte cells, stimulating the release of tumour necrosis factor-alpha from human blood, in gene therapy, or as molecular weight markers for protein electrophoresis purposes. The anti-PRO antibodies may be used in diagnostic assays for PRO, or for the affinity purification of PRO from recombinant cell culture or natural sources. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide
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 SAAALIPTGDGONLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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100.0%; Pred. No. 7.7e-135;
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| 705<br>705<br>705<br>705<br>705<br>805<br>805<br>805<br>805<br>805<br>805<br>805                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                              |
| 700000000000000000000000000000000000000                                                                                                                              | 27-MAR.1998;<br>31-MAR.1998;<br>31-MAR.1998;<br>01-APR.1998;<br>08-APR.1998;<br>08-APR.1998;<br>15-APR.1998;<br>21-APR.1998;<br>22-APR.1998;<br>22-APR.1998;<br>29-APR.1998;<br>29-APR.1998;<br>29-APR.1998;<br>05-MAY.1998;<br>07-MAY.1998;<br>07-MAY.1998;<br>07-MAY.1998;<br>07-MAY.1998;<br>07-MAY.1998;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | , , , , , , , , , , , , , , , , , , ,                                                                                                                                                                                        |
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This invention relates to a nucleotide sequence encoding an isolated secreted and/or transmembrane protein. The nucleotide sequences of the invention may have antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HIV, cytostatic and antidiabetic activities and may be used in gene therapy. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, cancer, of diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA probes, in the polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing. The present sequence represents a protein encoded by the nucleic acids of the
 Human, PRO; secreted protein; transmembrane protein; cytostatic; antiarthritic; osteopathic; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; curvical tumour; liver tumour; TNF-alpha release; arthritis; tumour necrosis factor alpha; chondrocyte cell; bone disorder; cartilage disorder; sports injury.
 New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Baton DL, Ferrara N, Filvaroff E;
,, Godowski PJ, Grimaldi JC, Gurney AL;
Napier MA, Roy MA, Tumas D, Wood WI;
 35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135; cive 0; Mismatches 0; Indels
 Human secreted/transmembrane protein, SEQ ID 34.
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 ABU65585 standard; protein; 440 AA
 Claim 1; Fig 24; 173pp; English
 22-MAY-2000; 2000WO-US014042.
28-UUL-2000; 2000WO-US020710.
01-DEC-2000; 2000WO-US032678.
28-FEB-2001; 2001WO-US065520.
25-MAY-2001; 2001US-00866028.
 Botstein D, Ea
1E, Goddard A,
 (first entry)
 Matches 150; Conservative
 Kljavin IJ,
 (GETH) GENENTECH INC
 2003-174140/17.
 Query Match
Best Local Similarity
 WPI; 2003-174140/
N-PSDB; ABX77101.
 Sequence 440 AA;
 Gerritsen ME,
 Homo sapiens
 19-MAY-2003
 Hillan KJ,
 Baker KP,
 invention
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 136
 RESULT
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 75
 Human, antiinflammatory, antiarteriosclerotic, cardiant, anti-infertility, anti-HIV, cytostatic, antidiabetic, transmembrane; antiinflammatory; anti-HIV; antiarteriosclerotic, cardiant; infertility; anti-infertility, cytostatic; antidiabetic; gene therapy; birth defect; inflammatory disease; organ failure; atherosclerosis; cardiac injury; premature aging; AIDS; cancer; diabetic complication.
 91
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
 ö
 Length 440;
 0; Indels
 Score 150; DB 6; Le
Pred. No. 7.7e-135;
 35.5%; Sco...
100.0%; Pred. No. ...
... 0; Mismatches
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 ABUS7246 standard; protein; 440 AA
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98US-0101738P.
98US-0101739P.
98US-0101922P.
98US-0101786P.
98US-0101786P.
98US-0102240P.
98US-0102310P.
98US-0102311P.
98US-0102571P.
98US-0102571P.
98US-0102564P.
98US-0102664P.
 2000WO-US003565.
2000WO-US004414.
2000WO-US005841.
2000WO-US008439.
 98WO-US019330.
98WO-US025108.
99WO-US012252.
 99WO-U3028301.
 99WO-US021090
 99WO-US028313
 99WO-US028409
 99WO-US030095
 2001US-00943762
 150; Conservative
 Human PRO355 protein.
 Similarity
 US2002142958-A1.
 11-FEB-2000; 22-FEB-2000; 202-MAR-2000; 30-MAR-2000; 200-MAR-2000; 200-MAR-2000; 200-MAR-2000; 200-MAR-2000; 200-MAR-2000; 2000; 200-MAR-2000;
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01-OCT-1998;
 30-AUG-2001;
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01-DEC-1998;
22-JUN-1999;
 15-SEP-1999;
30-NOV-1999;
30-NOV-1999;
 16-DEC-1999;
 04-APR-2003
 01-DEC-1999;
 01-OCT-1998;
 06-OCT-1998;
 03-OCT-2002
 ABU57246;
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 75
 91
 Human; secreted and transmembrane protein; PRO; TNF-alpha; tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour.
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larity 100.0%; Pred. No. 7.7e-135;
Conservative 0; Mismatches 0;
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Baker KP,

Pan J,

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Human; secreted protein; transmembrane protein; PRO; antiarthritic; vulnerary; tumour necrosis factor-alpha; chondrocyte cell proliferation; ohondrocyte cell differentiation; tumour; adrenal tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; cervical tumour; liver tumour; bone disorder; cartilage disorder;
 Human secreted/transmembrane protein, PRO355.
ABU55952 standard; protein; 440 AA.
 98US-0080107P.
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97WO-US020069
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 97US-00661
 arthritis; sports injury
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 07-MAY-1998
 30-JAN-2003
 1-MAR-1998
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 NOV-1997
 8-DEC-1997
 27-MAR-1998
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 05-MAY-1998
 ABUS5952;
 12-DEC-19
17-DEC-19
 05-NOV-1
 24 - NOV - 1
 DEC-
The invention discloses human nucleic acids encoding secreted and transmembrane (PRO) polypeptides, with or without their associated signal competition. Also disclosed is an antibody that specifically binds to the PRO polypeptide, a method for stimulating the release of tumour necrosis factor alpha (TNR-alpha) from human blood by contacting the blood with a CRO polypeptide, a method for stimulating the proliferation or differentiation of chodrocyte cells by contacting the blood with a PRO contactine a method for detecting the presence of a tumour in a mammal an oligonucleotide probe derived from any of the PRO nucleotide con an oligonucleotide probe derived from any of the PRO nucleotide and gene mapping, in generating antiense RNA and DNA, in preparing PRO polypeptides by recombinant techniques and in gene therapy (e.g. for replacement of defective gene). The PRO polypeptides are useful as concented and gene method as differentiation electrophoresis purposes, for creplacement of defective gene). The PRO polypeptides are useful as concented identification, as chromosome markers, as therapeutic agents, for stimulating the proliferation or differentiation of chondrocytes and detecting the presence, prevention and/or treatment of a tumour, such as adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour. The PRO polypeptides and nucleic acids may also be used diagnostically for in electronic format directly from USPTO at this patent can also be betained concented by an encaperation betained and and an encape of the concented by an encape of the concented by an encape of the concented by an encape by and processing the proliferation or differentiation or dispense of the concented by any and directly from USPTO at this patent can also be betained and an encape because by the proliferation by the proliferation by the proliferation by the proliferation or dispense by the proliferation by the proliferation or dispense by the proliferation or dispense by the proliferation or dispense by the proliferation
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 SAAALI PIGDGQNLFIKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 Three hundred and five nucleic acids encoding PRO polypeptides, useful for the manufacture of a medicament for diagnosing or treating tumor or for measuring or detecting expression of an associated gene.
 ', Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;
Smith V, Watanabe CK, Wood WI, Zhang Z;
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 Claim 11; Fig 34; 699pp; English
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 05-JUN-2000; 2000US-0209832P.
28-FEB-2001; 2001WO-US006520.
15-JAN-2002; 2002US-00052586.
 26-JUL-2002; 2002US-00205907
 (GETH) GENENTECH INC.
 WPI; 2003-479876/45.
 N-PSDB; ACD21185.
 Sequence 440 AA;
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 Homo sapiens.
 20-MAR-2003
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RESULT 67

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 8-JUN
 Human, PRO; cytostatic, chromosome mapping; gene mapping;
protein electrophoresis, tumour necrosis factor-alpha, TNF-alpha, blood;
chondrocyte differentiation; chondrocyte proliferation; tumour.
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 17-JUN-2002;
 16-MAY-2003
 13-FEB-2003
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 28-JUN-2002; 2002US-00184635
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 Human PRO polypeptide #17
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 Homo sapiens.
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Human, PRO, secreted polypeptide, transmembrane polypeptide, cytostatic, tumour necrosis factor-alpha; TNP-alpha; blood; tumour, chondrocyte cell; cancer; adrenal; lung; colon; breast; prostate; rectum; cervix; liver.

| 8US-00846439<br>8US-00855809<br>8US-00855809<br>8US-00855809<br>8US-0086039<br>8US-0086039<br>8US-0086039<br>8US-0087039<br>8US-0087039<br>8US-0087039<br>8US-0087039<br>8US-0087039 | 98035 - 0088323 P. 98035 - 0088323 P. 98035 - 0088326 P. 98035 - 0088212 P. 98035 - 0088212 P. 98035 - 0088213 P. 98035 - 008823 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008834 P. 98035 - 008934 P. 98035 - 008934 P. 98035 - 008934 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P. 98035 - 0089353 P.                                                                                 | 8025 0090429F<br>8035 0090429F<br>8035 0090444P<br>8035 0090444P<br>8035 0090440F<br>8035 0090690F<br>8035 ---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
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| 8US-0096757<br>8US-0096766<br>8US-0096817<br>8US-0096891<br>8US-0096949<br>8US-0096959<br>8US-0097052<br>8US-0097052<br>8US-00979554<br>8US-00979554 | 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 | 8US -0101475<br>8US -0101475<br>8US -0101739<br>8US -0101739<br>8US -0101739<br>8US -0101786<br>8US -0102207<br>8US -0102240<br>8US -0102240<br>8US -0102240<br>8US -0102240<br>8US -0102240<br>8US -0102240<br>8US -0102330<br>8US -0102330<br>8US -0102330<br>8US -0102340<br>8US -0102687                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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Query Match 35.5%; Score 150; DB 6; Length 440; Best Local Similarity 100.0%; Pred. No. 7.7e-135; Matches 150; Conservative 0; Mismatches 0; Indels

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 Human, PRO, secreted protein, transmembrane protein,
extracellular domain, tumour necrosis factor-alpha; TNF-alpha,
chondrocyte, proliferation, differentiation, cartilage disorder,
 Human secreted polypeptide PRO355, SEQ ID NO:34
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 99WO-US012252
 99US-0145698P
 2000WO-US004414
 2001WO-US006520
 (first entry)
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02-MAR-2000
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15-MAR-2000
 22-MAY-2000
 ABR69979;
 RESULT 71
 ABR69979
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adrenal tumour, lung tumour, colon tumour, breast tumour, prostate tumour, rectal tumour, cervical tumour or liver tumour) in a mammal. This method involves comparing the level of expression of the PRO polypeptide in test and control samples, where a higher level of expression of PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of a tumour. The PRO polypeptides are additionally useful for in drug screening to identify agonists and antagonists of PRO polypeptides. PRO nucleic acids are useful as hybridistation probes (for isolation of cDNA molecules), in chromosome and gene mapping, in the generation of antisense RNA and in gene therapy. The nucleic acids can also be used for mapping genes encoding
 ABR69963-ABR70267) and nucleic acids encoding them (ACC90994-ACC91298). The invention also relates to sequences at least 80% identical to the PRO
 stimulating the proliferation or differentiation of chondrocytes and as such may be used in the treatment of various bone and/or cartilage disorders such as arthritis and sports injuries. The PRO polypeptides may be used in a method for detecting the presence of a tumour (e.g., an
 nucleic acid and polypeptide sequences of the invention, recombinant vectors and host cells comprising a PRO nucleic acid, a method for the recombinant production of a PRO polypeptide, antibodice against a PRO polypeptide, and fusion proteins comprising a PRO polypeptide. Nucleic acids encoding PRO polypeptides of the invention were initially identified via homology screening using consensus sequences based on the extracellular domain sequences of interest were identified using oligonucleotides based on the consensus sequences, and cDNA clones were isolated and characterised. The PRO polypeptides are useful for stimulating release of tumour necrosis factor-alpha (TNR-alpha) from human blood and may thus be used in the treatment of conditions in which enhanced TNR-alpha release would be beneficial. They are also useful for the human blood and may thus be used in the treatment of conditions in which enhanced TNR-alpha release would be beneficial. They are also useful for the human blood and may thus be used in the treatment of conditions in which enhanced TNR-alpha release would be beneficial.
 therapeutically useful compounds. Sequences ABR69963-ABR70267 represent the human PRO secreted/transmembrane polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html
 invention relates to human PRO secreted/transmembrane polypeptides
 Gurney AL;
 PRO polypeptides, for genetic analysis of individuals with genetic disorders, and for generating either transgenic animals or knock-out animals which are useful in the development and screening of
 ಥ
 New secreted and transmembrane PRO polypeptide useful in preparing medicament for treating a condition that is responsive to the PRO polypeptide or anti-PRO antibody.
 35.5%; Score 150; DB 6; Length 440; 100.0%; Pred. No. 7.7e-135;
 Godowski PJ,
 KP, Chen J, Desnoyers L, Goddard A, Godor
Smith V, Watanabe CK, Wood WI, Zhang Z;
 100.0%; Pred.
 Claim 11; Fig 34; 707pp; English.
 2001WO-US021066.
2001WO-US021735.
 29-AUG-2001; 2001WO-US027099
15-JAN-2002; 2002US-00052586
2001WO-US017800
 (GETH) GENENTECH INC
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Gaps

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Indels

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Matches 150; Conservative

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chondrocyte cell, colon, breast, prostate, rectum, cervix, liver.
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 21-JUN-2002; 2002US-00176758
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 Human PRO polypeptide #17.
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 07-AUG-2003
 Homo sapiens.
 24-0CT-1997;
28-0CT-1997;
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Matches 150
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transmembrane polypeptides on antibody that specifically binds to a PRO invention also relates to an antibody that specifically binds to a PRO polypeptide a method for stimulating the release of tumour necrosis factor alpha (TMF-alpha) from human blood by contacting the blood with a PRO polypeptide and a method for stimulating the proliferation or differentiation of chondrocyte cells by contacting the cells with a PRO polypeptide. The polypeptides and polynucleotides are useful for detecting the presence of a tumour, such as an adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumour, and for treating such tumours. The polynucleotides are useful as hybridisation probes, in chromosome and gene mapping and in generating antisense RNA or DNA. The polypeptides are useful in tissue typing. Sequences ABOO1431.

Colypeptides are useful in tissue typing. Sequences ABOO1431.

ABOO1741 represent human PRO polypeptides of the invention. Note: The sequence data for this patent is also available in electronic format from
 Three hundred and five nucleic acids encoding secreted and transmembrane polypeptides, designated as PRO, useful for detecting the presence of, or treating tumor, e.g. adrenal, lung, colon, breast, prostate, rectal, cervical or liver tumor.
 Godowski PJ, Gurney AL;
 The invention relates to human PRO polypeptides (secreted and
 Desnoyers L, Goddard A, Godo
stanabe CK, Wood WI, Zhang Z;
 Claim 11; Fig 34; 707pp; English.
 Smith V, Watanabe CK,
 17-MAY-2000; 2000W0-US013705.
22-MAY-2000; 2000W0-US014042.
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2000WO-US005004.
2000WO-US005601.
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2000WO-US008439.
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99WO-US021090.
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 99WO-US028301
99WO-US028551
 2000WO-US004342
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 (GETH) GENENTECH INC.
 WPI; 2003-341328/32.
 Chen J,
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chondrocyte cell; tumour; adrenal; kidney; lung; colon; breast; prostate;
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 91
 Human; PRO; secreted protein; transmembrane protein; extracellular domain; tumour necrosis factor-alpha; rmr-alpha; chondrocyte; proliferation; differentiation; cartilage disorder; bone disorder; arthritis; sports injury; cancer; tumour; diagnosis; adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix; liver; drug screening; transgenic animal; genetic analysis; antiarthritic; vulnerary; gene therapy.
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
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 tch 35.5%; Score 150; DB 6; Le sal Similarity 100.0%; Pred. No. 7.7e-135; 150; Conservative 0; Mismatches 0;
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98US-0103449P.
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9703-0066772P.
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US-10-180-559-34
US-10-181-000-34
US-10-183-010-34
US-10-184-614-34
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US-10-184-632-34
US-10-184-636-34
 US-10-184-650-34
US-10-184-651-34
 US-10-187-600-34
 US-10-187-601-34
 US-10-176-990-34
 US-10-184-640-34
 US-10-187-588-34
 US-10-187-741-34
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ALIGNMENTS

RESULT 1 US-09-778-510-22

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PINGTIYFRDFRPLKDSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDFPQESYTT1 120
 361 GVVAVVVFAMLCLLIILGRYFARKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420
 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
 241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
 301 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTGAGEEGTIGAVDHAVIG 360
 361 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGQNNSEEKK 420
 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
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 1 AAPPGLRIKLILLILISAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 Gaps
 .
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 Length 423;
 Indels
 ö
 DB 16;
 APPLICANT: Baum, Peter R.
APPLICANT: Fanalow III, William C
TITLE OF INVENTION: MOLECULES DESIGNATED LDCAM
FILE SHERENCE: 2873-US
CURRENT APPLICATION NUMBER: US/10/622,237
CURRENT APPLICATION NUMBER: US/09/778,187B
PRIOR FILING DATE: 2001-02-06
PRIOR PILING DATE: 2001-02-06
PRIOR PILING DATE: 1999-08-05
PRIOR PILING DATE: 1998-08-07
PRIOR PILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Petentin version 3.1
SEQ ID NO 4
 0; Mismatches
 Score 423; I
Pred. No. 0;
 ; Sequence 4, Application US/10622237; Publication No. US20040204568A1; GENERAL INFORMATION:
 Query Match
Best Local Similarity 100.0%;
Matches 423; Conservative 0
 ORGANISM: mus musculus
 EYF 423
 421 EYF 423
 LENGTH: 423
 RESULT 4
US-10-622-237-4
 US-10-622-237-4
 61
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 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
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 YTVTSQLMLKVHKEDDGVPVI CQVEHPAVTGNLQTQRYLEVQYKPQVHI QMTYPLQGLTR
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 1 AAPPGLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 Gaps
 Gaps
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 ö
 DB 14; Length 423;
 Length 423;
 Indels
 Indels
 ;
0
 ö
 DB 9;
 ; Score 423; D; Pred. No. 0; 0; Mismatches
 0; Mismatches
 TITLE OF INVENTION: Molecules Designated B7L FILE REFERENCE: 2844-US CURRENT APPLICATION NUMBER: US/10/302,041 CURRENT FILING DATE: 2002-11-21 PRIOR FILING DATE: 2001-02-07 PRIOR PILING DATE: 2001-02-07 PRIOR APPLICATION NUMBER: PG/US99/17906 PRIOR APPLICATION NUMBER: PG/US99/17906 PRIOR PILING DATE: 1999-08-05 PRIOR PILING DATE: 1998-08-05 PRIOR PILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR FILING DATE: 1998-08-07 SPRIOR PILING DATE: 1998-08-07 SPRIOR PILING DATE: 1998-08-07 SPRIOR PILING DATE: 1998-08-07 SPRIOR PILING DATE: 1998-08-07 SPRIOR PILING DATE: 1998-08-07 SPRIOR DATE: 1998-08-07 SPRIO
 Score 423;
Pred. No. 0;
 ; Sequence 22, Application US/10302041; Publication No. US20030144478A1; GENERAL INFORMATION:
 100.0%;
 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 423; Conservative 0
 SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
 423; Conservative
 ORGANISM: Mus musculus US-10-302-041-22
 musculus
 Similarity
 423
 EYF 423
 TYPE: PRT
; ORGANISM: mus
US-09-778-1878-4
 RESULT 3
US-10-302-041-22
 LENGTH: 423
 241
 361
 61
 61
 121
 181
 181
 241
 301
 361
 421
 421
 Query Match
Best Local 8
 Matches
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 240
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 121 TVLVPPRNIMIDIQKOTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM 180
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 261
 241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
 APPLICANT: Padigaru, Muralidhara
TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
TITLE OF INVENTION: Using the Same
 9
 81
 22 AAPPGLRIRLILLILSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI
 142 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
 181 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 202 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 1 AAPPGLRLKLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 82 PNRQTIYFRDFRPLKDSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTI
 Gaps
 ..
0
 Length
 Indels
 100.0%; Score 423; DB 15;
100.0%; Pred. No. 0;
ive 0; Mismatches 0;
 TITLE OF INVENTION: USING LIE COMME
FILE REFERENCE: 21402-211
CURRENT APPLICATION NUMBER: US/10/015,115
CURRENT FILING DATE: 2002-09-23
PRIOR PILING DATE: 2000-11-13
PRIOR PLING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: 60/249,598
PRIOR APPLICATION NUMBER: 60/246,200
PRIOR APPLICATION NUMBER: 60/266,127
PRIOR PILING DATE: 2001-01-26
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-02
PRIOR PILING DATE: 2001-02-03
PRIOR PILING DATE: 2001-02-16
PRIOR PILING DATE: 2001-07-11
PRIOR PILING DATE: 2001-07-13
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PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
PRIOR PILING DATE: 2001-07-31
 Sequence 112, Application US/10015115 Publication No. US20030207800A1 GENERAL INFORMATION:
 Guo, Xiaojia
Kekuda, Ramesha
Gangolli, Esha A
Shimkets, Richard A
Taupier, Raymond J
Li, Li
 Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
 APPLICANT: Malyankar, Uriel M
 Query Match 100.
Best Local Similarity 100.
Matches 423; Conservative
 ORGANISM: Mus musculus
US-10-015-115-112
 421 EYF 423
 EYF 423
 US-10-015-115-112
 APPLICANT:
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 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGITR 240
 240
 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
 361 GVVAVVVPAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGONNSEEKK 420
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 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
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 Sequence 4, Application US/10898408
Publication No. US20050058642A1
GENERAL INFORMATION:
APPLICANT: GALIBERT, Laurent J.
TITLE OF INVENTION:
TITLE OF INVENTION: ANTAGONISTS AND AGONISTS OF LDCAM AND METHODS OF USE
FILE REFERENCE: 3467-A
CURRENT APPLICATION NUMBER: US/10/898,408
CURRENT FILING DATE: 2004-07-23
FRIOR APPLICATION NUMBER: 60490,027
FRIOR FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.2
 YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
YTVTSQLMLKVHKEDDGVPVICQVEHPAVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTR
 1 AAPPGLRLALLILLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
 1 AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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 DB 17; Length 423,
 Indels
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 100.0%; Score 423; D
100.0%; Pred. No. 0;
ive 0; Mismatches
 Best Local Similarity 100.
Matches 423; Conservative
 TYPE: PRT ORGANISM: mus musculus
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EYF 423
 EYF 423
 LENGTH: 423
 RESULT 5
US-10-898-408-4
 US-10-898-408-4
 241
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 SEQ ID NO 4
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 Query Match
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241 EGDAFELTCEAIGKPQPVMVTWVRVDDEMPQHAVLSGPNLFINNLNKTDNGTYRCEASNI 300
 ELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVN 120
 181 AVTGNLQTQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDD 240
 ELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQKDTAVEGEEIEVN 147
 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP 207
 208 AVTGNLQIQRYLEVQYKPQVHIQMTYPLQGLTREGDAFELTCEAIGKPQPVMVTWVRVDD 267
 180 TVLVPPRNLMIDIQKDTAVEGEEIEVNCTAMASKPATTIRWFKGNKELKGKSEVEEWSDM
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 CTAMASKPATTIRWFKGNKELKGKSEVEEWSDMYTVTSQLMLKVHKEDDGVPVICQVEHP
 28 NLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLKDSRFQLLNFSSS
 Gaps
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 Indels
 in Cancer
 DB 16;
 Sequence 145, Application US/10417375
Publication No. US20040219528A1
GENERAL INCORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in
FILE REFERENCE: 529452001600
CURRENT APPLICATION UNBER: US/10/417,375
CURRENT FILING DATE: 2003-04-15
NUMBER OF SEQ ID NOS: 176
SOFTMARE: FastSEQ for Windows Version 4.0
 Query Match 62.4%; Score 264; DB 16;
Best Local Similarity 100.0%; Pred. No. 6e-228;
Matches 264; Conservative 0; Mismatches C
 APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REFERENCE: PF489P2
CURRENT APPLICATION NUMBER: US/09/984,130
PRIOR APPLICATION NUMBER: 60/243,792
 EMPQHAVLSGPNLFINNLNKTDNG 264
 Sequence 39, Application US/09984130; Publication No. US20030055231A1; GENERAL INFORMATION:
 TYPE: PRT
ORGANISM: Mus musculus
US-10-417-375-145
 US-10-417-375-145
 US-09-984-130-39
 148
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 ### APPLICANT: iaupler, Kaymonu o

APPLICANT: Taupler, Kaymonu o

APPLICANT: Padigaru, Muralidhara

APPLICANT: Padigaru, Muralidhara

ITILE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of

TITLE OF INVENTION: Using the Same

FILE REPERENCE: 21402-21

CURRENT APPLICATION NUMBER: 60/249,153

PRIOR APPLICATION NUMBER: 60/249,598

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2001-01-02-02

PRIOR FILING DATE: 2001-01-02-06

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR PLING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-02-16

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-07-31

PRIOR FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 205

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 VGKAHSDYMLYVYDPPTTIPPPTTTTTTTTTTTTTTTTTTGSRAGEEGTIGAVDHAVIG 360
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 GVVAVVVFAMLCLLIILGRYFARHKGTYFTHEAKGADDAADADTAIINAEGGGNNSEEKK 441
 60 AAPPGLRLRLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN 119
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61 PNRQTIYFRDFRPLKDSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTI 120
 1 AAPPGLRLRLLLLLLSAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLN
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 Length 494;
 0; Indels
 Pred. No. 8.3e-298;
 DB 15;
 100.0%; Pred. nc.
 80.9%; Score 342;
 Sequence 113, Application US/10015115
Publication No. US20030207800A1
GENERAL INFORMATION:
 Shenoy, Suresh G
Spytek, Kimberly A
Zerhusen, Bryan D
Patturajan, Meera
Guo, Xiaojia
Kekuda, Ramesha
Gangolli, Esha A
Shimkets, Richard A
 Taupier, Raymond J
 Best Local Similarity 100.
Matches 342; Conservative
 ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-015-115-113
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 EYF 444
 361
 120
 382
 421
 Query Match
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
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 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: DiBlasio-Smith, Elizabeth
APPLICANT: Widom, Angela
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: 00766.000101
 0; Gaps
 Query Match 35.5%; Score 150; DB 16; Length 414; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels (
 Sequence 148, Application US/10417375
Publication No. US20040219528A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc Malandro
TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
FILE REPERENCE: S29452001600
CURRENT APPLICATION UNMERR: US/10/417,375
CURRENT FILING DATE: 2003-04-15
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 FILE KEFEKEMENE UO'66.UUUJU.

CURRENT PRILING DATE: 2004-04-09

PRIOR APPLICATION NUMBER: US 09/306,111

PRIOR PILING DATE: 1999-05-06

PRIOR PILING DATE: 1999-05-06

PRIOR PILING DATE: 1998-05-07

PRIOR PILING DATE: 1998-06-07

PRIOR PILING DATE: 1998-06-02

PRIOR PILING DATE: 1998-06-02

PRIOR PILING DATE: 1998-07-22

PRIOR PILING DATE: 1998-07-31

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PRIOR PILING DATE: 1998-07-31

PRIOR PILING DATE: 1998-07-31

PRIOR PILING DATE: 1998-08-10

PRIOR PILING DATE: 1998-08-11

NUMBER OF SED ID NOS: 180

SEQ ID NO 62

LENGTH: 414
 Merberg, David
Treacy, Maurice
Agostino, Michael J.
Steininger II, Robert J.
Bowman, Michael R.
DiBlasio-Smith, Elizabeth
 Sequence 62, Application US/10821273
Publication No. US20040248256A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCOy, John M.
APPLICANT: LaVallie, Edward R.
APPLICANT: COllins-Racie, Lisa A.
 RESULT 12
US-10-417-375-148
 US-10-821-273-62
 엄
 d
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSLSDEGRYFCQLYTDPPQESYTITVLVPPRNLMIDIQK 153
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 34 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 ö
 35.5%; Score 150; DB 10; Length 364; 100.0%; Pred. No. 9.4e-126; tive 0; Mismatches 0; Indels
 DB 10; Length 364;
 0; Indels
 35.5%; Score 150; DB 10; L
100.0%; Pred. No. 9.4e-126;
iive 0; Mismatches 0;
 Sequence 39, Application US/09836353A
Publication No. US20030129685A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 12 Human Secreted Proteins
FILE REPRENCE: PF48991
CURRENT FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/198,407
PRIOR FILING DATE: 2000-04-19
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1999-10-27
PRIOR APPLICATION NUMBER: 60/105,971
PRIOR FILING DATE: 1999-10-27
NUMBER: OF SEQ. ID NOS: 147
SOFTWARE: PATENTING DATE: 1999-10-27
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 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
PRIOR FILING DATE: 2000-10-30
PRIOR APPLICATION WUMBER: 09/836,353
PRIOR FILING DATE: 2001-04-16
PRIOR FILING DATE: 2000-04-19
PRIOR PLICATION NUMBER: 60/198,407
PRIOR PLICATION NUMBER: 60/198,407
PRIOR APPLICATION NUMBER: PCT/US99/25031
PRIOR PLING DATE: 1999-10-27
PRIOR PLING DATE: 1998-10-27
PRIOR PLING DATE: 1998-10-28
NUMBER OF SEC ID NOS: 149
SOFTWARE: PATENTIN VET. 2.0
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
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US-09-836-353A-39
 US-09-836-353A-39
 US-09-984-130-39
 SEQ ID NO 39
LENGTH: 364
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152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181

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us-10-622-237-4.oligo.rapb

NUMBER OF SEQ ID NOS: 176 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 148

LENGTH

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2548PICI CURRENT APPLICATION: NUMBER: US/09/944,449

CURRENT FILING DATE: 2001-09-26

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: 2001-05-25

PRIOR PLING DATE: December 13, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

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PRIOR PLING DATE: December 11, 1997
 FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
 APPLICATION NUMBER: PCT/US98/19330
 R FILING DATE: December 18, 1997
R APPLICATION NUMBER: 60/070,440
R FILING DATE: January 5, 1998
R APPLICATION NUMBER: 60/074,086
R FILING DATE: PEDRUARY 9, 1998
RR APPLICATION NUMBER: 60/074,092
 PILING DATE: December 1, 1998
APPLICATION NUMBER: 09/216,021
FILING DATE: December 16, 1998
 FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
 FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
 APPLICATION NUMBER: 60/113,296
 Sequence 61, Application US/0994449
Patent No. US20020102647A1
GENERAL INFORMATION:
 FILING DATE: February 9, 1998 APPLICATION NUMBER: 60/075,94
 FILING DATE: December 12, 1993
APPLICATION NUMBER: 60/069,69
 FILING DATE: December 17, 19
APPLICATION NUMBER: 60/069,8
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 APPLICATION NUMBER: 60/069,
 FILING DATE: December 16, 1 APPLICATION NUMBER: 60/069,
 FILING DATE: December 17, 1 APPLICATION NUMBER: 60/068,
 Grimaldi, Christopher
 FILING DATE: July 28, 1999
 FILING DATE: December 16
 FILING DATE: December 16
 Ferrara, Napoleone
Filvaroff, Ellen
 Baker, Kevin
Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 Godowski, Paul
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 FILING DATE:
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 153
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
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 Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 120
 Query Match 35.5%; Score 150; DB 9; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 0; Indels
 35.5%; Score 150; DB 16; L 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 CURRENT APPLICATION NUMBER: US/09/866,028
CURRENT FILING DATE: 2001-05-25
 Sequence 61, Application US/09866028
Patent No. US20020058309A1
GENERAL INFORMATION:
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Roy, Margaret
Tumas, Daniel
Wood, William
 Kljavin, Ivar
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-375-148
 Napier, Mary
 CRGANISM: Homo Sapien US-09-866-028-61
 US-09-866-028-61
 SEQ ID NO 61
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 APPLICANT:
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2548PIC1
 FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
FILING DATE: September 15, 1999
APPLICATION NUMBER: PCT/US99/28409
FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/29313
 FILING DATE: No. US20020110859Alember 30, 1999
APPLICATION NUMBER: PCT/US99/28301
 CURRENT APPLICATION NUMBER: US/09/44,457
CURRENT FILING DATE: 2001-09-26
PRIOR PILING DATE: 2001-09-26
PRIOR PLILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: DOCEMBER: 60/067,411
PRIOR PLILANG DATE: DECEMBER 1, 1997
PRIOR PLILANG DATE: DECEMBER 1, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PLILANG DATE: DECEMBER 11, 1997
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PRION APPLICATION NUMBER: 60/068 017
PRION APPLICATION NUMBER: 60/064 40
PRION APPLICATION NUMBER: 60/074, 40
PRION FILING DATE: January 5, 1998
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PRION FILING DATE: February 9, 1998
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PRION PRILING DATE: February 25, 1998
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PRION FILING DATE: December 16, 1998
 APPLICATION NUMBER: PCT/US00/03565
FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
 FILING DATE: March 3, 1999
APPLICATION NUMBER: PCT/US99/12252
 R FILING DATE: December 1, 1996
R PAPLICATION NUMBER: 09/216,021
R FILING DATE: December 16, 1998
R APPLICATION NUMBER: 09/218,517
R APPLICATION NUMBER: 09/254,311
RR APPLICATION NUMBER: 09/254,311
 FILING DATE: February 22, 2000
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,870
APPLICATE: December 17, 1997
APPLICATION NUMBER: 60/069,873
 FILING DATE: December 16, 1999
 FILING DATE: December1
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 76 DSRFQLLNFSSSBLKVSLTNVSISDBGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
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 35.5%; Score 150; DB 9; Length 440;
 0; Indels
IOR APPLICATION NUMBER: 09/218,31,
IOR FILING DATE: December 22, 1998
IOR FILING DATE: March 3, 1999/21252
ALOR FILING DATE: March 3, 1999/21252
ALOR FILING DATE: March 3, 1999/21252
ALOR FILING DATE: JOHN SPECIFICATION NUMBER: PCT/US99/21090
RIOR APPLICATION NUMBER: PCT/US99/28409
RIOR APPLICATION NUMBER: PCT/US99/28409
RIOR APPLICATION NUMBER: PCT/US99/28131
PRIOR FILING DATE: No. US20020102647Alember 30, 1999
PRIOR FILING DATE: No. US20020102647Alember 30, 1999
PRIOR FILING DATE: December 1, 1999
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PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US09/03565
PRIOR PELING DATE: PEDLARY 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/036691
PRIOR FILING DATE: PEDLARY 2, 2000
PRIOR PELING DATE: PEDLARY 2, 2000
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PRIOR PRILING DATE: December 1, 2000
PRIOR PRILING DATE: December 1, 2000
PRIOR PRILING DATE: December 1, 2000
PRIOR PRILING DATE: PEDLARY 28, 2001
PRIOR FILING DATE: PEDLARY 28, 2001
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PRIOR FILING DATE: PEDLARY 28, 2001
 Pred. No. 1.1e-125;
 100.0%; Pred.
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 61, Application US/09944457
Patent No. US20020110859A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botesin, David
APPLICANT: Eaton, Dan
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Gurney, Austin
Hillan, Kenneth
 Kljavin, Ivar
 TYPE: PRT
ORGANISM: Homo Sapien
 JS-09-944-449-61
 US-09-944-457-61
 APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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 APPLICANT:
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PRIOR PILLING DATE: DECEMBER 60/146, 220

PRIOR PILLING DATE: JULY 28, 1999, 28

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PRIOR PELICATION NUMBER: PCT/US98/19310

PRIOR PELICATION NUMBER: PCT/US98/25108

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PRIOR PELICATION NUMBER: 09/216,021

PRIOR PELICATION NUMBER: 09/216,129

PRIOR PELICATION NUMBER: 09/218,311

PRIOR APPLICATION NUMBER: 09/218,311

PRIOR APPLICATION NUMBER: PCT/US99/21090

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PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR APPLICATION NUMBER: PCT/US99/21030

PRIOR APPLICATION NUMBER: PCT/US99/21313

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PRIOR AP
 R FILING DATE: December 17, 1997
R APPLICATION NUMBER: 60/069,873
R FILING DATE: December 17, 1997
R APPLICATION NUMBER: 60/068,017
R FILING DATE: December 18, 1997
R APPLICATION NUMBER: 60/070,440
 PR FILING DATE: February 9, 1998

R PRILING DATE: February 9, 1998

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R APPLICATION NUMBER: 60/075, 945

R FILING DATE: February 25, 1998

R APPLICATION NUMBER: 60/113, 265

R FILING DATE: December 16, 1998

R FILING DATE: December 16, 1998

R APPLICATION NUMBER: 60/113, 296

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R APPLICATION NUMBER: 60/069,694
R FILING DATE: December 16, 1997
R FILING DATE: December 16, 1997
R FILING DATE: December 16, 1997
R APPLICATION NUMBER: 60/069,870
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 US-09-944-862-61
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 APPLICANT: Tunas baniel
APPLICANT: Tunas baniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/944,862
CURRENT FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PLING DATE: December 11, 1997
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 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
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 Length 440;
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 35.5%; Score 150; DB 9; Le
100.0%; Pred. No. 1.1e-125;
tive 0; Mismatches 0;
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PRIOR APPLICATION NUMBER: PCT/USO0/05841
PRIOR FILING DATE: March 2, 2000
PRIOR FILING DATE: March 30, 2000
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PRIOR FILING DATE: May 22, 2000
PRIOR PLICATION NUMBER: PCT/USO0/2010
PRIOR PLING DATE: July 28, 2000
PRIOR PILING DATE: UNWBER: PCT/USO0/32678
PRIOR PRILING DATE: December 1, 2000
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NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,278
FILING DATE: December 11, 1997
 APPLICATION NUMBER: 60/069,425
 Sequence 61, Application US/09944862
Patent No. US20020115145A1
GENERAL INFORMATION:
 Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Conservative
 Baker, Kevin
Botstein, David
 Hillan, Kenneth
 Gurney, Austin
 Godowski, Paul
 Kljavin, Ivar
Napier, Mary
 Roy, Margaret
 ; ORGANISM: Homo Sapien
US-09-944-457-61
 Eaton, Dan
 Query Match
Best Local Similarity
Matches 150; Conserv
 US-09-944-862-61
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 APPLICANT:
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35.5%; Score 150; DB 9; Length 440;

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FILING DATE: February 25, 1998
 ; Sequence 61, Application US/09945015; Patent No. US20020132768A1
 RESULT 18
US-09-945-015-61
 US-09-945-587-61
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 TILE REFERENCE: P2548PIC1
CURRENT APPLICATION NUMBER: US/09/945,587
CURRENT FILING DATE: 2001-09-26
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PRIOR PELLING DATE: PEDELUATY 9, 1998
 Sequence 61, Application US/09945587
Patent No. US20020127643A1
GENERAL INFORMATION:
 Grimaldi, Christopher
100.08;
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
 Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Kljavin, Ivar
 Roy, Margaret
 Tumas, Daniel
 Napier, Mary
 Best Local Similarity
 RESULT 17
US-09-945-587-61
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 IOR APPLICATION NUMBER: 60/146,222

IOR FILING DATE: Univ 28, 1998

IOR FILING DATE: Univ 28, 1998

IOR FILING DATE: Univ 28, 1998

IOR FILING DATE: September 16, 1998

IOR PELLING DATE: September 1, 1998

IOR APPLICATION NUMBER: PCT/US98/25108

IOR APPLICATION NUMBER: 09/216,021

IOR FILING DATE: December 12, 1998

IOR APPLICATION NUMBER: 09/218,517

IOR FILING DATE: December 22, 1998

IOR APPLICATION NUMBER: 09/218,517

IOR FILING DATE: Univ 22, 1999

IOR APPLICATION NUMBER: PCT/US99/12252

IOR FILING DATE: No. US20020127643Alember 30, 1999

IOR APPLICATION NUMBER: PCT/US99/28313

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IOR PILING DATE: PCT/US99/30095
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PRIOR FILING DATE: PEDRUARY 28, 20
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
 Matches 150; Conservative
 ORGANISM: Homo Sapien
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Best Local Similarity
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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FILING DATE: No. US2002013768Alember 30, 1999
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APPLICATION NUMBER: PCT/US99/30095
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100.0%; Pred. No. 1.1e-125;
iive 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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Patent No. US20020132981A1
 Godowski, Paul
Grimaldi, Christopher
 errara, Napoleone
ilvaroff, Ellen
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Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
 Goddard, Audrey
 Gerritsen, Mary
 Gurney, Austin
 Kljavin, Ivar
 Roy,Margaret
Tumas,Danie]
 Napier, Mary
) ORGANISM: Homo Sapien
US-09-945-015-61
 -09-944-396-61
 152
 APPLICANT
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 APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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CURRENT APPLICATION NUMBER: US/09/945,015
PRIOR APPLICATION NUMBER: US/06/028
PRIOR APPLICATION NUMBER: US/06/05/411
PRIOR APPLICATION NUMBER: US/06/05/411
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 FILING DATE: June 22, 1999
APPLICATION NUMBER: PCT/US99/21090
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FILING DATE: June 22, 1999
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Botstein, David
 Gurney, Austin
 Napier, Mary
Roy, Margaret
Tumas, Daniel
 Kljavin, Ivar
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CURRENT APPLICATION NUMBER: US/09/944,396

CURRENT FILING DATE: 2010-09-26

REIOR APLICATION NUMBER: 03/66,028

REIOR APLICATION NUMBER: 05/067,111

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REIOR PLINICATION NUMBER: 05/067,111

REIOR PLINICATION NUMBER: 05/069,134

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PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
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TYPE: PRT
ORGANISM: HOMO Sapien
 FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,432
CURRENT FILING DATE: 2001-09-26
 CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR PELICATION NUMBER: 60/067,411
PRIOR PELICATION NUMBER: 60/069,334
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PRIOR PELICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR PELICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR PLILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
 FILING DATE: December 12, 1997
APPLICATION WINBER: 60/069,696
FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,694
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,702
FILING DATE: December 16, 1997
 FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,425
 Sequence 61, Application US/09944432
Patent No. US20020142419A1
GENERAL INFORMATION:
 Grimaldi, Christopher
 Ferrara, Napoleone Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Gerritsen, Mary
 Goddard, Audrey
 i, Paul
 Kljavin, Ivar
Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
 Eaton, Dan
 Godowski
 JS-09-944-432-61
 US-09-944-396-61
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/943,762

CURRENT PILING DATE: 2001-09-26

PRIOR PILING DATE: 2001-05-25

PRIOR PILING DATE: December 3, 1997

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FILING DATE: December 17, 1997
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FILING DATE: December 18, 1997
APPLICATION NUMBER: 60/070,440
 PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/075,945
 FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
 APPLICATION NUMBER: 60/113,296
FILING DATE: December 22, 1998
APPLICATION NUMBER: 60/146,222
 Sequence 61, Application US/09943762
Patent No. US20020142958A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 PRIOR FILING DATE: February 25, 1996
PRIOR APPLICATION NUMBER: 60/112,85(
 FILING DATE: December 16, 199
APPLICATION NUMBER: 60/069,87
FILING DATE: December 17, 199
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Filvaroff, Ellen
 Gerritsen, Mary
 Gurney, Austin
 Kljavin, Ivar
Napier, Mary
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 1999
 No. US20020142419Alember 30, 1999
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FILING DATE: No. US20020142419Alember 30,
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; ORGANISM: Homo Sapien
US-09-944-432-61
 SEQ ID NO 61
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PRIOR FILING DATE: 2001-05-25
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FILING DATE: December 16, 1998
APPLICATION NUMBER: 09/218,517
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 Godowski, Paul
Grimaldi, Christopher
 Hillan, Kenneth
 Tumas, Daniel
Wood, William
 Kljavin, Ivar
 Roy,Margaret
 Napier, Mary
 APPLICANT:
APPLICANT:
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 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125;
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IOR APPLICATION NUMBER: PCT/US98/19330

IOR FILING DATE: September 16, 1998

IOR PELLING DATE: December 1, 1998

IOR FILING DATE: December 1, 1998

IOR FILING DATE: December 16, 1998

IOR PELLING DATE: December 22, 1998

IOR APPLICATION NUMBER: 09/218, 517

IOR FILING DATE: December 22, 1998

IOR APPLICATION NUMBER: 09/254, 311

IOR FILING DATE: March 3, 1999

IOR APPLICATION NUMBER: PCT/US99/12050

IOR FILING DATE: September 15, 1999

IOR APPLICATION NUMBER: PCT/US99/28013

IOR FILING DATE: No. US20020142958Alember 30, 1999

IOR PILING DATE: No. US20020142958Alember 30, 1999

IOR PELLING DATE: PCC-MDS9/28013

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PRIOR PILING DATE: September 15, 1999
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PRIOR PILING DATE: December 16, 1999
PRIOR PILING DATE: PELVISSONO(03565)
PRIOR PELING DATE: PECTION SONO(0414)
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PRIOR PILING DATE: PEDALARY 11, 2000
PRIOR PILING DATE: PEDALARY 11, 2000
PRIOR PILING DATE: PEDALARY 22, 2000
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PRIOR PILING DATE: PEDALARY 28, 2001
 Sequence 61, Application US/09944654
Patent No. US20020142959A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Baterin, David
APPLICANT: Eaton, Dan
 Eaton, Dan
Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Matches 150; Conservative
 NUMBER OF SEQ ID NOS: 120
 ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
 US-09-943-762-61
 RESULT 22
US-09-944-654-61
 SEQ ID NO 61
 16
 32
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 152
 TYPE: PRT
 APPLICANT:
APPLICANT:
APPLICANT:
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PRIOR PILICATION NUMBER: 00.146, 122
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PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
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PRIOR PILING DATE: December 1, 1998
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PRIOR FILING DATE: TOWN NUMBER: PCT/US99/21090
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PRIOR FILING DATE: FEBTUARY 11, 2000
PRIOR FILING DATE: FEBTUARY 21, 2000
PRIOR FILING DATE: FEBTUARY 22, 2000
PRIOR FILING DATE: PEDTUARY 22, 2000
PRIOR PLICATION NUMBER: PCT/US00/05841
PRIOR PLICATION NUMBER: PCT/US00/08439
PRIOR PLILING DATE: March 30, 2000
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 PRIOR FILING DATE: December1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
 APPLICATION NUMBER: 60/070,440
FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
FILING DATE: February 9, 1998
APPLICATION NUMBER: 60/074,092
 PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: 70.11.
 FILING DATE: February 25, 1998
APPLICATION NUMBER: 60/112,850
FILING DATE: December 16, 1998
APPLICATION NUMBER: 60/113,296
 PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
 FILING DATE: December 16, 1997
APPLICATION NUMBER: 60/069,703
 FILING DATE: December 16, 199
APPLICATION NUMBER: 60/669,87
APPLICATE: December 17, 199
APPLICATION NUMBER: 60/069,87
 FILING DATE: December 17, 199
APPLICATION NUMBER: 60/068,01
FILING DATE: December 18, 199
 FILING DATE: February 9, 1998 APPLICATION NUMBER: 60/075,94
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNIMIDIQK 135
 92 DSRPQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 APPLICANT: Napier Mary
APPLICANT: Roy, Margaret
APPLICANT: Tunas Panier
APPLICANT: Tunas Panier
APPLICANT: Tunas Panier
APPLICANT: Tunas Panier
APPLICANT: Wood, Milliam
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PITCATION NUMBER: US/09/943,851A
CURRENT APPLICATION NUMBER: US/09/866,028
PRIOR FILING DATE: 2001-06-25
PRIOR FILING DATE: 2001-05-25
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PEDT/US00/03565
PRIOR PLILING DATE: PEDT/US00/04414
PRIOR PLILING DATE: PEDT/USV 22, 2000
PRIOR PLILING DATE: March 2, 2000
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 Sequence 61, Application US/09943851A
Patent No. US20020150976A1
GENERAL INFORMATION:
 APPLICATION NUMBER: 60/067,411
 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Kljavin, Ivar
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 23
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92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPITGDGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK
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PRIOR APPLICATION NUMBER: 60/074,002
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: PEbruary 9, 1998
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PRIOR FILING DATE: December 16, 1998
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PRIOR PELING DATE: DECEMBER: 60/113,266
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 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 FILING DATE: January 5, 1998
APPLICATION NUMBER: 60/074,086
 ; ORGANISM: Homo Sapien
US-09-944-413-61
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 16 SAAALIPTGDGQNLFTKDVTVIBGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 75
 13 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548PICT CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
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 0; Indels
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100.0%; Pred. No. 1.1e-125;
ive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
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PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR PILING DATE: 2001-05-25
PRIOR PELING DATE: December 3, 1997
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PRIOR PRILING DATE: December 16, 1997
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 Sequence 61, Application US/09944413
Patent No. US20020156004A1
GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Roy, Margaret
 Tumas, Daniel
Wood, William
 TYPE: PRT
CORGANISM: Homo Sapien
US-09-943-851A-61
 Eaton, Dan
 RESULT 24
US-09-944-413-61
LENGTH: 440
 APPLICANT:
APPLICANT:
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Gaps

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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSGSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCOVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 35.5%; Score 150; DB 9; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels
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PRIOR PELICATION NUMBER: PCT/US99/12552
PRIOR PELICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: June 22, 1999
PRIOR FILING DATE: September 15, 1999
PRIOR FILING DATE: No. US20020165143Atember 30, 1999
PRIOR FILING DATE: No. US20020165143Atember 30, 1999
PRIOR FILING DATE: No. US20020165143Atember 30, 1999
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PRIOR FILING DATE: December 16, 1999
PRIOR FILING DATE: PCT/US99/30095
PRIOR FILING DATE: PCT/US09/01365
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PRIOR APPLICATION NUMBER: PCT/US00/034014
PRIOR PILING DATE: February 22, 2000
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PRIOR PILING DATE: May 22, 2000
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PRIOR PILING DATE: December 1, 2000
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 Sequence 61, Application US/09944896
Patent No. US20020168715A1
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match
Best Local Similarity 100.0
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Hillan, Kenneth
 Napier, Mary
 GENERAL INFORMATION:
 JS-09-944-896-61
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 APPLICANT:
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 APPLICANT: WOOD, WILLIAM
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 TILE REFERENCE: P2544BPIC1

CURRENT APPLICATION NUMBER: US/09/944,403

CURRENT FILING: DATE: 2001-05-26

PRIOR FILING DATE: 2001-05-25

PRIOR PELLOTATION NUMBER: 0/06/411

PRIOR FILING DATE: December 1, 1997

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 Sequence 61, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
 Grimaldi,Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Godowski, Paul
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 US-09-944-403-61
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Gaps ö

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TILL OF INVENTION: ACIDS ENCODING THE SAME CURRENT APPLICATION NUMBER: US/09/944,944

CURRENT APPLICATION NUMBER: US/08/66,028

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR PLING DATE: December 13, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997

PRIOR PLING DATE: December 11, 1997
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPIGGGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
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 35.5%; Score 150; DB 9; Le
ilarity 100.0%; Pred. No. 1.1e-125;
Conservative 0; Mismatches 0;
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/USOO/14042
PRIOR FILING DATE: May 22, 2000
PRIOR FILING DATE: May 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/USOO/32678
PRIOR PILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/USO1/6520
PRIOR FILING DATE: PEDTUARY 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 FILING DATE: December 11, 1997
APPLICATION NUMBER: 60/069,425
 FILING DATE: December 12, 1997
APPLICATION NUMBER: 60/069,696
FILING DATE: December 16, 1997
 Sequence 61, Application US/09944944
Patent No. US20020173463A1
GENERAL INFORMATION:
FILING DATE: March 30, 2000
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
 Gerritsen, Mary
 Kljavin, Ivar
 Tumas, Daniel
Wood, William
 Roy, Margaret
 Napier, Mary
 , ORGANISM: Homo Sapien
US-09-944-896-61
 Eaton, Dan
 Query Match
Best Local Similarity
Matches 150; Conserv
 US-09-944-944-61
 APPLICANT:
APPLICANT:
APPLICANT:
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76 DSRFQLLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPHTGGGNLFTKDVTVIEGEVATISCOVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,929
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR RILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
 Indels
 Query Match 35.5%; Score 150; DB 9; Le
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
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 Sequence 61, Application US/09944929
Publication No. US20020197612A1
GENERAL INFORMATION:
 Sequence 61, Application US/09944907; Publication No. US20020198147A1; GENERAL INFORMATION:
 Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
 Filvaroff, Ellen
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
 Roy, Margaret
Tumas, Daniel
Wood, William
 Gurney, Austin
 Kljavin, Ivar
 TYPE: PRT
ORGANISM: Homo Sapien
US-09-944-929-61
 RESULT 28
US-09-944-929-61
 US-09-944-907-61
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 APPLICANT:
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 35.5%; Score 150; DB 9; Length 440;
 Indels
 TOR FILING DATE: December 22, 1998

UR APPLICATION NUMBER: 09/254,311

IOR PILING DATE: March 3, 1999

IOR PILING DATE: March 3, 1999

IOR APPLICATION NUMBER: PCT/US99/1252

IOR APPLICATION NUMBER: PCT/US99/28109

IOR FILING DATE: September 15, 1999

IOR FILING DATE: No. US200201734634ember 30, 1999

IOR FILING DATE: No. US200201734634ember 30, 1999

IOR APPLICATION NUMBER: PCT/US99/28313

IOR APPLICATION NUMBER: PCT/US99/28301

IOR FILING DATE: December1, 1999

IOR APPLICATION NUMBER: PCT/US99/30095

IOR APPLICATION NUMBER: PCT/US99/30095

IOR APPLICATION NUMBER: PCT/US09/00565

IOR PILING DATE: December 16, 1999

IOR RILING DATE: December 11, 2000

IOR FILING DATE: PCHAUSY 11, 2000

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 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0;
PRIOR FILING DATE: December 16, 1997
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PRIOR FILING DATE: December 17, 1997
PRIOR FILING DATE: December 17, 1997
PRIOR PLICATION NUMBER: 60/069, 873
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PRIOR PLILING DATE: December 18, 1997
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PRIOR PLILING DATE: December 19, 1998
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PRIOR PLILING DATE: POT/US99/28313
PRIOR PLILING DATE: POT/US99/28313
PRIOR PLILING DATE: POT/US99/28313
PRIOR PLILING DATE: PEDPLAY 22, 2000
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PRIOR PLILING DATE: PEDPLAY 22, 2000
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PRIOR PLILING DATE: PEDPLAY 22, 2000
PRIOR PLILING DATE: PATCH SPC/US09/280/199
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PRIOR PLILING DATE: PATCH SPC/US09/280/199
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PRIOR PLILING DATE: PATCH SPC/US09/280/199
PRIOR PLILING DATE:
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 TYPE: PRT
ORGANISM: Homo Sapien
 US-09-944-944-61
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Gaps

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Length 440;

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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTXDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 0; Indels
 35.5%; Score 150; DB 10; L 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 RESULT 31
US-05-944-852-61
US-09-944-852-61
Sequence 61, Application US/09944852
Publication No. US20030083479A1
GENERAL INFORMATION
 Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
 Query Match
Best Local Similarity 100.0
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gerritsen, Mary
Goddard, Audrey
 Gurney, Austin
Hillan, Kenneth
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
 ; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-884-61
 ; ORGANISM: Homo Sapien
US-09-944-852-61
 Eaton, Dan
 Best Local Similarity
Matches 150; Conserv
 APPLICANT:
APPLICANT:
SEQ ID NO 61
 APPLICANT:
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 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE COF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548PLC1
CURRENT APPLICATION NUMBER: US/09/944,884
CURRENT FILING DATE: 2001-08-31
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 120
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
 0; Indels
 Query Match 35.5%; Score 150; DB 9; Le Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 ; Sequence 61, Application US/09944884; Publication No. US20030077698A1; GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Goddard, Audrey
Godowski, Paul
Grimaldi, Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Ferrara, Napoleone
 Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Gurney, Austin
Hillan, Kenneth
 Roy, Margaret
Tumas, Daniel
 Kljavin, Ivar
 Napier, Mary
 TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-907-61
 Eaton, Dan
 US-09-944-884-61
 16
 152
 APPLICANT:
APPLICANT:
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 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P25-4891C1
CURRENT PELLICATION NUMBER: US/09/944,852
CURRENT FILING DATE: 2001-08-31
PRIOR RPPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
SEQ ID NOS: 120
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LENGTH: 440
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 35.5%; Score 150; DB 10; L ilarity 100.0%; Pred. No. 1.1e-125; Conservative 0; Mismatches 0;
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92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
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 Length 440;
 Indels
PRIOR PELLING DATE: December 22, 1999
PRIOR PELLING DATE: March 3, 1999
PRIOR PELLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR PELLING DATE: June 22, 1999
PRIOR PELLING DATE: September 15, 1999
PRIOR PELLING DATE: September 15, 1999
PRIOR PELLING DATE: September 15, 1999
PRIOR PELLING DATE: No. US20030096742Alember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR PELLING DATE: December 1, 1999
PRIOR PELLING DATE: December 1, 1999
PRIOR PELLING DATE: Pebruary 11, 2000
PRIOR PELLING DATE: Pebruary 12, 2000
PRIOR PELLING DATE: Pebruary 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR PELLING DATE: Pebruary 22, 2000
PRIOR PELLING DATE: March 30, 2000
PRIOR PELLING DATE: March 30, 2000
PRIOR PELLING DATE: March 30, 2000
PRIOR PELLING DATE: March 30, 2000
PRIOR PELLING DATE: March 130, 2000
PRIOR PELLING DATE: March 130, 2000
PRIOR PELLING DATE: March 12000
PRIOR PELLING DATE: PEPRIOR POT/US00/14042
PRIOR PELLING DATE: PERLINGSON 14042
PRIOR PELLING DATE: PERLINGSON 12070
PRIOR PELLING DATE: PERLINGSON 12070
PRIOR PELLING DATE: PEPRIOR PELLINGSON 130, 2000
PRIOR PELLING DATE: PEPRIOR PERIOR PELLING DATE: PEPRIOR PELLING DATE: PEPRIOR PELLING DATE: PERLINGSON 1200
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PRIOR
 35.5%; Score 150; DB 10; I
100.0%; Pred. No. 1.1e-125;
tive 0; Mismatches 0;
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 61, Application US/09945584 Publication No. US20030211570A1 GENERAL INFORMATION:
 Godowski, Paul
Grimaldi, Christopher
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, ban
APPLICANT: Ferrara, Napoleone
APPLICANT: Fluvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Hillan, Kenneth
 Gurney, Austin
 Kljavin, Ivar
Napier, Mary
 ORGANISM: Homo Sapien
US-09-943-780-61
 US-09-945-584-61
 LENGTH: 440
TYPE: PRT
 APPLICANT:
APPLICANT:
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 Sequence 61, Application US/09943780 Publication No. US20030096742A1 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 US-09-943-780-61
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Gaps

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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P2549FILL CURRENT APPLICATION NUMBER: US/09/943,664
CURRENT FILING DATE: 2001-09-26
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
 35.5%; Score 150; DB 10; Length 4 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 PRIOR APPLICATION NUMBER: PCT/USO0/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR PILING DATE: May 22, 2000
PRIOR PILING DATE: May 22, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: July 28, 2000
PRIOR FILING DATE: December 1, 2000
PRIOR FILING DATE: Pebruary 28, 2001
PRIOR FILING DATE: Pebruary 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 61
LENGTH: 440
FILING DATE: March 2, 2000
APPLICATION NUMBER: PCT/US00/08439
 CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069335
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
PRIOR FILING DATE: December 11, 1997
 PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
 Sequence 61, Application US/09943664
Publication No. US20040091972A1
 Godowski, Paul
Grimaldi, Christopher
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 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
 Gurney, Austin
Hillan, Kenneth
Kljavin, Ivar
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Goddard, Audrey
 Napier, Mary
Roy, Margaret
Tumas, Daniel
Wood, William
 TYPE: PRT
CORGANISM: Homo Sapien
US-09-945-584-61
 Eaton, Dan
 GENERAL INFORMATION
 US-09-943-664-61
 APPLICANT:
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| THILL OF STRUCKTON SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC.
| THILL OF STRUCKTON NUMBER: 105/05/26/5.564
| PRIOR PAILCATION NUMBER: 105/06/26/345
| PRIOR PLILICATION NUMBER: 0010-05/26/345
| PRIOR PLILICATION NUMBER: 0010-05/26/345
| PRIOR PLILICATION NUMBER: 0000-05/344
| PRIOR PLILICATION NUMBER: 00/06/3134
| PRIOR PLILICATION NUMBER: 00/06/3134
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 FILING DATE: February 11, 2000
APPLICATION NUMBER: PCT/US00/04414
 APPLICATION NUMBER: PCT/US00/05841
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 Tumas, Daniel
Wood, William
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PRIOR PLILING DATE: DATE: DATE 10, 2000
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Score 150; DB 11; Length 440; Pred. No. 1.1e-125;

35.5%; S 100.0%;

Query Match Best Local Similarity

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32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYPRDFRPLK
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430R1C1
CURRENT APPLICATION NUMBER: US/10/052,586
CURRENT FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
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 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
Mismatches
 PRIOR APPLICATION NUMBER: 60/06220
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R APPLICATION NUMBER: 60/063870
 PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
 FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/064103
FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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 FILING DATE: 1997-10-28
APPLICATION NUMBER: 60/063544
 APPLICATION NUMBER: 60/066120
FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/066466
 APPLICATION NUMBER: 60/069425
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 APPLICANT: Smith, Victoria APPLICANT: Watanabe, Colin K. APPLICANT: Wood, William I. APPLICANT: Zhang 7...
 Godowski, Paul J. Gurney, Austin L.
Conservative
 Goddard, Audrey
 Pan, James
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DB 13; Length 440;

35.5%; Score 150;

Query Match

Gaps

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 76 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
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APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
ITILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF ILINEDATE: P3430R1C104
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 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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LENGTH: 440
TYPE: PRT
 Pred. No. 1.1e-125;
 Score 150; DB 14; I
Pred. No. 1.1e-125;
 35.5%; Score 150; DB 14;
 100.0%; Prec.
 136 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
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Wood, William I.
 Godowski, Paul J
 Gurney, Austin L
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Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 rype: PRT CORGANISM: Homo Sapien US-10-176-758-34
 ; ORGANISM: Homo Sapien
US-10-175-737-34
 RESULT 38
US-10-175-737-34
 APPLICANT:
 Query Match
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
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 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERDICE: P3430R1C42 CURRENT APPLICATION NUMBER: U5/10/174,590 CURRENT FILING DATE: 2002-06-18
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Publication No. US20030008353A1
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Godowski, Paul J
Gurney, Austin L
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J
APPLICANT: Gurney, Austin L
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-758-34
 JS-10-174-590-34
 SEQ ID NO 34
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 APPLICANT:
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APPLICATION NUMBER: 60/086486
 FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
 APPLICATION NUMBER: 60/086023
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TITLE OF INVERTIONS: ACIDS ENCODING THE SAME
FILE REFERENCE: P34-3001241
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; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
 Watanabe, Colin K. Wood, William I.
 Godowski, Paul J.
Gurney, Austin L.
 Pan, James
Smith, Victoria
 Goddard, Audrey
 Desnoyers, Luc
 Zhang, Zemin
 RESULT 39
US-10-174-581-34
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 APPLICANT:
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 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C68
CURRENT APPLICATION NUMBER: US/10/176,483
CURRENT FILING DATE: 2002-06-20
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35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGERIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10176483
Publication No. US20030017541A1
GENERAL INFORMATION:
 Sequence 34, Application US/10176749
Publication No. US20030017542A1
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Watanabe, Colin K. Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Watanabe, Colin K.
Wood, William I.
 Pan, James
Smith, Victoria
 Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT: Baker, Kevin P.
 ; ORGANISM: Homo Sapien
US-10-176-483-34
 Chen, Jian
 GENERAL INFORMATION:
 JS-10-176-749-34
 APPLICANT:
APPLICANT:
 16
 136
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 Length 440;
 Indels
 35.5%; Score 150; DB 14; L 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0;
 RAPPLICATION NUMBER: 60/087759
R FILING DATE: 1998-06-02
R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/086025
R APLICATION NUMBER: 60/086025
R APLICATION NUMBER: 60/086028
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
R FILING DATE: 1998-06-04
 R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088826
R FILING DATE: 1998-06-10
R APPLICATION NUMBER: 60/088861
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088863
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088863
R FILING DATE: 1998-06-11
R APPLICATION NUMBER: 60/088976
R FILING DATE: 1998-06-11
 FILING DATE: 1998-05-28
APPLICATION NUMBER: 66/087208
FILING DATE: 1998-05-28
APPLICATION NUMBER: 66/087609
FILING DATE: 1998-06-02
FILING DATE: 1998-05-22
APPLICATION NUMBER: 60/087098
 APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
 FILING DATE: 1998-06-04
APPLICATION UNMBER: 60/088655
FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/089722
 FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
 FILING DATE: 1998-06-16
APPLICATION NUMBER: 60/089514
 APPLICATION NUMBER: 60/089538
 FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
 FILING DATE: 1998-06-04
APPLICATION UNDBER: 60/088167
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088202
 FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088326
 FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088738
 FILING DATE: 1998-06-10
APPLICATION NUMBER: 60/088740
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 APPLICATION NUMBER: 60/089512
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 APPLICATION NUMBER: 60/088811
 APPLICATION NUMBER: 60/088824
 FILING DATE: 1998-06-05
 FILING DATE: 1998-06-10
 FILING DATE: 1998-06-10
 1998-06-10
 FILING DATE: 1998-06-16
 Query Match
Best Local Similarity 100.
 PRIOR
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OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC OF INVENTION: ACIDS ENCODING THE SAME

Zhang, Zemin

APPLICANT

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US-10-173-706-34
 US-10-176-915-34
 LENGTH: 440
 APPLICANT:
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 TYPE: PRT
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIBGBVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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0
 Length 440;
 Length 440;
 0; Indels
 0; Indels
 FILE REFERENCE: P3430RIC83
CURRENT APPLICATION NUMBER: US/10/176,914
CURRENT FILING DATE: 2002-06-20
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 Prior application removed - See File Wrapper or Palm, NUMBER OF SEQ ID NOS: 612; SEQ ID NO 34
LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-749-34
 35.5%; Score 150; DB 14; L
100.0%; Pred. No. 1.1e-125;
tive 0; Mismatches 0;
 35.5%; Score 150; DB 14; L
100.0%; Pred. No. 1.1e-125;
tive 0; Mismatches 0;
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 FILE REFERENCE: P3430R1C76
CURRENT APPLICATION NUMBER: US/10/176,749
CURRENT FILING DATE: 2002-06-20
 Sequence 34, Application US/10176914; Publication No. US20030017543A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-914-34
 US-10-176-914-34
 SEQ ID NO 34
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 136
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 APPLICANT:
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APPLICANT: wan, James
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TITLE OF INVENTION: ACIDS ENCODING THE SAME
TITLE OF INVENTION ACIDS ENCODING THE SAME
TITLE OF INVENTION ACIDS ENCODING THE SAME
STOR APPLICATION NUMBER: US/10/173,706
CURRENT APPLICATION NUMBER: US/10/173,706
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPITGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERRNER: 934.0RTC110
CURRENT APPLICATION NUMBER: US/10/176,915
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
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0
 Length 440;
 Score 150; DB 14; Lengtn *-; Pred. No. 1.1e-125;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Query Match
35.5%; Score 150; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 150; Conservative 0; Mismatches
Sequence 34, Application US/10173706
Publication No. US20030022293A1
GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 APPLICANT: Pan, Jämes
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Smith, victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: ADANG, Zemin I.
APPLICANT: ADANG, Zemin I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT APPLICATION NUMBER: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430FIC70 CURRENT APPLICATION NUMBER: US/10/176,482 CURRENT FILING DATE: 2002-06-20
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0; Indels
 Query Match
35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 136 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10176482
Publication No. US20030022296A1
GENERAL INFORMATION:
 Watanabe, Colin K.
Wood, William I.
Zhang, Zemin
 Godowski, Paul J.
Gurney, Aŭstin L.
 Gurney, Austin L.
 Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 Pan, James
Smith, Victoria
 Godowski, Paul
 APPLICANT: Baker, Kevin P.
 ORGANISM: Homo Sapien
 TYPE: PRT
ORGANISM: Homo Sapien
 Chen, Jian
 Pan, James
 US-10-176-482-34
 US-10-175-752-34
 SEQ ID NO 34
LENGTH: 440
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 Query Match
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTIIVLVPPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C45
CURRENT APPLICATION NUMBER: US/10/175,738
CURRENT APPLICATION NUMBER: US/10/175,738
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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 Query Match
35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 Query Match 35.5%; Score 150; DB 14; Length 4 Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEBIEVNCTAMASKPATTIRWFKGN 181
 RESULT 46
US-10-175-752-34
Sequence 34, Application US/10175752
Publication No US20030022295A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
 ; Sequence 34, Application US/10175738; Publication No. US20030022294A1; GENERAL INFORMATION:
 Watanabe, Colin K. Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Pan, James
Smith, Victoria
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
; ORGANISM: Homo Sapien
US-10-173-706-34
 TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 45
US-10-175-738-34
 US-10-175-738-34
 SEQ ID NO 34
 136
 92
 16
 92
 136
 152
 APPLICANT:
APPLICANT:
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNE: P343 ORIGGE CURRENT APPLICATION NUMBER: US/10/176,913 CURRENT FILING DATE: 2002-06-20 Prior Application removed - See file Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34 LENGTH: 440
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430R1C153
CURRENT APPLICATION NUMBER: US/10/180,552
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 32 SAAALIPTGDGQNLFTKDVIVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYPRDFRPLK
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10180552; Publication No. US/20030022300A1; GENERAL INFORMATION: APPLICANT: Baker Kevin P. APPLICANT: Chen, Jian
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 150, Conservative
 Desnoyers, Luc
Goddard, Audrey
 Zhang, Zemin
 ORGANISM: Homo Sapien
 ORGANISM: Homo Sapien
 RESULT 50
US-10-180-552-34
 US-10-180-552-34
 US-10-176-913-34
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
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 TYPE: PRT
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 DSRFQLLNFSSSBLKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYIDPPQESYTTITVLVPPRNLMIDIOK 151
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPIGGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERRNCE: P3430R1C86
CURRENT APPLICATION NUMBER: US/10/176,757
CURRENT FILING DATE: 2002-06-20
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 Gaps
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 Length 440;
 0; Indels
 35.5%; Score 150; DB 14; I
100.0%; Pred. No. 1.1e-125;
iive 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 RESULT 49
US-10-176-913-34
; Sequence 34, Application US/10176913
; Publication No. US20030022298A1
; Publication Nor.
; APPLICANT: Baker.Kevin P.
appLICANT: Chen, Jian
 ; Sequence 34, Application US/10176757; Publication No. US20030022297A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
 Watanabe, Colin K. Wood, William I.
 Query Match
Best Local Similarity 100.0
Matches 150; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 LENGTH: 440
TYPE: PRT
ORGANISM: Homo Sapien
 US-10-176-757-34
 APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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 136
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels (
 Length 440;
 Indels
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTI
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C40
CURRENT APPLICATION NUMBER: US/10/174,572
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 Query Match 35.5%; Score 150; DB 14; L Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10174572 Publication No. US20030027263A1 GENERAL INFORMATION:
 ; Sequence 34, Application US/10174579
; Publication No. US20030027264A1
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J. Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Goddard, Audrey
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-173-700-34
 ORGANISM: Homo Sapien
 Pan, James
 RESULT 54
US-10-174-579-34
 US-10-174-572-34
 SEQ ID NO 34
LENGTH: 440
 SEQ ID NO 34
LENGTH: 440
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 136
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 APPLICANT:
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 152
 TYPE: PRT
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C14
CURRENT APPLICATION NUMBER: US/10/173,700
CURRENT APPLICATION NUMBER: US/10/173,700
FILE PAPALICATION FOR SAME
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NUMBER OF SEQ ID NOS: 612
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P943-0911C147
CURRENT APPLICATION NUMBER: US/10/180,557
CURRENT FILING DATE: 2002-06-25
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0; Indels
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10173700 Publication No. US20030027262A1 GENERAL INFORMATION:
 Sequence 34, Application US/10180557
Publication No. US20030022301A1
GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Watanabe, Colin K. Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Best Local Similarity 100.
Matches 150, Conservative
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
 Pan, James
 RESULT 52
US-10-173-700-34
 US-10-180-557-34
 94
 APPLICANT:
APPLICANT:
 92
 136
 Query Match
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 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Query Match
35.5%; Score 150; DB
Best Local Similarity 100.0%; Pred. No. 1.1
Matches 150; Conservative 0; Mismatches
0; Mismatches
 Sequence 34, Application US/10174588 Publication No. US20030027266A1 GENERAL INFORMATION:
 Sequence 34, Application US/10175739
Publication No. US20030027267A1
GENERAL INFORMATION:
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
 APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
Matches 150; Conservative
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 US-10-174-588-34
 US-10-175-739-34
 US-10-174-588-34
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPIGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P34.09181C31
CURRENT APPLICATION NUMBER: US/10/174,579
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER: OF SEQ ID NOS: 612
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC36
CURRENT APPLICATION NUMBER: US/10/174,582
CURRENT FILING DATE: 2002-06-18
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 Gaps
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125;
 Length 440;
 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 35.5%; Score 150; DB 14;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10174582; Publication No. US20030027265A1; GENERAL INFORMATION:
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
 Desnoyers, Luc
 Baker, Kevin P.
Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-174~582-34
 Pan,James
 Best Local Similarity
 US-10-174-579-34
 US-10-174-582-34
 SEQ ID NO 34
 92
 92
 136
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 Query Match
 APPLICANT:
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 APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Smith, Victoria
APPLICANT: Matanabe Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: BECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C28
CURRENT APPLICATION NUMBER: US/10/174,588
CURRENT FILING DATE: 2002-06-18
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FILE RE
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRRQLLNPSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITULVPPRNLMIDIQK 151
 32 SAAALIPITGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 32 SAAALIPITGOONLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGONLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Gaps
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 ö
 Length 440;
 Score 150; DB 14; Lengtn 4:
Pred. No. 1.1e-125;
Pred. No. 1.1e-125;
Indels
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92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 FILE REFERENCE: P3430R1C52
CURRENT APPLICATION NUMBER: US/10/175,743
CURRENT FILING DATE: 2002-06-16
PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PILING DATE: 1997-09-18
PRIOR PLING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-01-18
PRIOR FILING DATE: 1997-01-17
PRIOR PILING DATE: 1997-01-17
PRIOR APPLICATION NUMBER: 60/06250
PRIOR PLING DATE: 1997-10-17
 PRIOR FILING DATE: 1997-10-24
PRIOR APPLICATION NUMBER: 60/063121
PRIOR FILING DATE: 1997-10-24
PRIOR PPLICATION NUMBER: 6//063486
PRIOR FILING DATE: 1997-10-24
 Sequence 34, Application US/10175743
Publication No. US20030027269A1
GENERAL INFORMATION:
 FILING DATE: 1997-10-21
APPLICATION NUMBER: 60/063540
FILING DATE: 1997-10-28
 APPLICATION NUMBER: 60/066466
FILING DATE: 1997-11-24
 FILING DATE: 1997-12-17
APPLICATION NUMBER: 60/068017
 APPLICATION NUMBER: 60/063870
 FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/064103
 APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066120
 APPLICATION NUMBER: 60/069425
 FILING DATE: 1997-12-18
APPLICATION NUMBER: 60/077450
 APPLICATION NUMBER: 60/063541
 APPLICATION NUMBER: 60/063544
 APPLICATION NUMBER: 60/063564
 APPLICATION NUMBER: 60/063734
 APPLICATION NUMBER: 60/066772
 Watanabe, Colin K. Wood, William I.
 FILING DATE: 1997-10-28
 FILING DATE: 1997-10-28
 1997-10-28
 FILING DATE: 1997-10-29
 FILING DATE: 1997-11-24
 FILING DATE: 1997-11-2;
 Godowski, Paul J.
Gurney, Austin L.
 FILING DATE: 1997-10-3
 1997-12-
 Desnoyers, Luc
Goddard, Audrey
 Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 FILING DATE:
 FILING DATE:
 JS-10-175-743-34
 136
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 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNE: P3430R1C46
CURRENT APPLICATION NUMBER: US/10/175,739
CURRENT FILING DATE: 2002-06-19
FILO Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3430NIC61
CURRENT APPLICATION NUMBER: US/10/175,740
CURRENT FILING DATE: 2002-06-18
 Gaps
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 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 Score 150; DB 14; L
Pred. No. 1.1e-125;
0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 35.5%; oc.
100.0%; Pred
0; M
 ; Sequence 34, Application US/10175740; Publication No. US20030027268A1; GENERAL INFORMATION:
 Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Conservative
Smith, Victoria
 Pan, James
Smith, Victoria
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-175-739-34
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-175-740-34
 Similarity
 RESULT 58
US-10-175-740-34
 150;
 LENGTH: 440
APPLICANT:
 92
 92
 Query Match
Best Local
 APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
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PRIOR PELING DATE: 1998-05-16
PRIOR PELING DATE: 1998-05-16
PRIOR PELING DATE: 1998-05-16
PRIOR PELING DATE: 1998-05-16
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135

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Gaps ; 0

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APPLICANT: APPLICANT:

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92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTIVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430781C92 CURRENT APPLICATION NUMBER: 105/10/176,747 CURRENT FILING DATE: 2002-06-20
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Length 440;
 Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
TYPE: PRT
 Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
LENGTH: 440
 Query Match 35.5%; Score 150; DB 14; I
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 CURRENT APPLICATION NUMBER: US/10/176,492
CURRENT FILING DATE: 2002-06-21
 Sequence 34, Application US/10176747
Publication No. US20030027273A1
GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Gurney, Austin L
 Goddard, Audrey
Godowski, Paul
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Desnoyers, Luc
 Zhang, Zemin
 ; ORGANISM: Homo Sapien
US-10-176-492-34
 ORGANISM: Homo Sapien
 Pan, James
 US-10-176-747-34
 APPLICANT:
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92 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQGSYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTIIVLVPPPRNLMIDIOK 151
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLINPRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C119
CURRENT APPLICATION NUMBER: U5/10/176,488
CURRENT APPLICATION NUMBER: U5/10/176,488
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
 APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C107
 Gaps
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 35.5%; Score 150; DB 14; Length 440;
 0; Indels
 Pred. No. 1.1e-125;
 100.0%; Pred. ...
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 US-10-176-488-34
Sequence 34, Application US/10176488
Publication No. US20030027271A1
GENERAL INFORMATION:
 ; Sequence 34, Application US/10176492; Publication No. US20030027272A1; GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Smith, Victoria
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 TYPE: PRT
ORGANISM: Homo Sapien
 Pan, James
 US-10-176-488-34
 RESULT 61
US-10-176-492-34
 SEQ ID NO 34
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 APPLICANT:
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92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 76 DSRFQLLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: APPLICANT: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERENCE: P3430R1C93
CURRENT APPLICATION NUMBER: US/10/176,987
CURRENT FILING DATE: 2002-06-21
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
 Query Match 35.5%; Score 150; DB 14; Length 440; Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 Score 150; DB 14; Lengtn 4:; Pred. No. 1.1e-125;
 Prior Application removed - See File Wrapper or Palm; NUMBER OF SEQ ID NOS: 612; SEQ ID NO 34; LENGTH: 440; TYPE: PRT; ORGANISM: Homo Sapien
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Query Match 35.5%; Score 150; DB Best Local Similarity 100.0%; Pred. No. 1.1 Matches 150; Conservative 0; Mismatches
 RESULT 65
US-10-176-987-34
; Sequence 34, Application US/10176987
; Publication No. US20030027278A1
; GEBERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
 Sequence 34, Application US/10176992; Publication No. US20030027279A1; GENERAL INFORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian APPLICANT: Desnoyers, Luc
 Godowski, Paul J.
Gurney, Austin L.
 Desnoyers, Luc
Goddard, Audrey
 US-10-176-992-34
US-10-176-985-34
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RIC103
CURRENT APPLICATION NUMBER: US/10/176,750
CURRENT FILING DATE: 2002-06-21
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ö
 Length 440;
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 FILE REFERENCE: P3430R1C99
CURRENT APPLICATION NUMBER: US/10/176,985
CURRENT FILING DATE: 2002-06-21
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 , DB 14; I
. 1.1e-125;
 35.5%; Score 150; DB 100.0%; Pred. No. 1.1 tive 0; Mismatches
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 ; Sequence 34, Application US/10176750; Publication No. US20030027274A1; GENERAL INFORMATION:
 ; Sequence 34, Application US/10176985; Publication No. US20030027277A1; GENERAL INFORMATION:
 APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Pan, James
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Matches 150; Conservative
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 TYPE: PRT
ORGANISM: Homo Sapien
 TYPE: PRT
ORGANISM: Homo Sapien
 Рап, Јашев
 Best Local Similarity
 US-10-176-750-34
 US-10-176-985-34
 SEQ ID NO 34
 92
 136
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 Query Match
 APPLICANT:
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DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRINIDIQK 151
 76 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3430F1C228
CURRENT APPLICATION NUMBER: US/10/184,658
CURRENT FILING DATE: 2002-06-28
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
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 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 Query Match 35.5%; Score 150; DB 14; 1
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0;
 136 DTAVEGERIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10184658
Publication No. US20030027281A1
GENERAL INFORMATION:
 Application US/10176991
 Watanabe, Colin K. Wood, William I.
 Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
 Gurney, Austin L.
 Smith, Victoria
 Goddard, Audrey
Godowski, Paul
 APPLICANT: Baker, Kevin P.
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 ORGANISM: Homo Sapien
 GENERAL INFORMATION
 Sequence 34, App. Publication No.
 US-10-184-658-34
 US-10-184-658-34
 APPLICANT:
APPLICANT:
 96
 92
 136
 152
 TYPE: PRT
 APPLICANT:
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 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P343.0R1C100 CURRENT APPLICATION NUMBER: US/10/176,992 CURRENT FILING DATE: 2002-06-21 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34
 APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 Length 440;
 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; Live 0; Mismatches 0; Indels
 0; Indels
 35.5%; Score 150; DB 14; L 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 Prior Application removed - See File Wrapper or NUMBER OF SEQ ID NOS: 612
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 FILE REFERENCE: P3430R1C89
CURRENT APPLICATION NUMBER: US/10/176,993
CURRENT FILING DATE: 2002-06-20
 Sequence 34, Application US/10176993; Publication No. US20030027280A1; GENERAL INFORMATION:
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J.
Gurney, Austin L.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Query Match 35.5
Best Local Similarity 100.
Matches 150; Conservative
 Matches 150; Conservative
Goddard, Audrey
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P.
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
US-10-176-992-34
 TYPE: PRT
ORGANISM: Homo Sapien
 Query Match
Best Local Similarity
 US-10-176-993-34
 SEQ ID NO 34
 APPLICANT:
APPLICANT:
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76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 APPLICANT: Zhang, Zemin TILE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND THE SAME FILE OF INVENTION: ACIDS ENCODING THE SAME FILE REPERBNCE: P343311C18 CURRENT APPLICATION NUMBER: US/10/173,705 CURRENT FILING DATE: 2002-06-17 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612 SEQ ID NO 34
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME
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 35.5%; Score 150; DB 14; Length 440; 100.0%; Pred. No. 1.1e-125; ive 0; Mismatches 0; Indels
 FILE REFERENCE: P3430R1C5
CURRENT APPLICATION NUMBER: US/10/173,697
CURRENT FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 Sequence 34, Application US/10173697
Publication No. US20030032102A1
GENERAL INFORMATION:
 Sequence 34, Application US/10173705
Publication No. US20030032103A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
 Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Godowski, Paul J.
Gurney, Austin L.
 Godowski, Paul J. Gurney, Austin L.
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 TYPE: PRT
ORGANISM: Homo Sapien
 Chen, Jian
 Pan, James
 US-10-173-705-34
 US-10-173-697-34
 US-10-173-697-34
 SEQ ID NO 34
LENGTH: 440
 APPLICANT:
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRPQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 91
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 16 SAAALIPTGDGQNLFTKDVTVIBGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P343-931C3
CURRENT APPLICATION NUMBER: US/10/173,695
CURRENT FILING DATE: 2002-06-17
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ITLE OF INVENTION: ACIDS ENCODING THE SAME
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 Length 440;
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 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
PLENGTH: 440
 Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 612
 35.5%; Score 150; DB 14; I 100.0%; Pred. No. 1.1e-125;
 35.5%; Score 150; DB 14; I 100.0%; Pred. No. 1.1e-125; tive 0; Mismatches 0;
 100.0%; Preu. ...
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 TITLE OF INVENTION: ACIDS ENCODING THE S. FILE REFERENCE: P3430R1C122
CURRENT APPLICATION NUMBER: US/10/176,991
CURRENT FILING DAIE: 2002-06-21
 ; Sequence 34, Application US/10173695; Publication No. US20030032101A1; GENERAL INFORMATION:
 Watanabe, Colin K.
Wood, William I.
 Gurney, Austin L.
Pan, James
Smith, Victoria
 Godowski, Paul J
 Best Local Similarity 100.
Matches 150; Conservative
 Query Match
Best Local Similarity 100.
Matches 150; Conservative
 Desnoyers, Luc
Goddard, Audrey
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 Zhang, Zemin
 ORGANISM: Homo Sapien
 TYPE: PRT
ORGANISM: Homo Sapien
 RESULT 70
US-10-173-695-34
 US-10-176-991-34
 US-10-173-695-34
 SEQ ID NO 34
 136
 TYPE: PRT
 APPLICANT:
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 Query Match
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRRQLINPSSSELKVSLINVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin Zemin TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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 Length 440;
 Length 440;
 Query Match 35.5%; Score 150; DB 14; Length 4. Best Local Similarity 100.0%; Pred. No. 1.1e-125; Matches 150; Conservative 0; Mismatches 0; Indels
 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 Score 150; DB 14; L
Pred. No. 1.1e-125;
 35.5%; Scor.
100.0%; Pred. No. 1...
'... 0; Mismatches
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 TRANSMEMBRA.
FILE REFERENCE: P3430R1C23
CURRENT APPLICATION NUMBER: US/10/174,576
CURRENT FILING DATE: 2002-06-18
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 ; Sequence 34, Application US/10174576
; Publication No. US20030032104A1
 Watanabe, Colin K. Wood, William I.
 Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Matches 150; Conservative
 Smith, Victoria
 APPLICANT: Baker, Kevin P.
 ; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-173-705-34
 TYPE: PRT
CORGANISM: Homo Sapien
US-10-174-576-34
 Query Match
Best Local Similarity
 Chen, Jian
 Pan, James
 GENERAL INFORMATION:
 RESULT 73
US-10-174-576-34
 RESULT 74
US-10-174-585-34
LENGTH: 440
 96
 92
 136
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 APPLICANT:
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 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
 APFLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Milliam I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C37
CURRENT APPLICATION NUMBER: US/10/174,585
CURRENT FILING DATE: 2002-06-18
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NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 16 SAAALIPIGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK
 APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1DA
CURRENT APPLICATION NUMBER: US/10/174,586
CURRENT FILING DATE: 2002-06-18
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 Query Match

35.5%; Score 150; DB 14; Length 440;
Best Local Similarity 100.0%; Pred. No. 1.1e-125;
Matches 150; Conservative 0; Mismatches 0; Indels
 35.5%; Score 150; DB 14; Length 440; llarity 100.0%; Pred. No. 1.1e-125; Conservative 0; Mismatches 0; Indels
 Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 34
 152 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 34, Application US/10174586
Publication No. US20030032106A1
GENERAL INFORMATION:
Desnoyers, Luc
Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Smith, Victoria
Watanabe, Colin K.
Wood, William I.
 Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
 Smith, Victoria
 Desnoyers, Luc
 APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
 ORGANISM: Homo Sapien
 ; ORGANISM: Homo Sapien
US-10-174-586-34
 Pan, James
 Pan,James
 Query Match
Best Local Similarity
Matches 150; Conserv
 RESULT 75
US-10-174-586-34
 JS-10-174-585-34
 LENGTH: 440
 APPLICANT:
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Sequence 34, Application US/10174585; Publication No. US20030032105A1; GENERAL INFORMATION:

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Oy 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75

Db 32 SAAALIPTGGGNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75

Oy 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPFRNLMIDIQK 135

Db 92 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPFRNLMIDIQK 151

Oy 136 DTAVEGEEIEVNCTAMASKDATTIRWFKGN 165

Db 152 DTAVEGEEIEVNCTAMASKDATTIRWFKGN 181

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Job time: 106.694 secs
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sequence 61, Application US/09866028

patent No. 6642560

GENERAL INFORMATION:

APPLICANT: Baker, Kevin

POTICANT: BOTELIN BOTELEIN DAVIG
 Grimaldi, Christopher
Gurney, Austin
Hillan, Kenneth
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary
Goddard, Audrey
Godowski, Paul
 Query Match
Best Local Similarity 100.
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 APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
 Kljavin, Ivar
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RRIOR FILING DATE: Pebruary 28, 2001
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 FILING DATE: July 28, 1999
APPLICATION NUMBER: PCT/US98/19330
FILING DATE: September 16, 1998
APPLICATION NUMBER: PCT/US98/25108
 RR FILING DATE: February 9, 1998
RR APPLICATION NUMBER: 60/075,945
RFILING DATE: February 25, 1998
RR PILING DATE: December 16, 1998
RFILING DATE: December 16, 1998
RFILING DATE: December 22, 1998
RFILING DATE: December 22, 1998
RR PADLICATION NUMBER: 60/113,296
 TYPE: PRT
CORGANISM: Homo Sapien
US-09-944-457-61
 92
 136
 152
 RESULT
 <u> </u> 8
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 TITLE OF INVENTION: SECRETE

TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: PS549FICH
FILE REFERENCE: PS549FICH
CURRENT APPLICATION NUMBER: US/09/944,457
CURRENT FILING DATE: 2001-09-26
PRIOR PELING DATE: 2001-05-26
PRIOR PELING DATE: 000-06-33
PRIOR PELING DATE: 000-06-33
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 11, 1997
PRIOR PELING DATE: December 12, 1997
PRIOR PELING DATE: December 16, 1997
PRIOR PELING DATE: December 16, 1997
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PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
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PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: December 17, 1997
PRIOR PELING DATE: PELCATION NUMBER: 60/069, 607
PRIOR PELING DATE: PELCATION NUMBER: 60/069, 607
PRIOR PELING DATE: PELCATION NUMBER: 60/069, 607
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
PRIOR PELING DATE: PELCATION NUMBER: 60/070, 407
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 151
 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 32 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 91
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 Length 440;
 0; Indels
 Score 150; DB 4; Le
Pred. No. 4.3e-132;
 35.5%; Scor.
100.0%; Pred. No. %...
... 0; Mismatches
 136 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 181
 RESULT 3
US-09-944-457-61
Sequence 61, Application US/09944457
Patent No. 6734288
; GENERAL INFORMATION:
 Godowski,Paul
Grimaldi,Christopher
 Ferrara, Napoleone
Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
 Query Match
Best Local Similarity 100.0
Matches 150, Conservative
 APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
 Hillan, Kenneth
 Gurney, Austin
 Kljavin, Ivar
 Roy, Margaret
Tumas, Daniel
 Napier, Mary
US-09-866-028-61
 92
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 152
 APPLICANT:
APPLICANT:
APPLICANT:
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GENERAL INFORMATION:
APPLICANT PETERSEN, CRROLYN
APPLICANT LEECH, JAMES
APPLICANT LEECH, JAMES
APPLICANT LEECH, JAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: WUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT PELLING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 9
LENGTH: 130
 Sequence 5, Application US/09060767B

Sequence 5, Application US/09060767B

Patent No. 6720152

GENERAL INFORMATION:

APPLICANT: Well, Gary

APPLICANT: Chandrashekar, Ramaswamy

TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION: Laganosis of Histoplasmosis Using Antigens Specific for TITLE OF INVENTION UNMERS: US/09/060,767B

CURRENT PELING DATE: 1998-04-15

PRIOR FILING DATE: 1997-04-15

NUMBER OF SEQ ID NOS: 9

SOFTWARR: Patentin version 3.0

SEQ ID NOS: 9
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 ch 3.3%; Score 14; DB 3; Length 130; l Similarity 100.0%; Pred. No. 3.3e-05; 14; Conservative 0; Mismatches 0; Indels
 Length 41;
 0; Indels
 DB 4; Le
1.3e-06;
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
 Query Match 3.5%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 1.3 Matches 15; Conservative 0; Mismatches
 RESULT 8
US-08-928-361B-14
; Sequence 14, Application US/08928361B
; Patent No. 6071518
 US-08-700-651-9; Sequence 9, Application US/08700651B; Patent No. 6015882
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 321 PPTTTTTTTTTT 335
 1 PPTTTTTTTTT 15
 322 PTTTTTTTTTT 335
 48 Priririririr 61
 Query Match
Best Local Similarity
 TYPE: PRT
ORGANISM: Leishmania
 RESULT 6
US-09-060-767B-5
 US-09-060-767B-5
 US-08-700-651-9
 FEATURE:
 Matches
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 Sequence 1, Application US/09930803

Patent No. 6596493

GENERAL INFORMATION:
APPLICANT: TREEVES, ROGER
APPLICANT: TREEVES, ROGER
APPLICANT: YOSHINORI, MUTAMAKI
APPLICANT: YOSHINORI, MUTAMAKI
APPLICANT: YOSHINORI, MUTAMAKI
APPLICANT: YOSHINORI, MUTAMAKI
TITLE OF INVENTION: DIGGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
FILE REFERENCE: JULI 770-1
CURRENT APPLICATION NUMBER: US/09/930,803
CURRENT FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 1
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLINFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIOK 153
 76 DSRFQLLNFSSSELKVSLTNVSISDEGRYFCQLYTDPPQESYTTITVLVPPRNLMIDIQK 135
 94 DSRFQLINFSSSELKVSLINVSISDEGRYFCQLYIDPPQESYTTITVLVPPRNLMIDIQK 153
 16 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 75
 34 SAAALIPTGDGQNLFTKDVTVIEGEVATISCQVNKSDDSVIQLLNPNRQTIYFRDFRPLK 93
 Gaps
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 Query Match 35.5%; Score 150; DB 4; Length 442; Best Local Similarity 100.0%; Pred. No. 4.3e-132; Matches 150; Conservative 0; Mismatches 0; Indels
 35.5%; Score 150; DB 4; Length 442;
 0; Indels
 APPLICANT:
Faum, Peter
Molecules Designated B7L1
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: 1999-08-05
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR PILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-05
PRIOR FILING DATE: 1999-08-07
PRIOR FILING DATE: 1999-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.0
 Best Local Similarity 100.0%; Pred. No. 4.3e-132; Matches 150; Conservative 0; Mismatches 0;
 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 154 DTAVEGEEIEVNCTAMASKPATTIRWFKGN 183
 DIAVEGEEIEVNCTAMASKPATTIRWFKGN 165
 Sequence 20, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
 ORGANISM: Homo sapiens
 TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-20
 SOFTWARE:
SEQ ID NO 20
LENGTH: 442
 US-09-778-510-20
 LENGTH: 442
 RESULT 5
US-09-930-803-1
 US-09-930-803-1
 136
 PRT
 136
 Query Match
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3.3%; Score 14; DB 3; Length 175; 100.0%; Pred. No. 4.4e-05;
 3.3%; Score 14; DB 4; Lo
100.0%; Pred. No. 3.3e-05;
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
 Query Match 3.3%; Score 14; DB Best Local Similarity 100.0%; Pred. No. 3.3 Matches 14; Conservative 0; Mismatches
 100.0%; Prec. ...
 E: PETERS, VERNY, JONES & BIKSA
385 Sherman Avenue, Suite 6
; PRIOR FILING DATE: 1995-04-03; NUMBER OF SEQ ID NOS: 115; SCQ ID NO 14; LENGTH: 130; TYPE: RT.
; ORDANISM: Cryptosporidium parvum US-09-588-995A-14
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 322 PTTTTTTTTTT 335
 322 PTTTTTTTTTTT 335
 48 PITITITITIT 61
 3.3%
Best Local Similarity 100.0
Matches 14; Conservative
 COUNTRY: USA
ZIP: 94306-1840
 STREET: 385 Sher
CITY: Palo Alto
STATE: CA
 US-08-928-361B-17
 US-08-700-651-12
 US-08-700-651-12
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), Carolyn PEPTIDES, GLYCOPROTEINS, PEPTIDES, POLYEPTIDES, GLYCOPROTEINS, THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BUELSON RICHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REPERENCE: 480.19-5
CURRENT FILING DATE: 2000-66-06
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR PILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/170,651
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR PILING DATE: 1996-08-14
 ö
 Score 14; DB 3; Length 130;
Pred. No. 3.3e-05;
 0; Indels
 STATE: ...
COUNTRY: USA
ZIP: 94306-1840
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPALIAL
SOFTWARE: PREADIN PRE-BREAT BROWN STATEM: PC-DOS/MS-DOS
SOFTWARE: PREADIN DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE DOCKET NUMBER: 30,518
REFERENCE DOCKET NUMBER: 30,518
REFERENCE DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1678
 APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 Mismatches
 US-09-588-995A-14; Application US/09588995A; Sequence 14, Application US/09588995A; Patent No. 6514697; GENERAL INFORMATION:
 3.3%; Scallarity 100.0%; P. Conservative 0;
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
 322 PTTTTTTTTTT 335
 LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 PTTTTTTTTT 61
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Query Match
Best Local Similarity
Matches 14; Conservat
 GENERAL INFORMATION:
 US-08-928-361B-14
 48
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DNAS AND RNAS

Gaps

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Length 130;

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COMPUTER READABLE FORM:
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Gaps ; 0

Indels

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NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 87 PTTTTTTTTT 100
 323 TTTTTTTTTT 336
 113 TTTTTTTTTT 126
 Query Match
Best Local Similarity 100.0 Matches 14; Conservative
 TYPE: PRT;
CRGANISM: Candida albicans
US-09-248-796A-21069
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 650-324-1678
 COUNTRY: USA
ZIP: 94306-1840
 US-08-928-361B-8
 RESULT 14
 ò
 g
 Sequence 17, Application US/09588995A

Sequence 17, Application US/09588995A

Sequence 17, Application US/09588995A

GENERAL INFORMATION:

APPLICANT: BETERSEN. CAROLYN

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

APPLICANT: BARNES, DEBRA A.

TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: INFECTIONS

TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 480.19-5

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT APPLICATION NUMBER: 08/025,171

PRIOR FILING DATE: 1997-09-12

PRIOR FILING DATE: 1997-09-12

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1996-08-14

PRIOR FILING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 115

SOSTWARE: Patentin Ver. 2.1
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 Query Match 3.3%; Score 14; DB 4; Length 175; Best Local Similarity 100.0%; Pred. No. 4.4e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 3; Length 175; 100.0%; Pred. No. 4.4e-05; tive 0; Mismatches 0; Indels
 SOFTWARE PATENTING STATEM STAT
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 ; ORGANISM: Cryptosporidium parvum
US-09-588-995A-17
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
 322 PTTTTTTTTT 335
 322 PTTTTTTTTTT 335
 LENGTH: 175 amino acids TYPE: amino acid
 Best Local Similarity 100.0
Matches 14; Conservative
 TOPOLOGY: linear
MOLECULE TYPE: protein
 RESULT 12
US-09-588-995A-17
 US-08-928-361B-17
 SEQ ID NO 17
LENGTH: 175
 TYPE: PRT ORGANISM:
 Query Match
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Wis-09-248-796A-21069

Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

Sequence 21069, Application US/09248796A

FRICANT: Keith Weinstock et al

TILLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANG.

TILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQUID NOS: 28208
 Sequence 8, Application US/08928361B

Sequence 8, Application US/08928361B

Fatent No. 6071518

GENERAL INFORMATION:

APPLICANT: Petersen, Carolyn

TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GIYCOPROTEINS,

TITLE OF INVENTION: PRATIMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: SPECIES INFECTIONS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: PETERS, VERNY, JONES & BIKSA

STREET: 385 Sherman Avenue, Suite 6

CITY: Palo Alto
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 Length 197;
 Indels
 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: Elem For Compatible
OPERATION SYSTEM: PC-005/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 3.3%; Score 14; DB 4; Le. 100.0%; Pred. No. 4.9e-05; iive 0; Mismatches 0;
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Sequence 8, Application US/09588995A Patent No. 6514697 GENERAL INFORMATION: APPLICANT: PETERSEN, CAROLYN
 322 PTTTTTTTTTT 335
 322 PTTTTTTTTTT 335
 70 Priritiritirii 83
 US-09-588-995A-8
 FEATURE:
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 Sequence 27, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
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TITLE O
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 Query Match 3.3%; Score 14; DB 3; Length 216; Best Local Similarity 100.0%; Pred. No. 5.3e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 3; Length 216; 100.0%; Pred. No. 5.3e-05;
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PATENTIN Release #1.0, Version #1.30
PLICATION NUMBER: US/08/928,361B
PILING DATE: 12-SEP-1997
 0; Mismatches
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
 100.08;
 322 PTTTTTTTTTT 335
 322 PTTTTTTTTTT 335
 LENGTH: 216 amino acids
TYPE: amino acid
STRANDEDNESS:
 70 PTTTTTTTTT 83
LENGTH: 216 amino acids
 14; Conservative
 TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
 TOPOLOGY: linear
MOLECULE TYPE: protein
 Query Match
Best Local Similarity
 RESULT 15
US-08-928-361B-27
 US-08-928-361B-27
 US-08-928-361B-8
 STATE: CA
 Matches
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RESULT 16 US-09-588-995A-8

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RESULT 17
US-08-700-651-15
is Sequence 15, Application US/08700651B
is Patent No. 6015882
is Patent No. 6015882
is Patent No. 6015882
is Patent No. 6015882
is Patent No. 6015882
is Patent No. 6015882
is Patent No. 6015882
is APPLICANT: DETENBY, CAROLYN
is APPLICANT: DETENBY, CAROLYN
is APPLICANT: MICHARD, C.
is APPLICANT: WICHARD, C.
is APPLICANT: WICHARD, C.
is TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
is TITLE OF INVENTION: INFECTIONS
is TITLE OF INVENTION: 1NFECTIONS
is TITLE OF INVENTIONS
is TITLE OF INVENTIONS
is TITLE OF INVENTIONS
is TITLE OF INVENTIONS
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APPLICANT: FETENSEM. CHANGEN
APPLICANT: PETENSEM. CHANGEN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, RIGHARD C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION UNMER: US/09/58,995A
CURRENT APPLICATION NUMBER: US/09/28,361
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 8

LENGTH: 216
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 Gaps
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 Ouery Match
3.3%; Score 14; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 5.3e-05;
Matches 14; Conservative 0; Mismatches 0; Indels
 Query Match 3.3%; Score 14; DB 3; Length 249; Best Local Similarity 100.0%; Pred. No. 6.1e-05; Matches 14; Conservative 0; Mismatches 0; Indels
 , OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-15
 ORGANISM: Cryptosporidium parvum
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 165 PTTTTTTTTTT 178
 엄
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Gaps
 APPLICANT: Chang, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith Plasmid Vectors for Cellular
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NOMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526ris
STREET: One Liberty Place 46th Floor
CITY: Philadelphia
 ;
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 Query Match 3.3%; Score 14; DB 1; Length 887; Best Local Similarity 100.0%; Pred. No. 0.00019; Matches 14; Conservative 0; Mismatches 0; Indels
 3.3%; Score 14; DB 4; Length 249;
100.0%; Pred. No. 6.1e-05;
tive 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/867,106
FILING DATE: 19220625
PRIOR APPLICATION NUMBER: PCTAU90/00530
FILING DATE: 02-NOV-1989
ATTORNEY/AGBNT INFORMATION:
NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
REFERENCE/DOCKET NUMBER: RICE-0002
RELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBHONE: 215-568-3439
INFORMATION FOR SEQ ID NO: 3:
 PRIOR FILING DATE: 1997-09-12
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 249
 PRIOR APPLICATION NUMBER: 08/928,361
 Sequence 3, Application US/07867106
Patent No. 5389526
GENERAL INFORMATION:
 TYPE: PRT ; ORGANISM: Cryptosporidium parvum US-09-588-995A-20
 322 PTTTTTTTTTT 335
 165 PÝTÝTÝTÝTÝTÝ 178
 322 PTTTTTTTTT 335
 LENGTH: 887 amino acids
 14; Conservative
 SEQUENCE CHARACTERISTICS
 TOPOLOGY: linear; MOLECULE TYPE: protein US-07-867-106-3
 Best_Local Similarity
Matches 14; Conserv
 USA
 COUNTRY:
ZIP: 1910
 US-07-867-106-3
 Query Match
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bequence 20, Application US/08928361B
| Patent No. 6071518
| CENERAL INFORMATION:
| APPLICANT: Petersen, Carolyn
| TITLE OF INVENTION: PEPTIDES, GLYCOPROTEINS,
| TITLE OF INVENTION: PEPTIDES, MUTANTS, VARIANTS, NALOGS AND FRAGMENTS
| TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
| TITLE OF INVENTION: SPECIES INFECTIONS
| NUMBER OF SEQUENCES: 30
| CORRESPONDENCE ADDRESS:
| ADDRESSE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6
| CITY: Palo Alto
 Sequence 20, Application US/09588995A

Sequence 20, Application US/09588995A

Batent No. 6514697

GENERAL INFORMATION:
APPLICANT: PETERSEN, CARCLYN
APPLICANT: GUT, JIRI
TITLE OF INVENTION: ISOLATES AND FITLE OF INVENTION:
TITLE OF INVENTION: ISOLATES AND FITLE OF INVENTION: ISOLATES AND FILE OF INVENTION: ISOLATES AND FILE OF INVENTION: ISOLATES AND FILE OF INVENTION: ISOLATES AND FILE OF INVENTION: ISOLATES AND FILE OF INVENTION: ISOLATES AND FILE REFERENCE: 480.19-5

CURRENT APPLICATION NUMBER: US/09/588,995A

CURRENT PILING DATE: 1997-03-27

PRIOR FILING DATE: 1997-03-27
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 Gaps
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 3.3%; Score 14; DB 3; Length 249;
100.0%; Pred. No. 6.1e-05;
tive 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FLING DATE: 12-SEP-1997
CLASSIFICATION:
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELECHONE: 650-324-1677
 322 PTTTTTTTTTT 335
 LENGTH: 249 amino acids TYPE: amino acid
 Query Match 3.3
Best Local Similarity 100.
Matches 14; Conservative
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 MOLECULE TYPE: protein
 linear
 USA
 STRANDEDNESS
 RESULT 18
US-08-928-361B-20
; Sequence 20, App
 US-08-928-361B-20
 RESULT 19
US-09-588-995A-20
 COUNTRY:
 165
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Sequence 5, Application US/08928361B
Facent No. 6071518
GENERAL INFORMATION:
APPLICANT: Perfersen, Carolyn
TITLE OF INVENTION: THEIR FUNCTIONAL MOTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: THEIR FUNCTIONAL MOTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
 APPLICANT: BARNES, CARCALIN
APPLICANT: BARNES, DBERA C.
APPLICANT: NELSON, RICHARD C.
APPLICANT: NELSON, RICHARD C.
APPLICANT: OUT, JITI
APPLICANT: OUT, JITI
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REPERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/58,995A
CURRENT FILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR PRILING DATE: 1996-08-14
PRIOR PRILING DATE: 1995-04-03
NUMBER: OF SEQ ID NOS: 115
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COURSE PRICED NOS: 120
COURSE PRICED NO
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 Gaps
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 3.3%; Score 14; DB 4; Length 1721;
100.0%; Pred. No. 0.00036;
tive 0; Mismatches 0; Indels
 3.3%; Score 14; DB 3; Length 1721;
100.0%; Pred. No. 0.00036;
tive 0; Mismatches 0; Indels
 Sequence 6, Application US/09588995A
Patent No. 6514697
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
 LENGTH: 1721 amino acids
TYPE: amino acid
STRANDEDNESS:
 322 PTTTTTTTTTT 335
 307 Pritririririi 320
 322 PITITITITIT 335
 307 PTTTTTTTTTTT 320
 650-324-1677
 Query Match
Best Local Similarity 100.0
Matches 14; Conservative
 Best Local Similarity 100.0
Matches 14; Conservative
 TOPOLOGY: linear MOLECULE TYPE: protein
 TELEPHONE:
 US-08-928-361B-6
 RESULT 24
US-08-928-361B-5
 RESULT 23
US-09-588-995A-6
 LENGTH: 1721
 US-09-588-995A-6
 SEQ ID NO 6
 Query Match
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 us-us-/uu-bal-5
Squence 5, Application US/08700651B
Patent No. 6015802
GENERAL INFORMATION:
APPLICANT: BEECH, JAMES
APPLICANT: BEECH, JAMES
APPLICANT: BECH, JANES
APPLICANT: GUT, JIRI
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: 1087-08-14
TITLE OF INVENTION: 1087-08-14
TITLE OF INVENTION: 1087-08-14
TITLE OF INVENTION: 1087-15-14
TITLE OF INVENTION: 1087-15-14
TITLE OF INVENTION: 1087-15-14
TITLE OF INVENTION: 1087-15-14
TITLE OF INVENTION: 1087-15-14
TITLE OF INVENTION: 1087-15-14
TITLE OF INVENTION: 1087-15-14-03
TITLE OF INVENTION: 1087-15-14-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SSQ ID NO 5
LENGTH: 1721
 THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM SPECIES INFECTIONS
 DNAS AND RNAS
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 Gaps
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 Score 14; DB 3; Length 1721;
Pred. No. 0.00036;
 , Carolyn POLYPEPTIDES, GLYCOPROTEINS,
 0; Indels
 STATE: CA
COUNTRY: USA
ZIP: 94306-1840
COMPUTER READBALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FT:ING DATE: 12-SEP-1997
 Sequence 6, Application US/08928361B
Patent No. 6071518
CENERAL INFORMATION:
FITTLE OF INVENTION: PEPTIDES, POLYPEPTIDES, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS; TITLE OF INVENTION: SPECIES INFECTIONS INVENTION: SPECIES INFECTIONS CORRESPONDENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCES: 30
CORRESPONDENCES: BTERS, VENY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
 3.3%; Scor.
100.0%; Pred. No. v.
0; Mismatches
 RECISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
 FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 , ORGANISM: Cryptosporidium parvum
US-08-700-651-5
 250 PITITITITIT 263
 322 PTTTTTTTTTT 335
 14; Conservative
 Query Match
Best Local Similarity
 Palo Alto
 RESULT 22
US-08-928-361B-6
 US-08-700-651-5
 307
 TYPE: PRT
 Matches
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ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,896

ER PILING DATE: 1997-06-06

ER FILING DATE: 1997-06-06

ER FILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER PELING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,895

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,895

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,991

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,991

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,991

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,882

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,893

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,893

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,893

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,893

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,893

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048,893
 EX FILING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/048,901

EX PILING DATE: 1997-06-06

EX PRILING DATE: 1997-06-06

EX PRILING DATE: 1997-06-06

EX PRILING DATE: 1997-06-06

EX ELING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/049,019

EX RILING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/049,019

EX PILING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/048,970

EX FILING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/048,972

EX PRILING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/048,972

EX PLING DATE: 1997-06-06

EX APPLICATION NUMBER: 60/048,972
 R FILING DATE: 1997-06-06
R RAPLICATION NUMBER: 60/049,373
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,875
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R FILING DATE: 1997-06-06
 RESULT 26
US-09-205-258-953
; Sequence 953, Application US/09205258
; Patent No. 6525174
 TTTT 335
 378 Piriririririr 391
 Best Local Similarity 100.
Matches 14; Conservative
 322 PTTTTT
 Query Match
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 ## Sequence 5, Application US/09588995A

| Sequence 5, Application US/09588995A
| Patent No. 6514697
| GENERAL INFORMATION:
| APPLICANT: PETERSEN, CAROLYN
| APPLICANT: BARNES, DEBRA A.
| APPLICANT: BARNES, DEBRA A.
| APPLICANT: BARNES, DEBRA A.
| APPLICANT: NELSON, RICHARD C.
| TITLE OF INVENTION: INFECTIONS FOR DIAGNOSIS OF CRYPTOSPORIDIUM
| TITLE OF INVENTION: INFECTIONS
| TITLE OF INVENTION: INFECTIONS
| TITLE OF INVENTION: INFECTIONS
| FILE REFERENCE: 480.19-5
| CURRENT FILING DATE: 1997-03-27
| PRIOR FILING DATE: 1997-03-27
| PRIOR FILING DATE: 1995-08-14
| PRIOR FILING DATE: 1995-08-14
| PRIOR FILING DATE: 1995-08-14
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| PRIOR FILING DATE: 1995-08-14
| PRIOR FILING DATE: 1995-08-14
| PRIOR
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 Gaps
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 Query Match 3.3%; Score 14; DB 3; Length 1837; Best Local Similarity 100.0%; Pred. No. 0.00038; Matches 14; Conservative 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRICK APPLICATION:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATORNEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUTCATION INFORMATION:
385 Sherman Avenue, Suite 6
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-5
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 TTTTTT
 378 PTTTTTTTTT 391
 / MOLECULE TYPE: protein US-08-928-361B-5
 amino acid
 linear
 Palo Alto
 322 PTTTTT
 USA
 RESULT 25
US-09-588-995A-5
 COUNTRY:
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Gaps
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0
3.3%; Score 14; DB 4; Length 1837;
100.0%; Pred. No. 0.00038;
tive 0; Mismatches 0; Indels
 APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
 CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER PILING DATE: 1998-06-04
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,881
EARLIER APPLICATION NUMBER: 60/048,881
EARLIER APPLICATION NUMBER: 60/048,880
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Sequence 23083, Application US/09248796A

Factor 23083, Application US/09248796A

Factor No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANF
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT PAPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 23083
 ö
 GENERAL INCORMATION:
APPLICANT: Weil, Gary
APPLICANT: Weil, Gary
APPLICANT: Weil, Gary
APPLICANT: Weil, Gary
APPLICANT: Weil, Gary
APPLICANT: Chandrashear, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
TITLE OF INVENTION NUMBER: US/09/060,767B
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 9-04-15
NUMBER OF SEQ ID NOS: 9-04-15
SOFTWARE: Patentin version 3.0
SEQ ID NO SEQ ID NOS: 9-04-15
LENGTH: 57
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 Length 57;
 3.1%; Score 13; DB 4; Length 57;
100.0%; Pred. No. 0.00014;
 0: Indels
 DB 3; Le
0.00014;
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 Pred. No. 0.0
Mismatches
 Sequence 9, Application US/09060767B Patent No. 6720152
 100.0%; PER
0;
 TYPE: PRT
ORGANISM: Histoplasma Capsulatum
 323 TITITITITI 335
 320 PPPTTTTTTT 332
 TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
 TYPE: PRT
ORGANISM: Candida albicans
 single
 TYPE: amino acid
STRANDEDNESS: si
 linear
 US-09-248-796A-23083
 MOLECULE TYPE:
 HYPOTHETICAL:
 TELEPHONE:
 ; ANTI-SENSE:
US-08-900-230-59
 TOPOLOGY:
 US-09-060-767B-9
 US-09-060-767B-9
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 Sequence 59, Application US/08900230
Patent No. 6329197
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham Lip
STREET: 1185 Avenue of The Americas
 Score 13; DB 4; Length 44;
Pred. No. 0.00011;
 COUNTK::

ZIF: 11036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/900,230
FTIING DATE: 23-JUL-1997
 3.1%; >\cdot\ 100.0%; Pred. No. \cdot\ \cdot
 NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-C/JPW/ADM
FELECOMMUNICATION INFORMATION:
EARLIER APPLICATION NUMBER: 60/048,917
BARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1997-06-06
BEARLIER APPLICATION NUMBER: 60/048,937
BEARLIER FILING DATE: 1997-06-06
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BEARLIER FILING DATE: 1997-06-06
BEARLIER FILING DATE: 1998-07-15
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BEARLIER FILING DATE: 1998-07-15
BEARLIER FILING DATE: 1998-07-15
BEARLIER FILING DATE: 1998-07-15
BEARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227

BEARLIER FILING DATE: 1998-07-30

SEQ ID NO 953

LENGTH: 44
 401 DADTAIINAEGGQ 413
 21 DADTAIINAEGGO 33
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 , TYPE: PRT
, ORGANISM: Homo sapiens
US-09-205-258-953
 New York
 CITY: New York
STATE: New Yorl
COUNTRY: U.S.A
 RESULT 27
US-08-900-230-59
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Sequence 19. Application US/08928361B
Sequence 19. Application US/08928361B
Patent No. 6071518
Patent No. 6071518
Patent No. 6071518
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
 ö
 18-09-588-995A-19
Sequence 19, Application US/09588995A
Sequence 19, Application US/09588995A
Patent No. 651469.
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: INFOCTIONS
TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
 Gaps
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 3.1%; Score 13; DB 3; Length 91;
100.0%; Pred. No. 0.00021;
ive 0; Mismatches 0; Indels
 COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRICA STEING TON:
PRICA STEING TON:
PRICA STEING TON:
REPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: VETTY, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
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REFERENCE/DOCKET NUMBER: 30,518
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REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 30,518
REFERENCE/DATA TON:
TELEBEHONE: 650-324-1677
 ADDRESSEE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6 CITY: Palo Alto
 TELEFAX: 650-324-16/8
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
 323 TTTTTTTTTTT 335
 323 TTTTTTTTTT 335
 18 TTTTTTTTT 30
 18 rrrrrrrrrrrr 30
 Best Local Similarity 100.
Matches 13; Conservative
 MOLECULE TYPE: protein
 amino acid
 linear
 USA
 STRANDEDNESS:
 ð
 TOPOLOGY:
 COUNTRY:
 LENGTH:
 Query Match
 ò
 g
 RESULT 30
US-09-248-796A-25289
is Sequence 25289, Application US/09248796A
is Patent No. 6747137
is GENERAL INFORMATION:
is APPLICANT: Keith Weinstock et al
itTILE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
itTILE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
itTILE OF INVENTION: NUMBER: US/09/248,796A
is CURRENT FILING DATE: 1999-02-12
is PRIOR APPLICATION NUMBER: US 60/074,725
is PRIOR PLILING DATE: 1998-08-13
is PRIOR PILING DATE: 1998-08-13
is NUMBER: US 60/096,409
is SEQ ID NOS: 28208
is SEQ ID NOS: 28208
is SEQ ID NOS 25289
 GLYCOPROTEINS, DNAS AND RNAS
 ö
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 APPLICANT: DETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: MELSON, RICHARD, C.
APPLICANT: MELSON, RICHARD, C.
APPLICANT: MUTAIT
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: NOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: NOR PROPHYLAXIS AND TREATMENT OF CRYPTOSPORIDIUM PARVUM FILE REFERENCE: 480.19-4(HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER PILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
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 Query Match 3.1%; Score 13; DB 3; Length 91; Best Local Similarity 100.0%; Pred. No. 0.00021; Matches 13; Conservative 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 4; Length 75; Best Local Similarity 100.0%; Pred. No. 0.00017; Matches 13; Conservative 0; Mismatches 0; Indels
 Length 63;
 0; Indels
 Score 13; DB 4; L
Pred. No. 0.00015;
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-14
 3.1%; Scor.
100.0%; Pred. No. co.
 Sequence 14, Application US/08700651B; Patent No. 6015882; GENERAL INFORMATION:
 ORGANISM: Cryptosporidium parvum
 322 PTTTTTTTTT 334
 323 TTTTTTTTTT 335
 36 Priririririr 48
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
US-09-248-796A-23083
 RESULT 31
US-08-700-651-14
 SEQ ID NO 14
LENGTH: 91
 FEATURE:
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APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOFROTEINS,
TITLE OF INVENTION: PHEN FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
STATE: CA
COUNTRY: USA
 TREATMENT OF Cryptosporidium parvum
 Gaps
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 Length 124;
 Indels
 GENERAL INCORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSCH, JAMES
TAPLICANT: NELSCH, VAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, G
TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF F
TITLE OF INVENTION: INFECTIONS
FILE REFRENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT APPLICATION NUMBER: 08/415,751
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 11
TYPE: PRT
TYPE: PRT
TYPE: PRT
CRACANISM: CTYPLOSPORIGIUM PATYUM
FEATURE:
CHARLINGRAMISM: CTYPLOSPORIGIUM PATYUM
FEATURE:
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CHARLINGRAMISM: CTYPLOSPORIGIUM
FEATURE:

 COMPUTER READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATE: US/08/928,361B
FILING DATE: 12-SEP-1997
Pred. No. 0.00024;
 Query Match
3.1%; Score 13; DB 3; Le
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0;
 Best Local Similarity 100.0%; Pred. No. 0.(
Matches 13; Conservative 0; Mismatches
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
 US-08-928-361B-16; Sequence 16, Application US/08928361B; Setent No. 6071518; GENERAL INFORMATION:
 Sequence 11, Application US/08700651B Patent No. 6015882
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 33 rrrrrrrrrrrr 45
 94306-1840
 RESULT 36
US-08-700-651-11
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 Sequence 36192, Application US/09270767
; Sequence 36192, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 36192
 Sequence 51409, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster:
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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 Score 13; DB 4; Length 106;
Pred. No. 0.00024;
 3.1%; Score 13; DB 4; Length 106;
 3.1%; Score 13; DB 4; Length 91;
100.0%; Pred. No. 0.00021;
ive 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 CURRENT APPLICATION NUMBER: US/09/588,995A CURRENT FILING DATE: 2000-06-06
 CURRENT FILING DATE: 2000-06-06
PRIOR APPLICATION NUMBER: 08/827,171
PRIOR PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-03-27
PRIOR APPLICATION NUMBER: 08/928,361
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR PILING DATE: 1996-08-14
PRIOR PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PARCHILIN Ver. 2.1
 ; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-36192
 ORGANISM: Drosophila melanogaster
 ORGANISM: Cryptosporidium parvum
 323 TTTTTTTTTT 335
 323 TTTTTTTTTTT 335
 Matches 13; Conservative
 Query Match
Best Local Similarity
 RESULT 34
US-09-270-767-36192
 RESULT 35
US-09-270-767-51409
 US-09-270-767-51409
 SEQ ID NO 51409
LENGTH: 106
 US-09-588-995A-19
 SEQ ID NO 19
LENGTH: 91
 TYPE: PRT
 Query Match
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TYPE: PRT
ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
 APPLICANT: NELSON, RICHARD, C.
 LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS:
 323 TTTTTTTTTT 335
 TOPOLOGY: linear MOLECULE TYPE: protein
 US-08-928-361B-12
 RESULT 40
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 GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM
TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: 08/927,171
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-12
PRIOR FILING DATE: 1995-04-03
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 16
LENGTH: 124
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 Gaps
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 Query Match 3.1%; Score 13; DB 3; Length 124; Best Local Similarity 100.0%; Pred. No. 0.00028; Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 124;
100.0%; Pred. No. 0.00028;
iive 0; Mismatches 0; Indels
FILING DATE: 13-SEP-1996

ATTONEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30,518
REGISTRATION NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 124 amino acids
TYPE: amino acids
TOPOLOGY: linear
TOPOLOGY: linear
 RESULT 38
US-09-588-995A-16
Gequence 16, Application US/09588995A
; Patent No. 6514697
 Sequence 7, Application US/08700651B; Patent No. 6015882; GENERAL INFORMATION: APPLICANT: PETERSEN, CAROLYN; APPLICANT: LEECH, JAMES
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 33 ririririririri 45
 Best Local Similarity 100.
Matches 13, Conservative
 US-08-928-361B-16
 US-09-588-995A-16
 RESULT 39
US-08-700-651-7
 Query Match
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Sequence 12, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
APPLICANT: Petersen, Carolyn
TITLE OF INVENTION: PEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: PER TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
OUNBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY: Palo Alto
 GLYCOPROTEINS, DNAS AND RNAS
AFFILIANS OF INVENTION: WACTINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: POR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-4(41), 651B
CURRENT AFPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
BARLIER PILING DATE: 1995-04-03
SOFTWARE: PARENT NEXT: 1995-04-03
SOFTWARE: PARENT NEXT: 2.0
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 Query Match
3.1%; Score 13; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 13; Conservative 0; Mismatches 0; Indels
 SIGHTS: CA
CUNTARY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPOTER: BATCHING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTONEY/AGENT INFORMATION:
NAME: Verny, Hana
REGISTRATION NUMBER: 30.518
REFERENCE/DOCKET NUMBER: 30.518
REFERENCE/DOCKET NUMBER: 480.76-1 (HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324.1677
 FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5
US-08-700-651-7
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Sequence 13, Application US/08928361B

Betent No. 6071518

GENERAL INFORMATION:

PAPLICANT: Petersen, Carolyn

TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,

TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM

TITLE OF INVENTION: SPECIES INFECTIONS
 Query Match 3.1%; Score 13; DB 3; Length 130; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 3; Length 130;
100.0%; Pred. No. 0.00029;
iive 0; Mismatches 0; Indels
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
 FEATURE:
; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-8
 TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, TITLE OF INVENTION: THEIR FUNCTIONAL MUTANITY TITLE OF INVENTION: FOR TREATMENT AND DETECT TITLE OF INVENTION: SPECIES INFECTIONS NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSE: PETERS, VERNY, JONES & BIKSA STREET: 385 Sherman Avenue, Suite 6 CITY: Palo Alto
 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
NAME: Verry, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 ; Sequence 13, Application US/09588995A; Patent No. 6514697
 ORGANISM: Cryptosporidium parvum
 INFORMATION FOR SEQ ID NO: 13:
 LENGTH: 130 amino acids
TYPE: amino acid
STRANDEDNESS:
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 Ouery Match
Best Local Similarity 100.C
Matches 13; Conservative
 39 ririririririr 51
 39 TTTTTTTTTTT 51
 SEQUENCE CHARACTERISTICS:
 650-324-1678
 TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-361B-13
 USA
 US-08-928-361B-13
 US-09-588-995A-13
 COUNTRY:
 TELEFAX:
 RESULT 44
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 g
 APPLICANT: DETERBEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: WISHON, RICHARD, C.
APPLICANT: GUT, JIRI
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS
TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
FILE REPERENCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
EARLIER APPLICATION NUMBER: US/08/15,751
EARLIER PILING DATE: 1997-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 8
 Sequence 12, Application US/09588995A

Patent No. 6514697

GERBEAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: WISCONTION: INPECTION C.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT GUT, JIRI
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION NUMBER: US/09/588,995A
CURRENT FILING DATE: 1997-03-27
FRIOR APPLICATION NUMBER: 08/926,361
FRIOR FILING DATE: 1997-09-12
FRIOR PILING DATE: 1997-09-12
FRIOR PILING DATE: 1997-09-12
FRIOR FILING DATE: 1997-09-12
FRIOR PILING DATE: 1995-08-14
FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE: 1995-08-14
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FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE: 1995-08-14
FRIOR FILING DATE:
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 Score 13; DB 3; Length 128;
Pred. No. 0.00028;
 Length 128;
 Query Match 3.1%; Score 13; DB 4; Length 128 Best Local Similarity 100.0%; Pred. No. 0.00028; Matches 13; Conservative 0; Mismatches 0; Indels
 0; Indels
 3.1%; scc.
100.0%; Pred. No. v
0; Mismatches
 US-08-700-651-8; Sequence 8, Application US/08700651B; Patent No. 6015882; GENERAL INFORMATION:
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 323 TTTTTTTTTT 335
 323 TITITITITI 335
 Query Match 3.1%
Best Local Similarity 100.0
Matches 13; Conservative
 37 TTTTTTTTTT 49
 37 İTİTİTİTİTİ 49
 RESULT 41
US-09-588-995A-12
US-08-928-361B-12
 US-09-588-995A-12
 LENGTH: 130
TYPE: PRT
 SEQ ID NO 12
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Sequence 15, Application US/08928361B
Patent No. 6071518
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: THEIR FUNCTIONAL MUTANTS, VARIANTS, ANALOGS AND FRAGMENTS
TITLE OF INVENTION: SPECIES INFECTIONS
TITLE OF INVENTION: SPECIES INFECTIONS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
CITY, Palo Alto
 US-09-588-995A-15

| Sequence 15, Application US/09588995A |
| Sequence 15, Application US/09588995A |
| Sequence 15, Application US/09588995A |
| GENERAL INFORMATION: |
| APPLICANT: BARNES, DEBRA A. |
| APPLICANT: BARNES, DEBRA A. |
| APPLICANT: WELSON, RICHARD C. |
| APPLICANT: GUT, JIRI METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND |
| TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM |
| TITLE OF INVENTION: INPECTIONS |
| FILE REPRESENTE: 2000-06-06 |
| CURRENT FILING DATE: 2000-06-06 |
| PRIOR PLILNG DATE: 1997-03-27 |
| PRIOR PLILNG DATE: 1997-03-27 |
| PRIOR FILING DATE: 1997-09-12 |
 Gaps
 .
0
 Length 138;
 0; Indels
 ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PLOPPY disk
COMPUTER: PLEM P. Compatible
OPERALING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION:
 DB 3; Le
0.00031;
 3.1%; Scort
100.0%; Pred. No. v.-
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTORNEY/AGENT INFORMATION:
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
 : 138 amino acids
amino acid
 323 TTTTTTTTTT 335
 Query Match
Best Local Similarity 100.
Matches 13, Conservative
 47 Triririririr 59
 TOPOLOGY: linear
MOLECULE TYPE: protein
 USA
 STRANDEDNESS:
 S
 US-08-928-361B-15
 US-08-928-361B-15
 COUNTRY:
 LENGTH:
 a
 JOHNSTON TO SERVING TREADY

JOHNSTON TO SERVING

APPLICANT: BETERSON, GRECLY

APPLICANT: BETESON, RICHARD, C.

APPLICANT: MELSON, RICHARD, C.

APPLICANT: MELSON, RICHARD, C.

APPLICANT: MELSON, RICHARD, C.

APPLICANT: MICHARD, C.

TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS

TITLE OF INVENTION: INFECTIONS

FILE REFERENCE: 480.19-4 (HV)

CURRENT APPLICATION NUMBER: US/08/700,651B

CURRENT PILING DATE: 1997-08-14

EARLIER PELLING DATE: 1995-04-03

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 10

LENGTH: 138
 TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE OF INVENTION: INPECTIONS
TITLE APPLICATION NUMBER: US/09/58,995A
CURRENT FILING DATE: 2000-06-06
PRIOR PILING DATE: 1997-03-27
PRIOR PILING DATE: 1997-03-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
PRIOR FILING DATE: 1996-08-14
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PRIOR FILING DATE: 1996-08-14
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 3.1%; Score 13; DB 3; Length 138; 100.0%; Pred. No. 0.00031; ive 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 4; Length 130; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 13; Conservative 0; Mismatches 0; Indels
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
 Sequence 10, Application US/08700651B
Patent No. 6015882
GENERAL INFORMATION:
 TYPE: PRT Cryptosporidium parvum US-09-588-995A-13
 ORGANISM: Cryptosporidium parvum
 BARNES, DEBRA A.
NELSON, RICHARD C.
GUT, JIRI
 CAROLYN
 323 TTTTTTTTTT 335
 323 TTTTTTTTTT 335
 39 rrrrrrrrrrrr 51
 47 ririririririr 59
 13; Conservative
 Query Match
Best Local Similarity
Matches 13; Conserv
GENERAL INFORMATION:
 RESULT 45
US-08-700-651-10
 US-08-700-651-10
 SEQ ID NO 13
LENGTH: 130
 RESULT 46
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323 TITITITITIT 335
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Sequence 21631, Application US/09248796A

Sequence 21631, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

CURRENT FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR PRILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 21631

LENGTH: 159
 APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: BARNES, DEBRA A.
APPLICANT: NELSON, RICHARD C.
APPLICANT: WELSON, RICHARD C.
TITLE OF INVENTION: METHODS FOR DETECTION OF CRYPTOSPORIDIUM SPECIES AND TITLE OF INVENTION: ISOLATES AND FOR DIAGNOSIS OF CRYPTOSPORIDIUM TITLE OF INVENTION: INFECTIONS
TITLE OF INVENTION: INFECTIONS
FILE REFERENCE: 480.19-5
CURRENT APPLICATION NUMBER: US/09/588,995A
CURRENT FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1997-09-12
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1995-08-14
PRIOR FILING DATE: 1995-08-14
SPRIOR FILING DATE: 1995-08-15
SPRIOR FILING DATE: 1995-08-15
SPRIOR FILING DATE: 1995-08-15
SPRIOR FILING DATE: 1995-08-15
SEQ ID NO 18
SEQ ID NO 18
LENGTH: 150
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 DB 4; Length 150; 0.00033;
 Query Match 3.1%; Score 13; DB 4; Length 159; Best Local Similarity 100.0%; Pred. No. 0.00035; Matches 13; Conservative 0; Mismatches 0; Indels
 3.1%; Score 13; DB 100.0%; Pred. No. 0.0; ive 0; Mismatches
 Sequence 18, Application US/09588995A
Patent No. 6514697
 ; TYPE: PRT
; ORGANISM: Cryptosporidium parvum
US-09-588-995A-18
 323 TTTTTTTTT 335
 324 TITITITITI 336
 Best Local Similarity 100.
Matches 13; Conservative
 62 rrrrrrrrrrrr 74
 ORGANISM: Candida albicans
 52 rrrrrrrrrrrri 64
 APPLICANT: PETERSEN,
 US-09-248-796A-21631
 US-09-248-796A-21631
 Query Match
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 US-08-928-361B-18
Sequence 18, Application US/08928361B
Sequence 18, Application US/08928361B
Sequence 18, Application US/08928361B
Sequence 18, Application
GENERAL INFORMATION:
TITLE OF INVENTION: PEPTIDES, POLYPEPTIDES, GLYCOPROTEINS,
TITLE OF INVENTION: FOR TREATMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
INVERTION: SPECIES INFECTIONS
INVERTION: SPECIES INFECTIONS
OCRRESPONDENCE ADDRESS:
ADDRESSEE: PETERS, VERNY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
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 Gaps
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0
 3.1%; Score 13; DB 4; Length 138; 100.0%; Pred. No. 0.00031; tive 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 3; Length 150; Best Local Similarity 100.0%; Pred. No. 0.00033; Matches 13; Conservative 0; Mismatches 0; Indels
 COUNTRY: USA
ZIP: 94306-1840
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/928,361B
FILING DATE: 12-SEP-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/026,062
FILING DATE: 13-SEP-1996
ATTONENEY/AGENT INFORMATION:
 NAME: Verny, Hana
REGISTRATION NUMBER: 30,518
REFERENCE/DOCKET NUMBER: 480.76-1(HV)
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-324-1677
PRIOR APPLICATION NUMBER: 08/700,651
PRIOR FILING DATE: 1996-08-14
PRIOR APPLICATION NUMBER: 08/415,751
PRIOR FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 15
LENGTH: 138
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 TELEFAX: 650-324-1678
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
 LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS:
 323 TTTTTTTTTT 335
 47 Tritiriririi 59
 Local Similarity 100.
hes 13; Conservative
 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-928-3618-18
 Palo Alto
 US-09-588-995A-15
 Query Match
Best Local S
Matches 13
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Sequence 17391, Application US/09248796A

Sequence 17391, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WOLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: WUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 17391

LENGTH: 216
 LOCATION: (212)
OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknov
 Sequence 24111, Application US/09248796A
| Patent No. 6747137
| GENERAL INFORMATION:
| APPLIATE OF INVENTION: NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANE; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 APPLICANT: Weil, Gary
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
FILE REFERENCE: BJCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT APPLICATION NUMBER: 0990-04-15
PRIOR PILING DATE: 1999-04-15
NUMBER: OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 211
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 3.1%; Score 13; DB 4; Length 211;
100.0%; Pred. No. 0.00045;
iive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 216; 100.0%; Pred. No. 0.00046; Pred. No. 0.10046; ive 0; Mismatches 0; Indels
 Sequence 3, Application US/09060767B Patent No. 6720152
 TYPE: PRT
ORGANISM: Histoplasma capsulatum
 320 PPPTTTTTTT 332
 323 TTTTTTTTTTT 335
 37 PPPTTTTTTT 49
 ORGANISM: Candida albicans FEATURE:
 Best Local Similarity 100.
Matches 13; Conservative
 13; Conservative
 Best Local Similarity
Matches 13; Conserv
 GENERAL INFORMATION:
 US-09-248-796A-17391
 NAME/KEY: UNSURE
 RESULT 55
US-09-248-796A-24111
 US-09-248-796A-17391
 US-09-060-767B-3
US-09-060-767B-3
 Query Match
 Query Match
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 RESULT 52
US-09-248-796A-16058
1 Sequence 16058, Application US/09248796A
2 Patent No. 6747137
3 GENERAL INFORMATION:
3 APPLICANT: Keith Weinstock et al
4 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
5 TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
6 CURRENT FILING DATE: 1999-02-12
7 CURRENT FILING DATE: 1999-02-13
8 PRIOR APPLICATION NUMBER: US 60/074,725
8 PRIOR PELING DATE: 1998-08-13
9 PRIOR FILING DATE: 1998-08-13
1 NUMBER OF SEQ ID NOS: 28208
1 SEQ ID NO 16058
1 LENGTH: 207
 Sequence 13. Application US/08700651B

Patent No. 601582
GENERAL INFORMATION:
APPLICANT: PETERSEN, CAROLYN
APPLICANT: DEECH, JAMES
APPLICANT: HEECH, JAMES
APPLICANT: HEECH, JAMES
TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: ROR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum
FILE OF INVENTION: WACCINES, ANTIBODIES, PROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: WACCINES, ANTIBODIES, PROTEINS, DNAS AND RNAS;
TITLE OF INVENTION: UNRECTIONS
FILE REPERBUCE: 480.19-4 (HV)
CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14

BARLIER APPLICATION NUMBER: 08/415,751

BARLIER PILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
SOFTWARE PATENTED PATENTIN VET: 2.0
 ; LOCATION: (204)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-16058
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 Gaps
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 3.1%; Score 13; DB 3; Length 162;
100.0%; Pred. No. 0.00035;
tive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 207; 100.0%; Pred. No. 0.00044; ive 0; Mismatches 0; Indels
 ; OTHER INFORMATION: mutant/variant of SEQ ID NO:5 US-08-700-651-13
 TYPE: PRT ORGANISM: Cryptosporidium parvum
 323 TTTTTTTTTT 335
 TTTTTTTTTT 335
 TTTTTTTTTT 88
 Best Local Similarity 100.
Matches 13; Conservative
 Conservative
 Best Local Similarity
Matches 13; Conserva
 RESULT 51
US-08-700-651-13
 SEQ ID NO 13
LENGTH: 162
 323
 Query Match
 Query Match
 FEATURE:
 RESULT 53
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US-09-248-796A-25055

US-09-248-796A-25055

Sequence 25055, Application US/09248796A

Sequence 25055, Application US/09248796A

Sequence 25055, Application US/09248796A

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

TITLE OF INVENTION: NUMBER: US/09/248,796A

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 22055

LENGTH: 292
 . LOCATION: (287), (288), (289)
, OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-25055
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 Gaps
 Gaps
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 Length 292;
 Indels
 Indels
Pred. No. 0.0006;
 3.1%; Score 13; DB 4; Le 00.08; Pred. No. 0.00081;
 3.1%; Score 13; DB 4; Lo
100.0%; Pred. No. 0.00061;
tive 0; Mismatches 0;
 Baum, Peter
TION: Molecules Designated B7L1
 TITE OF INVENTION: Molecules Designated B71
FILE OF INVENTION: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
PRIOR APPLICATION NUMBER: PCT/US99/17906
PRIOR APPLICATION NUMBER: 09/095,663
PRIOR PILING DATE: 1999-08-05
PRIOR PILING DATE: 1998-08-05
PRIOR FILING DATE: 1998-08-07
SOFTWARE: PALENTIN VOICE: 1998-08-07
SOFTWARE: PALENTIN VOICE: 20
 Query Match
Best Local Similarity 100.0%; Pred. No. ...
Marches 13; Conservative 0; Mismatches
 Best Local Similarity 100.0%; Pred. No. 0.(
Matches 13; Conservative 0; Mismatches
 Sequence 4, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
 323 TTTTTTTTTT 335
 401 DADTAIINAEGGQ 413
 375 papraiinaegeg 387
 323 TITITITITI 335
 TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
 Query Match
Best Local Similarity 100.
Matches 13; Conservative
 ORGANISM: Mus musculus
US-09-778-510-4
 NAME/KEY: UNSURE
 US-09-778-510-4
 TYPE: PRT
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 US-09-216-393B-344

Sequence 344, Application US/09216393B

Sequence 34694

Sequence 346694

GENERAL INFORMATION:

APPLICANT: Milhausen, Michael James

TITUE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER

TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER

TITLE NEFRENCE: TX-1-C2

CURRENT APPLICATION NUMBER: US/09/216,393B

CURRENT FILING DATE: 1997-12-19

NUMBER OF SEQ ID NOS: 366

SOFTWARE: PARCHIN VERSION 3.1

SEQ ID NO 344

LENGTH: 288
 DEPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THER
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
CURRENT FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: Patentin version 3.1
LENGTH: 288
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 Gaps
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 ;
 Score 13; DB 4; Length 247;
Pred. No. 0.00052;
 DB 4; Length 288;
 Length 288;
 0; Indels
 Score 13; DB 4; 1
Pred. No. 0.0006;
 3.1%; Scor.
100.0%; Pred. No. v...
0; Mismatches
 ; FILE REFERENCE: 107196.132; CURRENT APPLICATION NUMBER: US/09/248,796A; CURRENT FILING DATE: 1999-02-12; PRIOR APPLICATION NUMBER: US 60/074,725; PRIOR PILING DATE: 1998-02-13; PRIOR FILING DATE: 1998-02-13; PRIOR FILING DATE: 1998-08-13; NUMBER FILING DATE: 1998-08-13; SQ ID NO 24111
 Query Match 3.1%; Score 13; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 13; Conservative 0; Mismatches
 3.1%; Score 13;
 US-09-216-393B-341

Sequence 341, Application US/09216393B

; Patent No. 6514694

; GENERAL INFORMATION:
 323 TTTTTTTTTT 335
 164 rrrrrrrrrrrr 176
 TYPE: PRT
ORGANISM: Toxoplasma gondii
 323 TTTTTTTTTT 335
 TYPE: PRT ORGANISM: Toxoplasma gondii
 TYPE: PRT ORGANISM: Candida albicans
 58 Tririririi 70
 Conservative
 Local Similarity
les 13; Conservat
 US-09-248-796A-24111
 US-09-216-393B-341
 US-09-216-393B-344
 Query Match
Best Local S
Matches 13
 Query Match
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3.1%; Score 13; DB 4; Length 398;
100.0%; Pred. No. 0.00081;
tive 0; Mismatches 0; Indels
 PRIOR FILLING DATE: 1299-09-08
PRIOR PELICATION NUMBER: PCT/US99/20594
PRIOR PILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-15
PRIOR FILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-09-15
PRIOR PILING DATE: 1999-09-15
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PRIOR PILING DATE: 1999-13-09
PRIOR PILING DATE: 1999-13-09
PRIOR PILING DATE: 1999-13-09
PRIOR PILING DATE: 1999-13-09
 Goddard, A.
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Sequence 84, Application US/09905125A
Patent No. 6664376
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
 Ferrara, Napoleone
Filvaroff, Ellen
 Paoni, Nicholas F.
 FILING DATE: 1999-07-28
 Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
 Kljavin, Ivar J.
Mather, Jennie P.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Query Match 3.19
Best Local Similarity 100.
Matches 13, Conservative
 Desnoyers, Luc
Eaton, Dan L.
 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-905-125A-84
 US-09-907-794A-84
 APPLICANT:
APPLICANT:
APPLICANT:
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 IIILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IIILE OF INVENTION: Acids Encoding the Same
 Length 398;
 Indels
 TITLE OF INVENTION:
FILLE REFERENCE:
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07
FRIOR PILING DATE: 1999-08-05
PRIOR PILING DATE: 1998-08-07
PRIOR FILING DATE: 06/095,663
PRIOR FILING DATE: 1998-08-07
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SEQ TWARE: Patentin Ver. 2.0
SEQ TWARE: Patentin Ver. 2.0
 3.1%; Score 13; DB 4; Le
100.0%; Pred. No. 0.00081;
tive 0; Mismatches 0;
 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/907,794A
CURRENT FILING BATE: 2001-07-17
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
 ; Sequence 84, Application US/09907794A ; Patent No. 6635468
 Godowski, Paul J.
Grimaldi, Christopher J.
 Sequence 6, Application US/09778510; Patent No. 6512095; GENERAL INFORMATION: APPLICANT: Baum, Peter
 Stewart, Timothy A. Tumas, Daniel Williams, P. Mickey Wood, William, I.
 Gurney, Austin L.
Hillan, Kenneth, J.
Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 Ferrara, Napoleone
Filvaroff, Ellen
 Paoni, Nicholas F.
Roy, Margaret Ann
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGO 387
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Bustein, David
APPLICANT: Beton, Luc
APPLICANT: Baton, Dan L.
 Conservative
 Sherman
 Goddard, A.
 Query Match
Best Local Similarity
 TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-6
 Fong,
 13;
RESULT 60
US-09-778-510-6
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic ITLLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: 10466-14
 Gaps
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 Length 398;
 Indels
 Score 13; DB 4; L
Pred. No. 0.00081;
0; Mismatches 0;
 FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/902,775A

CURRENT FILING DATE: 2001-07-10

PRIOR APPLICATION NUMBER: US (0/143,048)

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-26

PRIOR FILING DATE: 1999-07-28

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-08

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-18

PRIOR FILING DATE: 1999-09-15

PRIOR FILING DATE: 1999-09-15

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PRIOR FILING DATE: 1999-11-30

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PRIOR FILING DATE: 1999-11-30

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PRIOR PRIOR PRIOR DATE: 1999-12-02

PRIOR PRIOR PRIOR DATE: 1999-12-02

PRIOR PRIOR PRIOR DATE: 1999-12-02

PRIOR PRIOR PRIOR DATE: 1999-12-02
 Godowski, Paul J.
Grimaldi, Christopher J.
 ; Sequence 84, Application US/09906700; Patent No. 6723535; GENERAL INFORMATION:
 100.08;
 Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 aoni, Nicholas F
 oy, Margaret Ann
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
 401 DADTAIINAEGGO 413
 375 DADTAIINAEGGO 387
 Query Match 3.1
Best Local Similarity 100.
Matches 13; Conservative
 TYPE: PRT
ORGANISM: Homo sapiens
 JS-09-902-775A-84
 US-09-906-700-84
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APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acid Encoding the Same
FILE REPERBRUE: 10466-14
FILE REPERBRUE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
CURRENT APPLICATION NUMBER: PCT/US00/0411
FRIOR APPLICATION NUMBER: PCT/US00/0411
FRIOR APPLICATION NUMBER: US 60/145,698
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR APPLICATION NUMBER: US 60/146,222
FRIOR PADLICATION NUMBER: US 60/146,222
FRIOR PADLICATION NUMBER: US 60/146,222
FRIOR PADLICATION NUMBER: US 60/146,222
FRIOR PADLICATION NUMBER: PCT/US99/2094
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
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FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-09-15
FRIOR PADLICATION NUMBER: PCT/US99/2809
FRIOR FILING DATE: 1999-09-15
FRIOR FILING DATE: 1999-01-20
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 3.1%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00081; ive 0; Mismatches 0; Indels
 Sequence 84, Application US/09902775A Patent No. 6686451 GENERAL INFORMATION:
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 401 DADTAIINAEGGQ 413
 Query Match
Best Local Similarity 100.0
 Genentech, Inc.
Ashkenazi, Avi
Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 TYPE: PRT
ORGANISM: Homo sapiens
 RESULT 63
US-09-902-775A-84
 US-09-905-125A-84
 APPLICANT:
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Mismatches

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Matches 13; Conservative
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 PPLICANT: Williams, P. Mickey
PPLICANT: Wood, William, I.
TLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
(TLE OF INVENTION: Acids Encoding the Same
 PRIOR PELICATION NUMBER: US 60/143,048

PRIOR PELICATION NUMBER: US 60/145,698

PRIOR PELING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-07-28

PRIOR PELING DATE: 1999-09-09

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR PELING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-09-15

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-10-05

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-29

PRIOR PELING DATE: 1999-11-29

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PRIOR PELING DATE: 1999-12-02

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PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02

PRIOR PELING DATE: 1999-12-02
 FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,700
CURRENT FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: PCT/USO0/04414
PRIOR FILING DATE: 2000-02-22
 Godowski, Paul J.
Grimaldi, Christopher J.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Gurney, Austin L.
Hillan, Kenneth, J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerber, Hanspeter
Gerritsen, Mary E
 Ashkenazi, Avi
Botstein, David
Desnoyers, Luc
Eaton, Dan L
 Wei-Qiang
 Sherman
 NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 TYPE: PRT
ORGANISM: Homo sapiens
US-09-906-700-84
 Goddard, A.
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Query Match 3.1%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00081;

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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, Williams, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: GNB.1618P2C12
CURRENT APPLICATION NUMBER: US/09/903,603A
CURRENT FILING DATE: 2001-07-11
 PRIOR FILING DATE: 2000-02-22
PRIOR FILING DATE: 1999-07-07
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR PILING DATE: 1999-07-26
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR PILING DATE: 1999-09-08
PRIOR PRIOR TILING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-08
PRIOR PELING DATE: 1999-09-13
PRIOR PILING DATE: 1999-09-13
PRIOR PELING DATE: 1999-09-13
PRIOR FILING DATE: 1999-09-13
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/21547
FILING DATE: 1999-09-15
 RIOR APPLICATION NUMBER: PCT/US99/23089
RIOR FILING DATE: 1999-10-05
RIOR APPLICATION NUMBER: PCT/US99/28214
 PRIOR APPLICATION NUMBER: PCT/US99/30095
 FILING DATE: 1999-12-16
APPLICATION NUMBER: PCT/US99/30911
 PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
 APPLICATION NUMBER: PCT/US99/30999
 PRIOR APPLICATION NUMBER: PCT/US00/04414
 PRIOR APPLICATION NUMBER: PCT/US99/28564
 US-09-903-603A-84; Sequence 84, Application US/09903603A; Patent No. 6767995
 Godowski, Paul J.
Grimaldi, Christopher J.
 Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
Roy, Margaret Ann
 Kenneth, J
 Perrara, Napoleone
 Gerritsen, Mary E.
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gurney, Austin L.
Hillan, Kenneth,
 FILING DATE: 1999-11-29
401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGO 387
 Kljavin, Ivar J
 Goddard, A.
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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 Query Match 3.1%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00081; Matches 13; Conservative 0; Mismatches 0; Indels
 FRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-11-30
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR PILING DATE: 1999-12-02
PRIOR PELING DATE: 1999-12-16
PRIOR PELING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 1999-12-20
PRIOR PILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
TYPE: PRT
 CURRENT APPLICATION NUMBER: US/09/909,064
CURRENT FILING DATE: 2001-07-18
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
 LICATION NUMBER: PCT/US99/28313
 FILING DATE: 1999-07-26
APPLICATION NUMBER: US 60/146,222
 Grimaldi, Christopher J. Gurney, Austin L.
 US-09-909-064-84
; Sequence 84, Application US/09909064
; Patent No. 6818449
 Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Kenneth, J
 Ferrara, Napoleone
Filvaroff, Ellen
 Gerritsen, Mary E.
Goddard, A.
 1999-07-26
 Gerber, Hanspeter
 Godowski, Paul J.
 Kljavin, Ivar J.
Mather, Jennie P.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 Desnoyers, Luc
Eaton, Dan L.
 Fong, Sherman
Gao, Wei-Qiang
 FILE REFERENCE: 10466-14
 ; ORGANISM: Homo sapiens
US-09-904-920A-84
 Pan, James
 Hillan,
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 APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
 Gaps
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 3.1%; Score 13; DB 4; Length 398; 100.0%; Pred. No. 0.00081; tive 0; Mismatches 0; Indels
 TILLE DEFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/904,920A

CURRENT FILING DATE: 2001-07-13

PRIOR PELING DATE: 2000-02-27

PRIOR PELING DATE: 2000-02-27

PRIOR PELING DATE: 1999-07-07

PRIOR PELING DATE: 1999-07-07

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-26

PRIOR PLING DATE: 1999-07-28

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PRIOR PLING DATE: 1999-07-8

PRIOR PLING DATE: 1999-09-08

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PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-13

PRIOR PLING DATE: 1999-09-15

PRIOR PRING DATE: 1999-09-15

PRIOR PRING DATE: 1999-09-15
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
 FILING DATE: 1999-09-15
APPLICATION NUMBER: PCT/US99/23089
FILING DATE: 1999-10-05
 APPLICATION NUMBER: PCT/US99/28214
 Sequence 84, Application US/09904920A Patent No. 6806352
 Godowski, Paul J.
Grimaldi, Christopher J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 Gurney, Austin L.
Hillan, Kenneth, J.
 Ferrara, Napoleone
Filvaroff, Ellen
 Nicholas F.
 Gao, Wei-Qiang
Gerber, Hanspeter
 Gerritsen, Mary E
 Kljavin, Ivar J.
Mather, Jennie P.
 401 DADTAIINAEGGO 413
 Query Match
Best Local Similarity 100.0
Matches 13, Conservative
 Pong, Sherman
 Eaton, Dan L.
 TYPE: PRT
CORGANISM: Homo sapiens
US-09-903-603A-84
 Goddard, A.
 Pan, James
Paoni, Nich
 Desnoyers,
 US-09-904-920A-84
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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
 Gaps
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 3.1%; Score 13; DB 4; Length 398; 00.00%; Pred. No. 0.00081; ve 0; Mismatches 0; Indels
 THILE DEFENDENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT APPLICATION NUMBER: US/09/905,381A

CURRENT FILING DATE: 2001-07-13

PRIOR PILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/145,048

PRIOR FILING DATE: 1999-07-07

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PRIOR PILING DATE: 1999-12-03

PRIOR PILING DATE: 1999-12-
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; Parent No. 6828146
 Query Match
3.1%; Sc
Best Local Similarity 100.0%; P:
Matches 13; Conservative 0;
 Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
 Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, A.
 Godowski, Paul J.
 401 DADTAIINAEGGQ 413
 375 DADTAIINAEGGQ 387
 GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 Desnoyers, Luc
Eaton, Dan L.
 TYPE: PRT
ORGANISM: Homo sapiens
 US-09-905-381A-84
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT
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 Gaps
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 Query Match 3.1%; Score 13; DB 4; Length 398; Best Local Similarity 100.0%; Pred. No. 0.00081; Matches 13; Conservative 0; Mismatches 0; Indels
PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1998-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR PLING DATE: 1999-09-15

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PRIOR PLING DATE: 1999-10-05

PRIOR PLING DATE: 1999-11-29

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-11-30

PRIOR PLING DATE: 1999-12-02

PRIOR PLING DATE: 1999-12-02

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PRIOR PLING DATE: 1999-12-06

PRIOR PRIOR PLING DATE: 1999-12-06

PRIOR PRIOR PLIN
 RESULT 68
US-09-905-381A-84
IS-09-905-381A-84
; Sequence 84, Application US/09905381A
; Patent No. 6818746
; GENERAL INFORMATION:
 Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth, J.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William, I.
 Desnoyers, Luc
Eaton, Dan L.
Ferrara, Napoleone
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Gerritsen, Mary E
 375 DADTAIINAEGGQ 387
 401 DADTAIINAEGGQ 413
 APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
 ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-064-84
 Goddard, A.
 APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
APPLICANT:
 APPLICANT
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Length 421;
 for Detecting Beta-Secretase
 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING BATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Ctr., 8th Floor CITY: San Francisco STATE: California
 ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Ctr., 8th Floor TTT: San Francisco STATE: California
 3.1%; Score 13; DB 2; L
100.0%; Pred. No. 0.00085;
 100.0%; Pred. ...
 NAME: Heslin, James M. REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
 Kirsten L.
 GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 2.
CORRESPONDENCE ADDRESS:
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirste
TITLE OF INVENTION: Assays for De
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townser
STREET: Two Embarcadero Ctr., 8
 Sequence 1, Application US/08660531
 : 415-326-2400
415-326-2422
 285 LNKTDNGTYRCEA 297
 272 LNKTDNGTYRCEA 284
 13; Conservative
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
) MOLECULE TYPE: protein US-08-659-984A-1
 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
 TYPE: amino acid
STRANDEDNESS: si
 linear
 Query Match
Best Local Similarity
Matches 13; Conserv
 USA
 Patent No. 6221645
 TELEPHONE:
 COUNTRY:
 US-08-660-531-1
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 APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/906,618
CURRENT FILING DATE: 2001-07-16
PRIOR PELLOR TOWNBER: PCT/USO0/04414
PRIOR PELLOR DATE: 1999-07-07
PRIOR PELLOR DATE: 1999-07-07
PRIOR PELLOR DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20944
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 Length 398;
 0; Indels
 Score 13; DB 4; L. Pred. No. 0.00081;
 PRIOR PILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR PILING DATE: 1999-07-28
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-09-08
PRIOR FILING DATE: 1999-09-08
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PRIOR PILING DATE: 1990-12-03
PRIOR PILING DATE: 1990-12-03
 Mismatches
 US-08-659-984A-1; Sequence 1, Application US/08659984A; Patent No. 5942400; GENERAL INFORMATION: APPLICANT: Anderson, John P.
 3.1%; Soc
Best Local Similarity 100.0%; P:
Matches 13; Conservative 0;
 Surney, Austin L.
Hillan, Kenneth, J.
 Kljavin, Ivar J.
Mather, Jennie P.
Pan, James
Paoni, Nicholas F.
 Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
 375 DADTAIINAEGGO 387
 401 DADTAIINAEGGQ 413
 ORGANISM: Homo sapiens
US-09-906-618-84
 RESULT 70
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Gaps

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SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:

```
Length 444;
 0; Indels
 GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Reim, Pamela S.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LIP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
 SOFTWARE: PATENTIN FEDERAGE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
CLASSIFICATION: 436
FILING DATE: US/08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
 E: Townsend and Townsend and Crew LLP Two Embarcadero Ctr., 8th Floor
 Score 13; DB 2; L
Pred. No. 0.00089;
 3.1%; Scot.
100.0%; Pred. No. co.
0; Mismatches
 REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAK: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
 ZIP: 9411-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 Sequence 5, Application US/08660531
Patent No. 6221645
 29,541
 444 amino acids
 285 LNKTDNGTYRCEA 297
 Query Match
Best Local Similarity 100.0
Matches 13, Conservative
 NAME: Heslin, James M. REGISTRATION NUMBER: 3
 TYPE: amino acid
STRANDEDNESS: single
 TOPOLOGY: linear MOLECULE TYPE: protein
 STREET: Two Embarcad
CITY: San Francisco
STATE: California
 CORRESPONDENCE ADDRESS
 COUNTRY:
 US-08-660-531-5
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 Gaps
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 3.1%; Score 13; DB 3; Length 421; 100.0%; Pred. No. 0.00085; tive 0; Mismatches 0; Indels
 3.1%; Score 13; DB 4; Length 432;
100.0%; Pred. No. 0.00087;
 RESULT 73

US-08-659-984A-5

US-08-659-984A-5

Sequence 5, Application US/08659984A

Patent No. 5942400

GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
 0; Indels
 US-09-778-510-2

Sequence 2, Application US/09778510

Sequence 2, Application US/09778510

Sequence 2, Application US/09778510

Sequence 2, Application US/09778510

GENERAL INFORMATION:

TITLE OF INVERMION:

FILE REPERENCE:

CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE:

PRIOR FILING DATE:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS:

SOFTWARE:

SEQ TRANCE:

BENGTHARE:

BENGTHARE:

SEQ ID NO:

LENGTH: 432
 Query Match 3.1%, No. 0.0 Best Local Similarity 100.0%; Pred. No. 0.0
 15270-002210US
 FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-UN-1995
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/660,531
 NAME: Healin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
 TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
 LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
 285 LNKTDNGTYRCEA 297
 272 LNKTDNGTYRCEA 284
 401 DADTAIINAEGGQ 413
 409 DADTAIINAEGGQ 421
 Best Local Similarity 100.
Matches 13, Conservative
 TOPOLOGY: linear MOLECULE TYPE: protein
 TYPE: PRT
ORGANISM: Homo sapien
 US-09-778-510-2
 US-08-660-531-1
 Query Match
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0; Gaps

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RESULT 75

US-09-248-796A-22504

JECTOR APPLICATION US/09248796A

Sequence 22504, Application US/09248796A

Sequence 22504, Application US/09248796A

Setent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1999-02-13

PRIOR FILING DATE: 1999-02-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 22504
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 0; Gaps
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 3.1%; Score 13; DB 3; Length 444; 100.0%; Pred. No. 0.00089; tive 0; Mismatches 0; Indels
 Query Match 3.1%; Score 13; DB 4; Length 543; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 13; Conservative 0; Mismatches 0; Indels
 15270-002210US
 Search completed: June 28, 2005, 10:22:32 Job time : 31.341 secs
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Healin, James N.

REGISTRATION NUMBER: 29,541

REFERENCE/DOCKET NUMBER: 15270

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2422

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 444 amino acids

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-660-531-5
 295 LNKTDNGTYRCEA 307
 323 TTTTTTTTT 335
 285 LNKTDNGTYRCEA 297
 372 rriririririri 384
 ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-22504
 Query Match
Best Local Similarity 100.
Matches 13; Conservative
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